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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypep-
tides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

DESCRIPTION
PROTEIN KINASES

FIELD OF THE INVENTION

5 The present invention relates to novel kinase polypeptides, nucleotide sequences encoding the novel kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

BACKGROUND OF THE INVENTION

10 The following description of the background of the invention is provided to aid in understanding the invention, but is not admitted to be or to describe prior art to the invention.

 Cellular signal transduction is a fundamental mechanism whereby external stimuli that regulate diverse cellular processes are relayed to the interior of cells. One of the key
15 biochemical mechanisms of signal transduction involves the reversible phosphorylation of proteins, which enables regulation of the activity of mature proteins by altering their structure and function.

 Protein phosphorylation plays a pivotal role in biological signal transduction. Among the biological functions controlled by protein phosphorylation are the following:
20 cell division; differentiation and death (apoptosis); cell motility and cytoskeletal structure; control of DNA replication, transcription, splicing and translation; protein translocation events from the endoplasmic reticulum and Golgi apparatus to the membrane and extracellular space; protein nuclear import and export; regulation of metabolic reactions, etc. Abnormal protein phosphorylation is widely recognized to be causally linked to the
25 etiology of many diseases including cancer as well as immunologic, neuronal and metabolic disorders.

 The most common phospho-acceptor amino acid residues are serine, threonine and tyrosine. Phosphorylation in histidine has also been observed in bacteria. The presence of a phosphate moiety modulates protein function in multiple ways. A common mechanism
30 includes changes in the catalytic properties (V_{\max} and K_m) of an enzyme leading to its activation or inactivation. A second widely recognized mechanism involves promoting protein-protein interactions. An example of this is the tyrosine autophosphorylation of the

ligand-activated EGF receptor tyrosine kinase. This event triggers the high-affinity binding to the phosphotyrosine residue on the receptor's C-terminal intracellular domain to the SH2 motif of the adaptor molecule Grb2. Grb2 in turn binds through its SH3 motif to a second adaptor molecule, such as SHC. The formation of this ternary complex
5 activates the signaling events that are responsible for the biological effects of EGF. Serine and threonine phosphorylation events have also been recently recognized to exert their biological function through protein-protein interaction events mediated by the high-affinity binding of phosphoserine and phosphothreonine to WW motifs present in a large variety of proteins (Lu, P.J. *et al.* (1999) *Science* 283:1325-1328). A third important
10 outcome of protein phosphorylation is changes in the subcellular localization of the substrate. As an example, nuclear import and export events in a large diversity of proteins are regulated by protein phosphorylation (Drier E.A. *et al.* (1999) *Genes Dev* 13: 556-568).

Protein kinases are one of the largest families of eukaryotic proteins with several
15 hundred known members. These proteins share a 250-300 amino acid domain that can be subdivided into 12 distinct subdomains that comprise the common catalytic core structure. These conserved protein motifs have recently been exploited using PCR-based and bioinformatic strategies leading to a significant expansion of the known kinases. Multiple
20 alignment of the sequences in the catalytic domain of protein kinases and subsequent parsimony analysis permits their segregation into a dendrogram reflecting the relatedness of their catalytic domains (Fig. 1). In this manner, related kinases are clustered into distinct branches or subfamilies including: tyrosine kinases, cyclic-nucleotide-dependent kinases, calcium/calmodulin kinases, cyclin-dependent kinases and MAP-kinases, serine-threonine kinase receptors, and several other less defined subfamilies.

25 We have recently completed a systematic analysis of the protein kinases present in *C. elegans*, the multicellular organism whose entire DNA sequence has been determined. We identified 473 unique kinase profiles including 398 full-length conventional kinases, and 20 additional proteins that may function as atypical protein kinases. (Plowman G.D. *et al.* (1999), *Proc. Natl. Acad. Sci.* 96:13603-13610).

30 Using parsimony analysis, the protein kinases may be divided into 4 major groups: AGC, CAMK, CMGC and tyrosine kinases. In addition, there are a number of minor yet distinct families, including the STE and casein kinase 1, families related to worm- or

fungus-specific kinases, and a family designated "other" to represent several smaller families. In addition, we designate an "atypical" family to represent protein kinases whose catalytic domain has little or no primary sequence homology to conventional kinases, including the A6 kinases and PI3 kinases.

5 The AGC kinases are basic amino acid-directed enzymes that phosphorylate residues found proximal to Arg and Lys. Examples of this group are the cyclic nucleotide-dependent kinases, G protein kinases, NDR or DBF2 and the ribosomal S6 kinases.

10 The CAMK group kinases are also basic amino acid-directed kinases. They include the Ca²⁺/calmodulin-regulated and AMP-dependent protein kinases, myosin light chain kinases, checkpoint 2 kinases (CHK2) and EMK-related protein kinases. The EMK family of STK are involved in the control of cell polarity, microtubule stability and cancer. One member of the EMK family, C-TAK1 has been reported to control entry into mitosis by activating Cdc25C which in turn dephosphorylates Cdc2.

15 CMGC group kinases are "proline-directed" enzymes phosphorylating residues that exist in a proline-rich context. They include the cyclin-dependent kinases (CDKs), mitogen-activated kinases (MAPKs), GSK3s and CLKs. Most CMGC kinases have larger-than-average kinase domains owing to the presence of insertions within subdomains X and XI.

20 The tyrosine kinase group encompass both cytoplasmic (i.e. src) as well as transmembrane receptor tyrosine kinases (i.e. EGF receptor). These kinases play a pivotal role in the signal transduction processes that mediate cell proliferation, differentiation and apoptosis.

25 Group members that define smaller, yet distinct phylogenetic branches of conventional kinases include the elongation factor 2 kinases (EIFKs); homologues of the yeast sterile family kinases (STE) which refers to 3 classes of kinases which lie sequentially upstream of the MAPKs; mixed lineage kinases (MLKs); Lim-domain containing kinases (LIMKs); Calcium-calmodulin kinase kinases (CAMKK), dual-specific tyrosine kinases (DYRK), integrin receptor associated kinase (IRAK); testis-specific kinases (TSK); UNC-51 related kinases (UNC); several families that are close
30 homologues to worm (C26C2.1, YQ09, ZC581.9, YFL033c, C24A1.3), Drosophila (SLOB), or yeast (YDOD_sp, YGR262_sc) kinases, and others that are "unique" and don't cluster into any obvious family.

SUMMARY OF THE INVENTION

Through a search of the EST database for homologies to the conserved catalytic kinase domain of protein kinases, hundreds of mammalian members of known and previously unidentified protein kinase families and groups have been identified as part of the present invention. Multiple alignment and parsimony analysis of the catalytic domain reveals that approximately half of these protein kinases cluster into 10 known groups, with the other half perhaps defining novel groups. Classification in this manner has proven highly accurate not only in predicting motifs present in the remaining non-catalytic portion of each protein, but also in their regulation, substrates, and signaling pathways. The present invention includes the partial or complete sequence of new protein kinases, their classification, predicted or deduced protein structure, and a strategy for elucidating their biologic and therapeutic relevance.

Thus, a first aspect of the invention features an isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,

SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to nucleic acid is meant a polymer of nucleotides conjugated to each other, including DNA and RNA, that is isolated from a natural source or that is synthesized. The isolated nucleic acid of the present invention is unique in the sense that it is not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular (*i.e.*, chromosomal) environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only nucleotide chain present, but that it is essentially free (about 90 - 95% pure at least) of non-nucleotide material naturally associated with it, and thus is distinguished from isolated chromosomes.

By the use of the term "enriched" in reference to nucleic acid is meant that the specific DNA or RNA sequence constitutes a significantly higher fraction (2 - 5 fold) of the total DNA or RNA present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other DNA or RNA present, or by a preferential increase in the amount of the specific DNA or RNA sequence, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other DNA or RNA sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term "significant" is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other nucleic acids of about at least 2 fold, more preferably at least 5 to 10 fold or even more. The term also does not imply that there is no DNA or RNA from other sources. The other source DNA may, for example, comprise DNA from a yeast or bacterial genome, or a cloning vector such as pUC19. This term distinguishes from naturally occurring events, such as viral infection, or tumor type

growths, in which the level of one mRNA may be naturally increased relative to other species of mRNA. That is, the term is meant to cover only those situations in which a person has intervened to elevate the proportion of the desired nucleic acid.

It is also advantageous for some purposes that a nucleotide sequence be in purified form. The term "purified" in reference to nucleic acid does not require absolute purity (such as a homogeneous preparation). Instead, it represents an indication that the sequence is relatively more pure than in the natural environment (compared to the natural level this level should be at least 2-5 fold greater, *e.g.*, in terms of mg/mL). Individual clones isolated from a cDNA library may be purified to electrophoretic homogeneity. The claimed DNA molecules obtained from these clones could be obtained directly from total DNA or from total RNA. The cDNA clones are not naturally occurring, but rather are preferably obtained via manipulation of a partially purified naturally occurring substance (messenger RNA). The construction of a cDNA library from mRNA involves the creation of a synthetic substance (cDNA) and pure individual cDNA clones can be isolated from the synthetic library by clonal selection of the cells carrying the cDNA library. Thus, the process which includes the construction of a cDNA library from mRNA and isolation of distinct cDNA clones yields an approximately 10^6 -fold purification of the native message. Thus, purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated.

By a "kinase polypeptide" is meant 10 (preferably 20, more preferably 40, most preferably 75) or more contiguous amino acids set forth in an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,

SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
5 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
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SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
10 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional
15 derivatives thereof as described herein. For sequences for which the full-length sequence
is not given, the remaining sequences can be determined using methods well-known to
those in the art and are intended to be included in the invention. In certain aspects,
polypeptides of 100, 200, 300 or more amino acids are preferred. The kinase polypeptide
can be encoded by a full-length nucleic acid sequence or any portion of the full-length
20 nucleic acid sequence, so long as a functional activity of the polypeptide is retained. By
“functional” domain is meant any region of the polypeptide that may play a regulatory or
catalytic role as predicted from amino acid sequence homology to other proteins or by the
presence of amino acid sequences that may give rise to specific structural conformations
(*i.e.*, coiled-coils). For some purposes, polypeptide domains are preferred, including, but
25 not limited to, N-terminal, catalytic/kinase and C-terminal.

The amino acid sequence will be substantially similar to a sequence selected from
the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID
NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
30 NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID
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NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID
NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID
NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding
20 full-length amino acid sequence, or fragments thereof. A sequence that is substantially
similar to a sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
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By "identity" is meant a property of sequences that measures their similarity or relationship. Identity is measured by dividing the number of identical residues between two sequences (either full-length or a defined domain) by the total number of residues in the known sequence, or the domain of the known sequence, and multiplying the product by 100. Thus, two copies of exactly the same sequence have 100% identity, but sequences that are less highly conserved, and have replacements and substitutions, have a lower degree of identity. "Gaps" are spaces in an alignment that can result from aligning a novel sequence with a known sequence when the novel sequence has additions or deletions of amino acids in comparison with the known sequence. These gaps do not factor into the assessment of % identity using the above calculation.

Those skilled in the art will recognize that several computer programs are also available for determining sequence identity using standard parameters, for example, Blast (Altschul, *et al.* (1997) *Nucleic Acids Res.* 25:3389-3402), Blast2 (Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-410), and Smith-Waterman (Smith, *et al.* (1981) *J. Mol. Biol.* 147:195-197).

In preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding a kinase polypeptide comprising a nucleotide sequence that: (a) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID

NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
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10 NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID
NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID
NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID
NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID
NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will
15 have at least 75% identity (preferably 90%, more preferably at least 95% and most
preferably 99-100%) to the sequence selected from the group consisting of those set forth
in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
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NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
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NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
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5 NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c)
10 hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes
a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an
amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
15 NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
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NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
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25 NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
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NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
30 NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID

NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID

NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (e) is the complement of the nucleotide sequence of (d); (f) encodes a polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID

NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.) A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID

NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ

ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID

NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof.

A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235,

SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, where the domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (g) is the complement of the nucleotide sequence of (f); (h) encodes a polypeptide having an amino acid sequence selected from the group consisting

of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,

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15 SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
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SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at
20 least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-
100%) to the sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
25 NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
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NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
5 NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
10 NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242; (b) is the complement of the nucleotide sequence of (a); (c) hybridizes under
15 highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally
occurring kinase polypeptide; (d) encodes a kinase polypeptide having an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
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20 NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
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30 NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
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NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or fragments thereof. A sequence that is substantially similar to a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,

SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 will have at least 75% identity (preferably 90%, more preferably at least 95% and most preferably 99-100%) to the sequence of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more of the domains selected from the group consisting of a N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; or (i) is the

complement of the nucleotide sequence of (h). The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.

The term "complement" refers to two nucleotides that can form multiple favorable interactions with one another. For example, adenine is complementary to thymine as they can form two hydrogen bonds. Similarly, guanine and cytosine are complementary since they can form three hydrogen bonds. A nucleotide sequence is the complement of another nucleotide sequence if all of the nucleotides of the first sequence are complementary to all of the nucleotides of the second sequence.

The term "domain" refers to a region of a polypeptide that contains a particular function. For instance, N-terminal or C-terminal domains of signal transduction proteins can serve functions including, but not limited to, binding molecules that localize the signal transduction molecule to different regions of the cell or binding other signaling molecules directly responsible for propagating a particular cellular signal. Some domains can be expressed separately from the rest of the protein and function by themselves, while others must remain part of the intact protein to retain function. The latter are termed functional regions of proteins and also relate to domains.

The term "N-terminal domain" refers to the extracatalytic region located between the initiator methionine and the catalytic domain of the protein kinase. The N-terminal domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the N-terminal boundary of the catalytic domain. Depending on its length, the N-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose N-terminal domain has been shown to play a regulatory role is PAK65, which contains a CRIB motif used for Cdc42 and rac binding (Burbelo, P.D. *et al.* (1995) J. Biol. Chem. 270, 29071-29074). The N-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the amino-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. Further, in some cases, portions of the N-terminal domains of the protein kinases of the invention have not been identified since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined and using the approaches described herein the N-terminal domain can be identified.

The term "catalytic domain" or "kinase domain" refers to a region of the protein kinase that is typically 25-300 amino acids long and is responsible for carrying out the phosphate transfer reaction from a high-energy phosphate donor molecule such as ATP or GTP to itself (autophosphorylation) or to other proteins (exogenous phosphorylation).

5 The catalytic domain of protein kinases is made up of 12 subdomains that contain highly conserved amino acid residues, and are responsible for proper polypeptide folding and for catalysis. The catalytic domain can be identified following a Smith-Waterman alignment of the protein sequence against the non-redundant protein database. The catalytic/kinase domains of the protein kinases of the invention are identified in Table 2, herein. Further, 10 in some cases, the complete sequence of the catalytic/kinase domains of the protein kinases of the invention may not have been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the catalytic/kinase domain can be identified.

15 The term "catalytic activity", as used herein, defines the rate at which a kinase catalytic domain phosphorylates a substrate. Catalytic activity can be measured, for example, by determining the amount of a substrate converted to a phosphorylated product as a function of time. Catalytic activity can be measured by methods of the invention by holding time constant and determining the concentration of a phosphorylated substrate 20 after a fixed period of time. Phosphorylation of a substrate occurs at the active-site of a protein kinase. The active-site is normally a cavity in which the substrate binds to the protein kinase and is phosphorylated.

The term "substrate" as used herein refers to a molecule phosphorylated by a kinase of the invention. Kinases phosphorylate substrates on serine/threonine or tyrosine 25 amino acids. The molecule may be another protein or a polypeptide.

The term "C-terminal domain" refers to the region located between the catalytic domain and the carboxy-terminal amino acid residue of the protein kinase. The C-terminal domain can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein database to define the C-terminal boundary of 30 the catalytic domain or of any functional C-terminal extracatalytic domain. Depending on its length and amino acid composition, the C-terminal domain may or may not play a regulatory role in kinase function. An example of a protein kinase whose C-terminal

domain may play a regulatory role is PAK3 which contains a heterotrimeric G_i subunit-binding site near its C-terminus (Leeuw, T. *et al.* (1998) *Nature*, 391, 191-195). The C-terminal domain of a protein kinase of the invention is that portion of the protein kinase to the carboxy-terminal side of the kinase domain where the kinase domain is identified in Table 2, herein. In some cases, the C-terminal domains of the protein kinases of the invention have not been provided since the entire sequence is not available. However, with the methods described herein, the full-length sequences of the kinases of the invention can be determined, and using the approaches described herein, the C-terminal domain can be identified.

The term "signal transduction pathway" refers to the molecules that propagate an extracellular signal through the cell membrane to become an intracellular signal. This signal can then stimulate a cellular response. The polypeptide molecules involved in signal transduction processes are typically receptor and non-receptor protein tyrosine kinases, receptor and non-receptor protein phosphatases, SRC homology 2 and 3 domains, phosphotyrosine binding proteins (SRC homology 2 (SH2) and phosphotyrosine binding (PTB and PH) domain containing proteins), proline-rich binding proteins (SH3 domain containing proteins), nucleotide exchange factors, and transcription factors.

The term "coiled-coil structure region" as used herein, refers to a polypeptide sequence that has a high probability of adopting a coiled-coil structure as predicted by computer algorithms such as COILS (Lupas, A. (1996) *Meth. Enzymology* 266:513-525). Coiled-coils are formed by two or three amphipathic α -helices in parallel. Coiled-coils can bind to coiled-coil domains of other polypeptides resulting in homo- or heterodimers (Lupas, A. (1991) *Science* 252:1162-1164). Coiled-coil-dependent oligomerization has been shown to be necessary for protein function including catalytic activity of serine/threonine kinases (Roe, J. *et al.* (1997) *J. Biol. Chem.* 272:5838-5845). Coiled-coil regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "proline-rich region" as used herein, refers to a region of a protein kinase whose proline content over a given amino acid length is higher than the average content of this amino acid found in proteins (*i.e.*, >10%). Proline-rich regions are easily discernable by visual inspection of amino acid sequences and quantitated by standard computer

sequence analysis programs such as the DNASTar program EditSeq. Proline-rich regions have been demonstrated to participate in regulatory protein -protein interactions. Among these interactions, those that are most relevant to this invention involve the "PxxP" proline rich motif found in certain protein kinases (*i.e.*, human PAK1) and the SH3 domain of the adaptor molecule Nck (Galisteo, M.L. *et al.* (1996) J. Biol. Chem. 271:20997-21000).
5 Other regulatory interactions involving "PxxP" proline-rich motifs include the WW domain (Sudol, M. (1996) Prog. Biophys. Mol. Bio. 65:113-132). Proline rich regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of
10 the invention.

The term "spacer region" as used herein, refers to a region of the protein kinase located between predicted functional domains. The spacer region has no detectable homology to any amino acid sequence in the database, and can be identified by using a Smith-Waterman alignment of the protein sequence against the non-redundant protein
15 database to define the C- and N-terminal boundaries of the flanking functional domains. Spacer regions may or may not play a fundamental role in protein kinase function. Precedence for the regulatory role of spacer regions in kinase function is provided by the role of the src kinase spacer in inter-domain interactions (Xu, W. *et al.* (1997) Nature 385:595-602). Spacer regions in the proteins of the invention can be identified using these
20 methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "insert" as used herein refers to a portion of a protein kinase that is absent from a close homolog. Inserts may or may not be the product alternative splicing of exons. Inserts can be identified by using a Smith-Waterman sequence alignment of the
25 protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Inserts may play a functional role by presenting a new interface for protein-protein interactions, or by interfering with such interactions. Insert regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of
30 the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

The term "C-terminal tail" as used herein, refers to a C-terminal domain of a protein kinase, that by homology extends or protrudes past the C-terminal amino acid of its closest homolog. C-terminal tails can be identified by using a Smith-Waterman sequence alignment of the protein sequence against the non-redundant protein database, or by means of a multiple sequence alignment of homologous sequences using the DNASTar program Megalign. Depending on its length, a C-terminal tail may or may not play a regulatory role in kinase function. C-terminal tail regions in the proteins of the invention can be identified using these methods. They may be present as sub-domains of the N-terminal, kinase, or C-terminal domains of the polypeptides of the invention.

Various low or high stringency hybridization conditions may be used depending upon the specificity and selectivity desired. These conditions are well-known to those skilled in the art. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides, more preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 50 contiguous nucleotides, most preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 100 contiguous nucleotides. In some instances, the conditions may prevent hybridization of nucleic acids having more than 5 mismatches in the full-length sequence.

By stringent hybridization assay conditions is meant hybridization assay conditions at least as stringent as the following: hybridization in 50% formamide, 5X SSC, 50 mM NaH_2PO_4 , pH 6.8, 0.5% SDS, 0.1 mg/mL sonicated salmon sperm DNA, and 5X Denhart solution at 42 °C overnight; washing with 2X SSC, 0.1% SDS at 45 °C; and washing with 0.2X SSC, 0.1% SDS at 45 °C. Under some of the most stringent hybridization assay conditions, the second wash can be done with 0.1X SSC at a temperature up to 70 °C (pg. 421, Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein including any figures, tables, or drawings.). However, other applications may require the use of conditions falling between these sets of conditions. Methods of determining the conditions required to achieve desired hybridizations are well-known to those with ordinary skill in the art, and are based on several factors, including but not limited to, the sequences to be hybridized and the samples to be tested.

In other preferred embodiments, the invention features isolated, enriched, or purified nucleic acid molecules encoding kinase polypeptides, further comprising a vector or promoter effective to initiate transcription in a host cell. The invention also features recombinant nucleic acid, preferably in a cell or an organism. The recombinant nucleic acid may contain a sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a functional derivative thereof and a vector or a promoter effective to initiate transcription in a host cell. The recombinant nucleic acid can alternatively contain a transcriptional initiation region functional in a cell, a sequence complementary to an RNA sequence encoding a kinase polypeptide and a transcriptional termination region functional in a cell. Specific

vectors and host cell combinations are discussed herein. The recombinant nucleic acid can also contain the full-length sequence encoding the protein kinase, or a domain, for example.

The term "vector" relates to a single or double-stranded circular nucleic acid molecule that can be transfected into cells and replicated within or independently of a cell genome. A circular double-stranded nucleic acid molecule can be cut and thereby linearized upon treatment with restriction enzymes. An assortment of nucleic acid vectors, restriction enzymes, and the knowledge of the nucleotide sequences cut by restriction enzymes are readily available to those skilled in the art. A nucleic acid molecule encoding a kinase can be inserted into a vector by cutting the vector with restriction enzymes and ligating the two pieces together.

The term "transfecting" defines a number of methods to insert a nucleic acid vector or other nucleic acid molecules into a cellular organism. These methods involve a variety of techniques, such as treating the cells with high concentrations of salt, an electric field, detergent, or DMSO to render the outer membrane or wall of the cells permeable to nucleic acid molecules of interest or use of various viral transduction strategies.

The term "promoter" as used herein, refers to nucleic acid sequence needed for gene sequence expression. Promoter regions vary from organism to organism, but are well known to persons skilled in the art for different organisms. For example, in prokaryotes, the promoter region contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

In preferred embodiments, the isolated nucleic acid comprises, consists essentially of, or consists of a nucleic acid sequence set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35,

SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ
ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID
NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51,
SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ
5 ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID
NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67,
SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ
ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID
NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83,
10 SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ
ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID
NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99,
SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104,
SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109,
15 SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114,
SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119,
SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, encodes
an amino acid sequence selected from the group consisting of those set forth in SEQ ID
NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
20 NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
25 NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID
NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID
NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID
NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID
30 NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID
NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID
NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID

NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID
NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID
NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID
NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID
5 NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID
NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID
NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID
NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID
NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID
10 NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ
ID NO:242, or the corresponding full-length amino acid sequence, a functional derivative
thereof, or at least 10, 20, 40, 50, 75, 100, 200, 300 or 500 contiguous amino acids of a
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
15 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
20 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
25 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID
NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID
NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID
30 NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID
NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID
NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID

NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length sequences or derivatives thereof. The nucleic acid may be isolated from a natural source by cDNA cloning or by subtractive hybridization. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the nucleic acid may be synthesized by the triester method or by using an automated DNA synthesizer.

The term "mammal" refers preferably to such organisms as mice, rats, rabbits, guinea pigs, sheep, and goats, more preferably to cats, dogs, monkeys, and apes, and most preferably to humans.

In yet other preferred embodiments, the nucleic acid is a conserved or unique region, for example those useful for: the design of hybridization probes to facilitate identification and cloning of additional polypeptides, the design of PCR probes to facilitate cloning of additional polypeptides, obtaining antibodies to polypeptide regions, and designing antisense oligonucleotides.

By "conserved nucleic acid regions", are meant regions present on two or more nucleic acids encoding a kinase polypeptide, to which a particular nucleic acid sequence can hybridize under lower stringency conditions. Examples of lower stringency conditions suitable for screening for nucleic acid encoding kinase polypeptides are provided in Berger *et al.* (1987) Guide to Molecular Cloning Techniques, Meth. Enzym. vol. 152, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables. Preferably, conserved regions differ by no more than 5 out of 20 nucleotides, even more preferably 2 out of 20 nucleotides or most preferably 1 out of 20 nucleotides.

By "unique nucleic acid region" is meant a sequence present in a nucleic acid coding for a kinase polypeptide that is not present in a sequence coding for any other naturally occurring polypeptide. Such regions preferably encode 10 (preferably 25, more preferably 50, most preferably 75) or more contiguous amino acids selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,

SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
5 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
10 SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
15 SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
20 SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or functional derivatives thereof.
25 In particular, a unique nucleic acid region is preferably of mammalian origin and
preferably human.

A second aspect of the invention features a nucleic acid probe for the detection of
nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is
selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
30 SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,

SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,
5 SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
10 SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
15 SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
20 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the nucleic acid
probe encodes a kinase polypeptide that is a fragment of the protein encoded by an amino
acid sequence selected from the group consisting of those set forth in SEQ ID NO:122,
SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127,
25 SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132,
SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137,
SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142,
SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147,
SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152,
30 SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157,
SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162,
SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167,

SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172,
SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177,
SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,
SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,
5 SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
10 SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
15 SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242, or the corresponding full-length amino acid sequences. The nucleic acid probe
contains a nucleotide base sequence that will hybridize to a sequence selected from the
group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ
ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9,
20 SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ
ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID
NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25,
SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ
ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID
25 NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41,
SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ
ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID
NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57,
SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ
30 ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID
NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73,
SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ

ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequence, or a functional derivative thereof.

In preferred embodiments, the nucleic acid probe hybridizes to nucleic acid encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID

NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or functional derivatives thereof.

Methods for using the probes include detecting the presence or amount of kinase RNA in a sample by contacting the sample with a nucleic acid probe under conditions such that hybridization occurs and detecting the presence or amount of the probe bound to kinase RNA. The nucleic acid duplex formed between the probe and a nucleic acid sequence coding for a kinase polypeptide may be used in the identification of the sequence of the nucleic acid detected (Nelson *et al.*, in *Nonisotopic DNA Probe Techniques*, Academic Press, San Diego, Kricka, ed., p. 275, 1992, hereby incorporated by reference herein in its entirety, including any drawings, figures, or tables). Kits for performing such methods may be constructed to include a container means having disposed therein a nucleic acid probe.

In a third aspect, the invention describes a recombinant cell or tissue comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,

SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
5 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
10 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242. In such cells, the nucleic acid may be under the control of the
genomic regulatory elements, or may be under the control of exogenous regulatory
elements including an exogenous promoter. By "exogenous" it is meant a promoter that is
15 not normally coupled *in vivo* transcriptionally to the coding sequence for the kinase
polypeptides.

The polypeptide is preferably a fragment of the protein encoded by an amino acid
sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID
NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID
20 NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID
NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID
NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID
NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID
NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID
25 NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID
NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID
NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID
NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID
NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID
30 NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID
NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID
NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID

NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence. By "fragment," is meant an amino acid sequence present in a kinase polypeptide. Preferably, such a sequence comprises at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,

SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
5 SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or of the corresponding full-
length amino acid sequence, or a functional derivative thereof.

In a fourth aspect, the invention features an isolated, enriched, or purified kinase
polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
10 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
15 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
20 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
25 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
30 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ

ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

By "isolated" in reference to a polypeptide is meant a polymer of amino acids (2 or more amino acids) conjugated to each other, including polypeptides that are isolated from a natural source or that are synthesized. The isolated polypeptides of the present invention are unique in the sense that they are not found in a pure or separated state in nature. Use of the term "isolated" indicates that a naturally occurring sequence has been removed from its normal cellular environment. Thus, the sequence may be in a cell-free solution or placed in a different cellular environment. The term does not imply that the sequence is the only amino acid chain present, but that it is essentially free (about 90 - 95% pure at least) of non-amino acid material naturally associated with it.

By the use of the term "enriched" in reference to a polypeptide is meant that the specific amino acid sequence constitutes a significantly higher fraction (2 - 5 fold) of the total amino acid sequences present in the cells or solution of interest than in normal or diseased cells or in the cells from which the sequence was taken. This could be caused by a person by preferential reduction in the amount of other amino acid sequences present, or by a preferential increase in the amount of the specific amino acid sequence of interest, or by a combination of the two. However, it should be noted that enriched does not imply that there are no other amino acid sequences present, just that the relative amount of the sequence of interest has been significantly increased. The term significant here is used to indicate that the level of increase is useful to the person making such an increase, and generally means an increase relative to other amino acid sequences of about at least 2-fold, more preferably at least 5- to 10-fold or even more. The term also does not imply that there is no amino acid sequence from other sources. The other source of amino acid sequences may, for example, comprise amino acid sequence encoded by a yeast or bacterial genome, or a cloning vector such as pUC19. The term is meant to cover only those situations in which man has intervened to increase the proportion of the desired amino acid sequence.

It is also advantageous for some purposes that an amino acid sequence be in purified form. The term "purified" in reference to a polypeptide does not require absolute purity (such as a homogeneous preparation); instead, it represents an indication that the sequence is relatively purer than in the natural environment. Compared to the natural level

this level should be at least 2-5 fold greater (*e.g.*, in terms of mg/mL). Purification of at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. The substance is preferably free of contamination at a functionally significant level, for example 90%, 95%, or 99% pure.

5 In preferred embodiments, the kinase polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,
10 SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
15 SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
20 SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
25 SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
30 SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequences. Preferably, the kinase polypeptide contains at least 10, 20, 40, 50, 75, 100, 200, or 300 contiguous

amino acids a sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof.

In preferred embodiments, the kinase polypeptide comprises an amino acid sequence having (a) an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ

ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ
ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ
ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ
ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ
5 ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ
ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165. SEQ
ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ
ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ
ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ
10 ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ
ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ
ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ
ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ
ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ
15 ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ
ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ
ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ
ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ
ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ
20 ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ
ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ
ID NO:241, and SEQ ID NO:242; (b) an amino acid sequence selected from the group
consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ
ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ
25 ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ
ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ
ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ
ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ
ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ
30 ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ
ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ
ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ

ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail; (c) an amino acid sequence of a domain of a polypeptide selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID
NO:242 where the domain is selected from the group consisting of an N-terminal domain,
a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich
region, a spacer region, an insert, and a C-terminal tail; or (d) an amino acid sequence
15 selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123,
SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
20 SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,
SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
25 SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
30 SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,

SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, an insert, and a C-terminal tail. (The domain demarcations of the polypeptides of the invention are indicated in Table 2 by reference to the kinase domain.)

The polypeptide can be isolated from a natural source by methods well-known in the art. The natural source may be mammalian, preferably human, blood, semen, or tissue, and the polypeptide may be synthesized using an automated polypeptide synthesizer. The isolated, enriched, or purified kinase polypeptide is preferably selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ

ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242A.

In some embodiments the invention includes a recombinant kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,

SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. By "recombinant kinase polypeptide" is meant a polypeptide produced by recombinant DNA techniques such that it is distinct from a naturally occurring polypeptide either in its location (*e.g.*, present in a different cell or tissue than found in nature), purity or structure. Generally, such a recombinant polypeptide will be present in a cell in an amount different from that normally observed in nature.

In a fifth aspect, the invention features an antibody (*e.g.*, a monoclonal or polyclonal antibody) having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain or fragment where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ

ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. In preferred embodiments, the antibody binds specifically to domains of kinase polypeptides, that are defined *supra*.

By “specific binding affinity” is meant that the antibody binds to the target kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions. Antibodies or antibody fragments are polypeptides that contain regions that can bind other polypeptides. The term “specific binding affinity” describes an antibody that binds to a kinase polypeptide with greater affinity than it binds to other polypeptides under specified conditions.

The term “polyclonal” refers to antibodies that are heterogenous populations of antibody molecules derived from the sera of animals immunized with an antigen or an antigenic functional derivative thereof. For the production of polyclonal antibodies, various host animals may be immunized by injection with the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species.

“Monoclonal antibodies” are substantially homogenous populations of antibodies to a particular antigen. They may be obtained by any technique which provides for the production of antibody molecules by continuous cell lines in culture. Monoclonal antibodies may be obtained by methods known to those skilled in the art (Kohler *et al.*, Nature 256:495-497, 1975, and U.S. Patent No. 4,376,110, both of which are hereby incorporated by reference herein in their entirety including any figures, tables, or drawings).

The term “antibody fragment” refers to a portion of an antibody, often the hyper variable region and portions of the surrounding heavy and light chains, that displays specific binding affinity for a particular molecule. A hyper variable region is a portion of an antibody that physically binds to the polypeptide target.

Antibodies or antibody fragments having specific binding affinity to a kinase polypeptide or domains of a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by probing the sample with the antibody under conditions suitable for kinase-antibody immunocomplex formation and detecting the presence and/or amount of the antibody conjugated to the

kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include antibodies or antibody fragments specific for the kinase as well as a conjugate of a binding partner of the antibodies or the antibodies themselves.

An antibody or antibody fragment with specific binding affinity to a kinase polypeptide of the invention can be isolated, enriched, or purified from a prokaryotic or eukaryotic organism. Routine methods known to those skilled in the art enable production of antibodies or antibody fragments, in both prokaryotic and eukaryotic organisms. Purification, enrichment, and isolation of antibodies, which are polypeptide molecules, are described above.

Antibodies having specific binding affinity to a kinase polypeptide of the invention may be used in methods for detecting the presence and/or amount of kinase polypeptide in a sample by contacting the sample with the antibody under conditions such that an immunocomplex forms and detecting the presence and/or amount of the antibody conjugated to the kinase polypeptide. Diagnostic kits for performing such methods may be constructed to include a first container containing the antibody and a second container having a conjugate of a binding partner of the antibody and a label, such as, for example, a radioisotope. The diagnostic kit may also include notification of an FDA approved use and instructions therefor.

In a sixth aspect, the invention features a hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide or a kinase polypeptide domain, where the polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID

NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242; and where the domains are defined as above. By "hybridoma" is meant an immortalized cell line that is capable of secreting an antibody, for example an antibody to a kinase of the invention. In preferred embodiments, the antibody to the kinase comprises a sequence of amino acids that is able to specifically bind a kinase polypeptide of the invention.

In a seventh aspect, the invention features a kinase polypeptide binding agent able to bind to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187,

SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199,
SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197,
SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202,
SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207,
5 SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212,
SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217,
SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222,
SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227,
SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232,
10 SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237,
SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID

NO:242. The binding agent is preferably a purified antibody that recognizes an epitope
present on a kinase polypeptide of the invention. Other binding agents include molecules
that bind to kinase polypeptides and analogous molecules that bind to a kinase
15 polypeptide. Such binding agents may be identified by using assays that measure kinase
binding partner activity, such as those that measure PDGFR activity.

The invention also features a method for screening for human cells containing a
kinase polypeptide of the invention or an equivalent sequence. The method involves
identifying the novel polypeptide in human cells using techniques that are routine and
20 standard in the art, such as those described herein for identifying the kinases of the
invention (*e.g.*, cloning, Southern or Northern blot analysis, in situ hybridization, PCR
amplification, etc.).

In an eighth aspect, the invention features methods for identifying a substance that
modulates kinase activity comprising the steps of: (a) contacting a kinase polypeptide
25 selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124,
SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129,
SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134,
SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139,
SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144,
30 SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149,
SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154,
SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159,

SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164,
SEQ ID NO:165. SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169,
SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174,
SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179,
5 SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184,
SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189,
SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194,
SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199,
SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204,
10 SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209,
SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214,
SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219,
SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224,
SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229,
15 SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234,
SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239,
SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 with a test substance; (b)
measuring the activity of said polypeptide; and (c) determining whether said substance
modulates the activity of said polypeptide.

20 The term “modulates” refers to the ability of a compound to alter the function of a
kinase of the invention. A modulator preferably activates or inhibits the activity of a
kinase of the invention.

The term “activates” refers to increasing the cellular activity of the kinase. The
term inhibit refers to decreasing the cellular activity of the kinase. Kinase activity is
25 preferably the interaction with a natural binding partner.

The term “modulates” also refers to altering the function of kinases of the
invention by increasing or decreasing the probability that a complex forms between the
kinase and a natural binding partner. A modulator preferably increases the probability that
such a complex forms between the kinase and the natural binding partner, more preferably
30 increases or decreases the probability that a complex forms between the kinase and the
natural binding partner depending on the concentration of the compound exposed to the

kinase, and most preferably decreases the probability that a complex forms between the kinase and the natural binding partner.

The term "complex" refers to an assembly of at least two molecules bound to one another. Signal transduction complexes often contain at least two protein molecules bound to one another. For instance, a protein tyrosine receptor protein kinase, GRB2, SOS, RAF, and RAS assemble to form a signal transduction complex in response to a mitogenic ligand.

The term "natural binding partner" refers to polypeptides, lipids, small molecules, or nucleic acids that bind to kinases in cells. A change in the interaction between a kinase and a natural binding partner can manifest itself as an increased or decreased probability that the interaction forms, or an increased or decreased concentration of kinase/natural binding partner complex.

The term "contacting" as used herein refers to mixing a solution comprising the test compound with a liquid medium bathing the cells of the methods. The solution comprising the compound may also comprise another component, such as dimethyl sulfoxide (DMSO), which facilitates the uptake of the test compound or compounds into the cells of the methods. The solution comprising the test compound may be added to the medium bathing the cells by utilizing a delivery apparatus, such as a pipet-based device or syringe-based device.

In a ninth aspect, the invention features methods for identifying a substance that modulates kinase activity in a cell comprising the steps of: (a) expressing a kinase polypeptide in a cell, wherein said polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,

SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
5 SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
10 SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
15 and SEQ ID NO:242; (b) adding a test substance to said cell; and (c) monitoring a change
in cell phenotype or the interaction between said polypeptide and a natural binding
partner.

The term “expressing” as used herein refers to the production of kinases of the
invention from a nucleic acid vector containing kinase genes within a cell. The nucleic
20 acid vector is transfected into cells using well known techniques in the art as described
herein.

In a tenth aspect, the invention provides methods for treating a disease or abnormal
condition by administering to a patient in need of such treatment a substance that
modulates the activity of a polypeptide selected from the group consisting of SEQ ID
25 NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID
NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID
NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID
NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID
30 NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID
NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID
NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID

NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242. Preferably, the disease is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer. Also included are metabolic disorders, such as diabetes mellitus, and reproductive disorders, such as infertility.

Preferably, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, and organ transplantation. Preferably the disease or disorder is selected from the group consisting of immune-related diseases and disorders, myocardial infarction, cardiomyopathies, stroke, renal failure, and oxidative stress-related neurodegenerative disorders. Most preferably, the immune-related diseases and disorders are selected from the group consisting of rheumatoid arthritis, chronic inflammatory bowel disease, chronic inflammatory pelvic disease, multiple sclerosis, asthma, osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity, and organ transplantation.

Substances useful for treatment of disorders or diseases preferably show positive results in one or more in vitro assays for an activity corresponding to treatment of the disease or disorder in question. Substances that modulate the activity of the polypeptides

preferably include, but are not limited to, antisense oligonucleotides and inhibitors of protein kinases.

The term “preventing” refers to decreasing the probability that an organism contracts or develops an abnormal condition.

5 The term “treating” refers to having a therapeutic effect and at least partially alleviating or abrogating an abnormal condition in the organism.

 The term “therapeutic effect” refers to the inhibition or activation factors causing or contributing to the abnormal condition. A therapeutic effect relieves to some extent one or more of the symptoms of the abnormal condition. In reference to the treatment of
10 abnormal conditions, a therapeutic effect can refer to one or more of the following: (a) an increase in the proliferation, growth, and/or differentiation of cells; (b) inhibition (*i.e.*, slowing or stopping) of cell death; (c) inhibition of degeneration; (d) relieving to some extent one or more of the symptoms associated with the abnormal condition; and (e) enhancing the function of the affected population of cells. Compounds demonstrating
15 efficacy against abnormal conditions can be identified as described herein.

 The term “abnormal condition” refers to a function in the cells or tissues of an organism that deviates from their normal functions in that organism. An abnormal condition can relate to cell proliferation, cell differentiation or cell survival. An abnormal condition may also include irregularities in cell cycle progression, *i.e.*, irregularities in
20 normal cell cycle progression through mitosis and meiosis.

 Abnormal cell proliferative conditions include cancers such as fibrotic and mesangial disorders, abnormal angiogenesis and vasculogenesis, wound healing, psoriasis, diabetes mellitus, and inflammation.

 Abnormal differentiation conditions include, but are not limited to
25 neurodegenerative disorders, slow wound healing rates, and slow tissue grafting healing rates.

 Abnormal cell survival conditions relate to conditions in which programmed cell death (apoptosis) pathways are activated or abrogated. A number of protein kinases are associated with the apoptosis pathways. Aberrations in the function of any one of the
30 protein kinases could lead to cell immortality or premature cell death.

The term "aberration", in conjunction with the function of a kinase in a signal transduction process, refers to a kinase that is over- or under-expressed in an organism, mutated such that its catalytic activity is lower or higher than wild-type protein kinase activity, mutated such that it can no longer interact with a natural binding partner, is no longer modified by another protein kinase or protein phosphatase, or no longer interacts with a natural binding partner.

The term "administering" relates to a method of incorporating a compound into cells or tissues of an organism. The abnormal condition can be prevented or treated when the cells or tissues of the organism exist within the organism or outside of the organism. Cells existing outside the organism can be maintained or grown in cell culture dishes. For cells harbored within the organism, many techniques exist in the art to administer compounds, including (but not limited to) oral, parenteral, dermal, injection, and aerosol applications. For cells outside of the organism, multiple techniques exist in the art to administer the compounds, including (but not limited to) cell microinjection techniques, transformation techniques, and carrier techniques.

The abnormal condition can also be prevented or treated by administering a compound to a group of cells having an aberration in a signal transduction pathway to an organism. The effect of administering a compound on organism function can then be monitored. The organism is preferably a mouse, rat, rabbit, guinea pig, or goat, more preferably a monkey or ape, and most preferably a human.

In an eleventh aspect, the invention features methods for detection the expression of a polypeptide in a sample as a diagnostic tool for diseases or disorders, wherein the method comprises the steps of: (a) contacting the sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ

ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding the polypeptide, fragments thereof, and the complements of the sequences and fragments; and (b) detecting the presence or amount of the probe:target region hybrid as an indication of the disease.

In preferred embodiments of the invention, the disease or disorder is selected from the group consisting of rheumatoid arthritis, atherosclerosis, autoimmune disorders, organ transplantation, myocardial infarction, cardiomyopathies, stroke, renal failure, oxidative stress-related neurodegenerative disorders, metabolic disorder including diabetes, reproductive disorders including infertility, and cancer.

The kinase "target region" is a nucleotide base sequence selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID

NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121, or the corresponding full-length sequences, a functional derivative thereof, or a fragment thereof to which the nucleic acid probe will specifically hybridize. Specific hybridization indicates that in the presence of other nucleic acids the probe only hybridizes detectably with the kinase of the invention's target region. Putative target regions can be identified by methods well known in the art consisting of alignment and comparison of the most closely related sequences in the database.

In preferred embodiments the nucleic acid probe hybridizes to a kinase target region encoding at least 6, 12, 75, 90, 105, 120, 150, 200, 250, 300 or 350 contiguous amino acids of the sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID

NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or the corresponding full-length amino acid sequence, or a functional derivative thereof. Hybridization

conditions should be such that hybridization occurs only with the kinase genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having more than 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

Hybridization conditions should be such that hybridization occurs only with the genes in the presence of other nucleic acid molecules. Under stringent hybridization conditions only highly complementary nucleic acid sequences hybridize. Preferably, such conditions prevent hybridization of nucleic acids having 1 or 2 mismatches out of 20 contiguous nucleotides. Such conditions are defined *supra*.

The diseases for which detection of kinase genes in a sample could be diagnostic include diseases in which kinase nucleic acid (DNA and/or RNA) is amplified in comparison to normal cells. By "amplification" is meant increased numbers of kinase

DNA or RNA in a cell compared with normal cells. In normal cells, kinases are typically found as single copy genes. In selected diseases, the chromosomal location of the kinase genes may be amplified, resulting in multiple copies of the gene, or amplification. Gene amplification can lead to amplification of kinase RNA, or kinase RNA can be amplified in the absence of kinase DNA amplification.

“Amplification” as it refers to RNA can be the detectable presence of kinase RNA in cells, since in some normal cells there is no basal expression of kinase RNA. In other normal cells, a basal level of expression of kinase exists, therefore in these cases amplification is the detection of at least 1-2-fold, and preferably more, kinase RNA, compared to the basal level.

The diseases that could be diagnosed by detection of kinase nucleic acid in a sample preferably include cancers. The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

Another aspect of the invention involves a method of agonizing (stimulating) or antagonizing a target of the invention and a natural binding partner associated activity in a mammal comprising administering to said mammal an agonist or antagonist to one of the above disclosed polypeptides in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of the protein of the present invention activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize associated functions is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein polypeptides. Some small organic molecules form a class of compounds that modulate the function of protein polypeptides. Examples of molecules that have been reported to inhibit the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published

November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1), seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*), all of which are incorporated by reference herein, including any drawings.

Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein inhibitors only weakly inhibit function. In addition, many inhibit a variety of protein kinases and will therefore cause multiple side-effects as therapeutics for diseases.

Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin, naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar groups including hydroxylated alkyl, phosphate, and ether substituents. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon

& Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives, both of which are incorporated by reference herein, including any drawings.

5 Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722
10 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris
15 *et al.* J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.* J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J. Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*,
20 Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); and Sikora *et al.*, Analytical Biochem. 172:344-355 (1988), all of which are incorporated
25 herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432
30 (1993); and Burke *et al.* BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen et al., Clin. Exp. Immunol. 91:141-156 (1993); Anafi et al., Blood 82:12:3524-3529 (1993); Baker et al., J. Cell Sci. 102:543-555 (1992); Bilder et al., Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton et al., Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert et al., Experimental
5 Cell Research 199:255-261 (1992); Dong et al., J. Leukocyte Biology 53:53-60 (1993); Dong et al., J. Immunol. 151(5):2717-2724 (1993); Gazit et al., J. Med. Chem. 32:2344-2352 (1989); Gazit et al., "J. Med. Chem. 36:3556-3564 (1993); Kaur et al., Anti-Cancer Drugs 5:213-222 (1994); Kaur et al., King et al., Biochem. J. 275:413-418 (1991); Kuo et al., Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992);
10 Lyall et al., J. Biol. Chem. 264:14503-14509 (1989); Peterson et al., The Prostate 22:335-345 (1993); Pillemer et al., Int. J. Cancer 50:80-85 (1992); Posner et al., Molecular Pharmacology 45:673-683 (1993); Rendu et al., Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring et al., J. Biol.
15 Chem. 269(36):22470-22472 (1994); and Yoneda et al., Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996,
20 incorporated herein by reference in its entirety, including any drawings.

Methods of Treating a Disease (Enablement - i.e., Dosing)

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number
25 WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being
30 treated, the particular composition being used and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be

formulated in animal models to achieve a circulating concentration range that initially takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors and major organs can also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows:

1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, Journal of American Veterinary Medical Assoc., 202:229-249, 1993).

Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness or toxicity. Gross abnormalities in tissue are noted and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

In a final aspect, the invention features a method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein the method comprises: (a) comparing a nucleic acid target region encoding the kinase polypeptide in
10 a sample, where the kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID
15 NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID
20 NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID

NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding the kinase polypeptide, or one or more fragments thereof; and (b) detecting differences in sequence or amount between the target region and the control target region, as an indication of the disease or disorder. Preferably, the disease or disorder is selected from the group consisting of immune-related diseases and disorders, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders, and cancer. Immune-related diseases and disorders include, but are not limited to, those discussed previously.

The term “comparing” as used herein refers to identifying discrepancies between the nucleic acid target region isolated from a sample, and the control nucleic acid target region. The discrepancies can be in the nucleotide sequences, *e.g.* insertions, deletions, or point mutations, or in the amount of a given nucleotide sequence. Methods to determine these discrepancies in sequences are well-known to one of ordinary skill in the art. The “control” nucleic acid target region refers to the sequence or amount of the sequence found in normal cells, *e.g.* cells that are not diseased as discussed previously.

The term also includes anti-sense molecules drawn thereto.

The invention has been described broadly and generically herein. Each of the narrower species and subgeneric groupings falling within the generic disclosure also form part of the invention. This includes the generic description of the invention with a proviso or negative limitation removing any subject matter from the genus, regardless of whether or not the excised material is specifically recited herein. For example, in some instances the nucleotide sequence of particular kinase polypeptides may not be part of a preferred embodiment.

The summary of the invention described above is not limiting and other features and advantages of the invention will be apparent from the following detailed description of the invention, and from the claims.

BRIEF DESCRIPTION OF THE FIGURES

Figures 1A to 1BB shows the amino acid sequences of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

Figures 2A to 2MMMM shows the nucleic acid sequences of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID

NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates in part to kinase polypeptides, nucleic acids encoding such polypeptides, cells containing such nucleic acids, antibodies to such polypeptides, assays utilizing such polypeptides, and methods relating to all of the foregoing. The present invention is based upon the isolation and characterization of new kinase polypeptides. The polypeptides and nucleic acids may be produced using well-known and standard synthesis techniques when given the sequences presented herein.

I. The Nucleic Acids of the Invention

Included within the scope of this invention are the functional equivalents of the herein-described isolated nucleic acid molecules. The degeneracy of the genetic code permits substitution of certain codons by other codons that specify the same amino acid and hence would give rise to the same protein. The nucleic acid sequence can vary

substantially since, with the exception of methionine and tryptophan, the known amino acids can be coded for by more than one codon. Thus, portions or all of the kinase genes of the invention could be synthesized to give a nucleic acid sequence significantly different from one selected from the group consisting of those set forth in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, SEQ ID NO:120, and SEQ ID NO:121. The encoded amino acid sequence thereof would, however, be preserved.

In addition, the nucleic acid sequence may comprise a nucleotide sequence which results from the addition, deletion or substitution of at least one nucleotide to the 5'-end and/or the 3'-end of the nucleic acid sequence shown in SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:7, SEQ ID

NO:8, SEQ ID NO:9, SEQ ID NO:10, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13,
SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ
ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:23, SEQ ID
NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29,
5 SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ
ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID
NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45,
SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ
ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID
10 NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61,
SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ
ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID
NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77,
SEQ ID NO:78, SEQ ID NO:79, SEQ ID NO:80, SEQ ID NO:81, SEQ ID NO:82, SEQ
15 ID NO:83, SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:86, SEQ ID NO:87, SEQ ID
NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:92, SEQ ID NO:93,
SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:98, SEQ
ID NO:99, SEQ ID NO:100, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID
NO:104, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:107, SEQ ID NO:108, SEQ ID
20 NO:109, SEQ ID NO:110, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID
NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID
NO:119, SEQ ID NO:120, and SEQ ID NO:121, or a derivative thereof. Any nucleotide
or polynucleotide may be used in this regard, provided that its addition, deletion or
substitution does not alter the amino acid sequence of SEQ ID NO:122, SEQ ID NO:123,
25 SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128,
SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133,
SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138,
SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143,
SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148,
30 SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153,
SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158,
SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163,

SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168,
SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173,
SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178,
SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183,
5 SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188,
SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193,
SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198,
SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203,
SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208,
10 SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213,
SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218,
SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223,
SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228,
SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233,
15 SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238,
SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, that is encoded
by the nucleotide sequence. For example, the present invention is intended to include any
nucleic acid sequence resulting from the addition of ATG as an initiation codon at the 5'-
end of the inventive nucleic acid sequence or its derivative, or from the addition of TTA,
20 TAG or TGA as a termination codon at the 3'-end of the inventive nucleotide sequence or
its derivative. Moreover, the nucleic acid molecule of the present invention may, as
necessary, have restriction endonuclease recognition sites added to its 5'-end and/or 3'-
end.

Such functional alterations of a given nucleic acid sequence afford an opportunity
25 to promote secretion and/or processing of heterologous proteins encoded by foreign
nucleic acid sequences fused thereto, for example. All variations of the nucleotide
sequence of the kinase genes of the invention and fragments thereof permitted by the
genetic code are, therefore, included in this invention.

Further, it is possible to delete codons or to substitute one or more codons with
30 codons other than degenerate codons to produce a structurally modified polypeptide, but
one which has substantially the same utility or activity as the polypeptide produced by the
unmodified nucleic acid molecule. As recognized in the art, the two polypeptides are

functionally equivalent, as are the two nucleic acid molecules that give rise to their production, even though the differences between the nucleic acid molecules are not related to the degeneracy of the genetic code. This is discussed further in the "Functional Derivatives" section, herein.

5 Finally, many of the nucleic acid molecules of the invention are provided as a partial sequence only (Fig. 2A through 2QQ). However, it is standard for one of ordinary skill in the art to obtain a full-length sequence when provided with a partial sequence. Similarly, when provided with a partial or full-length sequence it is standard for one of ordinary skill in the art to obtain nucleic acid sequence coding for homologous proteins.
10 Therefore, these nucleic acid molecules are also part of the invention.

 The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore
15 presumably define new protein kinase groups.

 Additional characteristics may be found, *inter alia*, in the tables, namely Table 1, Table 2, Table 3 and Table 4, shown below.

20 II. Nucleic Acid Probes, Methods, and Kits for Detection of Protein Kinases.

 A nucleic acid probe of the present invention may be used to probe an appropriate chromosomal or cDNA library by usual hybridization methods to obtain other nucleic acid molecules of the present invention. A chromosomal DNA or cDNA library may be prepared from appropriate cells according to recognized methods in the art (cf. "Molecular Cloning: A Laboratory Manual", second edition, Cold Spring Harbor Laboratory,
25 Sambrook, Fritsch, & Maniatis, eds., 1989).

 In the alternative, chemical synthesis can be carried out in order to obtain nucleic acid probes having nucleotide sequences that correspond to N-terminal, kinase or C-terminal portions, for example, of the amino acid sequence of the polypeptide of interest. The synthesized nucleic acid probes may be used as primers in a polymerase chain
30 reaction (PCR) carried out in accordance with recognized PCR techniques, essentially according to PCR Protocols, "A Guide to Methods and Applications", Academic Press,

Michael, *et al.*, eds., 1990, utilizing the appropriate chromosomal or cDNA library to obtain the fragment of the present invention.

One skilled in the art can readily design such probes based on the sequence disclosed herein using methods of computer alignment and sequence analysis known in the art ("Molecular Cloning: A Laboratory Manual", 1989, *supra*). The hybridization probes of the present invention can be labeled by standard labeling techniques such as with a radiolabel, enzyme label, fluorescent label, biotin-avidin label, chemiluminescence, and the like. After hybridization, the probes may be visualized using known methods.

The nucleic acid probes of the present invention include RNA, as well as DNA probes, such probes being generated using techniques known in the art. The nucleic acid probe may be immobilized on a solid support. Examples of such solid supports include, but are not limited to, plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, and acrylic resins, such as polyacrylamide and latex beads. Techniques for coupling nucleic acid probes to such solid supports are well known in the art.

The test samples suitable for nucleic acid probing methods of the present invention include, for example, cells or nucleic acid extracts of cells, or biological fluids. The samples used in the above-described methods will vary based on the assay format, the detection method and the nature of the tissues, cells or extracts to be assayed. Methods for preparing nucleic acid extracts of cells are well known in the art and can be readily adapted in order to obtain a sample that is compatible with the method utilized.

One method of detecting the presence of nucleic acids of the invention in a sample comprises (a) contacting said sample with the above-described nucleic acid probe under conditions such that hybridization occurs, and (b) detecting the presence of said probe bound to said nucleic acid molecule. One skilled in the art would select the nucleic acid probe according to techniques known in the art as described above. Samples to be tested include but should not be limited to RNA samples of human tissue.

A kit for detecting the presence of nucleic acids of the invention in a sample comprises at least one container means having disposed therein the above-described nucleic acid probe. The kit may further comprise other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound nucleic acid probe. Examples of detection reagents include, but are not limited to

radiolabelled probes, enzymatic labeled probes (horseradish peroxidase, alkaline phosphatase), and affinity labeled probes (biotin, avidin, or streptavidin).

In detail, a compartmentalized kit includes any kit in which reagents are contained in separate containers. Such containers include small glass containers, plastic containers or strips of plastic or paper. Such containers allow the efficient transfer of reagents from one compartment to another compartment such that the samples and reagents are not cross-contaminated and the agents or solutions of each container can be added in a quantitative fashion from one compartment to another. Such containers will include a container which will accept the test sample, a container which contains the probe or primers used in the assay, containers which contain wash reagents (such as phosphate buffered saline, Tris-buffers, and the like), and containers which contain the reagents used to detect the hybridized probe, bound antibody, amplified product, or the like. One skilled in the art will readily recognize that the nucleic acid probes described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

III. DNA Constructs Comprising a Protein Kinase Nucleic Acid Molecule and Cells Containing These Constructs.

The present invention also relates to a recombinant DNA molecule comprising, 5' to 3', a promoter effective to initiate transcription in a host cell and the above-described nucleic acid molecules. In addition, the present invention relates to a recombinant DNA molecule comprising a vector and an above-described nucleic acid molecule. The present invention also relates to a nucleic acid molecule comprising a transcriptional region functional in a cell, a sequence complementary to an RNA sequence encoding an amino acid sequence corresponding to the above-described polypeptide, and a transcriptional termination region functional in said cell. The above-described molecules may be isolated and/or purified DNA molecules.

The present invention also relates to a cell or organism that contains an above-described nucleic acid molecule and thereby is capable of expressing a polypeptide. The polypeptide may be purified from cells that have been altered to express the polypeptide. A cell is said to be "altered to express a desired polypeptide" when the cell, through genetic manipulation, is made to produce a protein which it normally does not produce or

which the cell normally produces at lower levels. One skilled in the art can readily adapt procedures for introducing and expressing either genomic, cDNA, or synthetic sequences into either eukaryotic or prokaryotic cells.

A nucleic acid molecule, such as DNA, is said to be "capable of expressing" a polypeptide if it contains nucleotide sequences which contain transcriptional and translational regulatory information and such sequences are "operably linked" to nucleotide sequences which encode the polypeptide. An operable linkage is a linkage in which the regulatory DNA sequences and the DNA sequence sought to be expressed are connected in such a way as to permit gene sequence expression. The precise nature of the regulatory regions needed for gene sequence expression may vary from organism to organism, but shall in general include a promoter region which, in prokaryotes, contains both the promoter (which directs the initiation of RNA transcription) as well as the DNA sequences which, when transcribed into RNA, will signal synthesis initiation. Such regions will normally include those 5'-non-coding sequences involved with initiation of transcription and translation, such as the TATA box, capping sequence, CAAT sequence, and the like.

If desired, the non-coding region 3' to the sequence encoding a kinase of the invention may be obtained by the above-described methods. This region may be retained for its transcriptional termination regulatory sequences, such as termination and polyadenylation. Thus, by retaining the 3'-region naturally contiguous to the DNA sequence encoding a kinase of the invention, the transcriptional termination signals may be provided. Where the transcriptional termination signals are not satisfactorily functional in the expression host cell, then a 3' region functional in the host cell may be substituted.

Two DNA sequences (such as a promoter region sequence and a sequence encoding a kinase of the invention) are said to be operably linked if the nature of the linkage between the two DNA sequences does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the promoter region sequence to direct the transcription of a gene sequence encoding a kinase of the invention, or (3) interfere with the ability of the gene sequence of a kinase of the invention to be transcribed by the promoter region sequence. Thus, a promoter region would be operably linked to a DNA sequence if the promoter were capable of effecting transcription of that DNA sequence.

Thus, to express a gene encoding a kinase of the invention, transcriptional and translational signals recognized by an appropriate host are necessary.

The present invention encompasses the expression of a gene encoding a kinase of the invention (or a functional derivative thereof) in either prokaryotic or eukaryotic cells.

5 Prokaryotic hosts are, generally, very efficient and convenient for the production of recombinant proteins and are, therefore, one type of preferred expression system for kinases of the invention. Prokaryotes most frequently are represented by various strains of *E. coli*. However, other microbial strains may also be used, including other bacterial strains.

10 In prokaryotic systems, plasmid vectors that contain replication sites and control sequences derived from a species compatible with the host may be used. Examples of suitable plasmid vectors may include pBR322, pUC118, pUC119 and the like; suitable phage or bacteriophage vectors may include γ gt10, γ gt11 and the like; and suitable virus vectors may include pMAM-neo, pKRC and the like. Preferably, the selected vector of the present invention has the capacity to replicate in the selected host cell.

15 Recognized prokaryotic hosts include bacteria such as *E. coli*, *Bacillus*, *Streptomyces*, *Pseudomonas*, *Salmonella*, *Serratia*, and the like. However, under such conditions, the polypeptide will not be glycosylated. The prokaryotic host must be compatible with the replicon and control sequences in the expression plasmid.

20 To express a kinase of the invention (or a functional derivative thereof) in a prokaryotic cell, it is necessary to operably link the sequence encoding the kinase of the invention to a functional prokaryotic promoter. Such promoters may be either constitutive or, more preferably, regulatable (*i.e.*, inducible or derepressible). Examples of constitutive promoters include the *int* promoter of bacteriophage λ , the *bla* promoter of the β -lactamase gene sequence of pBR322, and the *cat* promoter of the chloramphenicol acetyl transferase gene sequence of pPR325, and the like. Examples of inducible prokaryotic promoters include the major right and left promoters of bacteriophage λ (P_L and P_R), the *trp*, *recA*, *lacZ*, *lacI*, and *gal* promoters of *E. coli*, the α -amylase (Ulmanen *et al.*, J. Bacteriol. 162:176-182, 1985) and the ζ -28-specific promoters of *B. subtilis* (Gilman *et al.*, Gene Sequence 32:11-20, 1984), the promoters of the bacteriophages of *Bacillus* (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, Inc., NY, 1982), and *Streptomyces* promoters (Ward *et al.*, Mol. Gen. Genet. 203:468-478, 1986). Prokaryotic

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promoters are reviewed by Glick (Ind. Microbiot. 1:277-282, 1987), Cenatiempo (Biochimie 68:505-516, 1986), and Gottesman (Ann. Rev. Genet. 18:415-442, 1984).

Proper expression in a prokaryotic cell also requires the presence of a ribosome-binding site upstream of the gene sequence-encoding sequence. Such ribosome-binding sites are disclosed, for example, by Gold *et al.* (Ann. Rev. Microbiol. 35:365-404, 1981). The selection of control sequences, expression vectors, transformation methods, and the like, are dependent on the type of host cell used to express the gene. As used herein, "cell", "cell line", and "cell culture" may be used interchangeably and all such designations include progeny. Thus, the words "transformants" or "transformed cells" include the primary subject cell and cultures derived therefrom, without regard to the number of transfers. It is also understood that all progeny may not be precisely identical in DNA content, due to deliberate or inadvertent mutations. However, as defined, mutant progeny have the same functionality as that of the originally transformed cell.

Host cells which may be used in the expression systems of the present invention are not strictly limited, provided that they are suitable for use in the expression of the kinase polypeptide of interest. Suitable hosts may often include eukaryotic cells. Preferred eukaryotic hosts include, for example, yeast, fungi, insect cells, mammalian cells either *in vivo*, or in tissue culture. Mammalian cells which may be useful as hosts include HeLa cells, cells of fibroblast origin such as VERO or CHO-K1, or cells of lymphoid origin and their derivatives. Preferred mammalian host cells include SP2/0 and J558L, as well as neuroblastoma cell lines such as IMR 332, which may provide better capacities for correct post-translational processing.

In addition, plant cells are also available as hosts, and control sequences compatible with plant cells are available, such as the cauliflower mosaic virus 35S and 19S, and nopaline synthase promoter and polyadenylation signal sequences. Another preferred host is an insect cell, for example the *Drosophila* larvae. Using insect cells as hosts, the *Drosophila* alcohol dehydrogenase promoter can be used (Rubin, Science 240:1453-1459, 1988). Alternatively, baculovirus vectors can be engineered to express large amounts of kinases of the invention in insect cells (Jasny, Science 238:1653, 1987; Miller *et al.*, In: Genetic Engineering, Vol. 8, Plenum, Setlow *et al.*, eds., pp. 277-297, 1986).

Any of a series of yeast expression systems can be utilized which incorporate promoter and termination elements from the actively expressed sequences coding for glycolytic enzymes that are produced in large quantities when yeast are grown in mediums rich in glucose. Known glycolytic gene sequences can also provide very efficient transcriptional control signals. Yeast provides substantial advantages in that it can also carry out post-translational modifications. A number of recombinant DNA strategies exist utilizing strong promoter sequences and high copy number plasmids which can be utilized for production of the desired proteins in yeast. Yeast recognizes leader sequences on cloned mammalian genes and secretes peptides bearing leader sequences (*i.e.*, pre-peptides). Several possible vector systems are available for the expression of kinases of the invention in a mammalian host.

A wide variety of transcriptional and translational regulatory sequences may be employed, depending upon the nature of the host. The transcriptional and translational regulatory signals may be derived from viral sources, such as adenovirus, bovine papilloma virus, cytomegalovirus, simian virus, or the like, where the regulatory signals are associated with a particular gene sequence which has a high level of expression. Alternatively, promoters from mammalian expression products, such as actin, collagen, myosin, and the like, may be employed. Transcriptional initiation regulatory signals may be selected which allow for repression or activation, so that expression of the gene sequences can be modulated. Of interest are regulatory signals which are temperature-sensitive so that by varying the temperature, expression can be repressed or initiated, or are subject to chemical (such as metabolite) regulation.

Expression of kinases of the invention in eukaryotic hosts requires the use of eukaryotic regulatory regions. Such regions will, in general, include a promoter region sufficient to direct the initiation of RNA synthesis. Preferred eukaryotic promoters include, for example, the promoter of the mouse metallothionein I gene sequence (Hamer *et al.*, J. Mol. Appl. Gen. 1:273-288, 1982); the TK promoter of Herpes virus (McKnight, Cell 31:355-365, 1982); the SV40 early promoter (Benoist *et al.*, Nature (London) 290:304-31, 1981); and the yeast gal4 gene sequence promoter (Johnston *et al.*, Proc. Natl. Acad. Sci. (USA) 79:6971-6975, 1982; Silver *et al.*, Proc. Natl. Acad. Sci. (USA) 81:5951-5955, 1984).

Translation of eukaryotic mRNA is initiated at the codon that encodes the first methionine. For this reason, it is preferable to ensure that the linkage between a eukaryotic promoter and a DNA sequence which encodes a kinase of the invention (or a functional derivative thereof) does not contain any intervening codons which are capable of encoding a methionine (*i.e.*, AUG). The presence of such codons results either in the formation of a fusion protein (if the AUG codon is in the same reading frame as the kinase of the invention coding sequence) or a frame-shift mutation (if the AUG codon is not in the same reading frame as the kinase of the invention coding sequence).

A nucleic acid molecule encoding a kinase of the invention and an operably linked promoter may be introduced into a recipient prokaryotic or eukaryotic cell either as a nonreplicating DNA or RNA molecule, which may either be a linear molecule or, more preferably, a closed covalent circular molecule. Since such molecules are incapable of autonomous replication, the expression of the gene may occur through the transient expression of the introduced sequence. Alternatively, permanent expression may occur through the integration of the introduced DNA sequence into the host chromosome.

A vector may be employed which is capable of integrating the desired gene sequences into the host cell chromosome. Cells which have stably integrated the introduced DNA into their chromosomes can be selected by also introducing one or more markers which allow for selection of host cells which contain the expression vector. The marker may provide for prototrophy to an auxotrophic host, biocide resistance, *e.g.*, antibiotics, or heavy metals, such as copper, or the like. The selectable marker gene sequence can either be directly linked to the DNA gene sequences to be expressed, or introduced into the same cell by co-transfection. Additional elements may also be needed for optimal synthesis of mRNA. These elements may include splice signals, as well as transcription promoters, enhancers, and termination signals. cDNA expression vectors incorporating such elements include those described by Okayama (Mol. Cell. Biol. 3:280-, 1983).

The introduced nucleic acid molecule can be incorporated into a plasmid or viral vector capable of autonomous replication in the recipient host. Any of a wide variety of vectors may be employed for this purpose. Factors of importance in selecting a particular plasmid or viral vector include: the ease with which recipient cells that contain the vector may be recognized and selected from those recipient cells which do not contain the vector;

the number of copies of the vector which are desired in a particular host; and whether it is desirable to be able to "shuttle" the vector between host cells of different species.

Preferred prokaryotic vectors include plasmids such as those capable of replication in *E. coli* (such as, for example, pBR322, ColEI, pSC101, pACYC 184, π VX; "Molecular Cloning: A Laboratory Manual", 1989, *supra*). *Bacillus* plasmids include pC194, pC221, pT127, and the like (Gryczan, In: The Molecular Biology of the Bacilli, Academic Press, NY, pp. 307-329, 1982). Suitable *Streptomyces* plasmids include p1J101 (Kendall *et al.*, J. Bacteriol. 169:4177-4183, 1987), and streptomyces bacteriophages such as ϕ C31 (Chater *et al.*, In: Sixth International Symposium on Actinomycetales Biology, Akademiai Kiado, Budapest, Hungary, pp. 45-54, 1986). *Pseudomonas* plasmids are reviewed by John *et al.* (Rev. Infect. Dis. 8:693-704, 1986), and Izaki (Jpn. J. Bacteriol. 33:729-742, 1978).

Preferred eukaryotic plasmids include, for example, BPV, vaccinia, SV40, 2-micron circle, and the like, or their derivatives. Such plasmids are well known in the art (Botstein *et al.*, Miami Wntr. Symp. 19:265-274, 1982; Broach, In: "The Molecular Biology of the Yeast *Saccharomyces*: Life Cycle and Inheritance", Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, p. 445-470, 1981; Broach, Cell 28:203-204, 1982; Bollon *et al.*, J. Clin. Hematol. Oncol. 10:39-48, 1980; Maniatis, In: Cell Biology: A Comprehensive Treatise, Vol. 3, Gene Sequence Expression, Academic Press, NY, pp. 563-608, 1980).

Once the vector or nucleic acid molecule containing the construct(s) has been prepared for expression, the DNA construct(s) may be introduced into an appropriate host cell by any of a variety of suitable means, *i.e.*, transformation, transfection, conjugation, protoplast fusion, electroporation, particle gun technology, calcium phosphate-precipitation, direct microinjection, and the like. After the introduction of the vector, recipient cells are grown in a selective medium, which selects for the growth of vector-containing cells. Expression of the cloned gene(s) results in the production of a kinase of the invention, or fragments thereof. This can take place in the transformed cells as such, or following the induction of these cells to differentiate (for example, by administration of bromodeoxyuracil to neuroblastoma cells or the like). A variety of incubation conditions can be used to form the peptide of the present invention. The most preferred conditions are those which mimic physiological conditions.

IV. The Proteins of the Invention

A variety of methodologies known in the art can be utilized to obtain the polypeptides of the present invention. The polypeptides may be purified from tissues or cells that naturally produce the polypeptides. Alternatively, the above-described isolated nucleic acid fragments could be used to express the kinases of the invention in any organism. The samples of the present invention include cells, protein extracts or membrane extracts of cells, or biological fluids. The samples will vary based on the assay format, the detection method, and the nature of the tissues, cells or extracts used as the sample.

Any eukaryotic organism can be used as a source for the polypeptides of the invention, as long as the source organism naturally contains such polypeptides. As used herein, "source organism" refers to the original organism from which the amino acid sequence of the subunit is derived, regardless of the organism the subunit is expressed in and ultimately isolated from.

One skilled in the art can readily follow known methods for isolating proteins in order to obtain the polypeptides free of natural contaminants. These include, but are not limited to: size-exclusion chromatography, HPLC, ion-exchange chromatography, and immuno-affinity chromatography.

Further, the polypeptides of the invention include the full-length polypeptides that can be identified from the full-length or partial sequences encoded by SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182,

SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 (Figure 1). In addition, the polypeptides of the invention include the domains of these polypeptides, including, but not limited to, the N-terminal, kinase/catalytic, and C-terminal domains.

The characteristics of the protein kinase nucleic acid sequences of the invention are provided in Table 1. The protein kinases fall into 10 known groups: AGC, CAMK, CKI, CMGC, dsPK, EIFK, LIMK, MLK, STE and TK. In addition, there are a significant number of protein kinases that do not belong to any of the known groups, and therefore presumably define new protein kinase groups.

Additional characteristics are shown in, *inter alia*, the tables, namely Table 1, Table 2, Table 3 and Table 4, provided below.

V. Antibodies, Hybridomas, Methods of Use and Kits for Detection of Protein Kinases

The present invention relates to an antibody having binding affinity to a kinase of the invention. The polypeptide may have an amino acid sequence selected from the group consisting of those set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ

ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or a functional derivative thereof, or at least 9 contiguous amino acids thereof (preferably, at least 20, 30, 35, or 40 or more contiguous amino acids thereof). Alternatively, the antibody may bind to a part of the polypeptide not provided in the sequences above, but that is present in the full-length sequence of the polypeptide and that is easily obtained using methods standard in the art. Further, the antibody may bind specifically to particular domains of one or more of the kinases of the invention, including, but not limited to, the N-terminal, kinase/catalytic, or C-terminal domains.

The present invention also relates to an antibody having specific binding affinity to a kinase or kinase domain of the invention. Such an antibody may be isolated by comparing its binding affinity to a kinase of the invention with its binding affinity to other polypeptides. Those that bind selectively to a kinase of the invention would be chosen for use in methods requiring a distinction between a kinase of the invention and other

polypeptides. Such methods could include, but should not be limited to, the analysis of altered kinase expression in tissue containing other polypeptides.

The kinases of the present invention can be used in a variety of procedures and methods, such as for the generation of antibodies, for use in identifying pharmaceutical compositions, and for studying DNA/protein interaction.

The kinases of the present invention can be used to produce antibodies or hybridomas. One skilled in the art will recognize that if an antibody is desired, such a peptide could be generated as described herein and used as an immunogen. The antibodies of the present invention include monoclonal and polyclonal antibodies, as well fragments of these antibodies, and humanized forms. Humanized forms of the antibodies of the present invention may be generated using one of the procedures known in the art such as chimerization or CDR grafting.

The present invention also relates to a hybridoma that produces the above-described monoclonal antibody, or binding fragment thereof. A hybridoma is an immortalized cell line that is capable of secreting a specific monoclonal antibody.

In general, techniques for preparing monoclonal antibodies and hybridomas are well known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1984; St. Groth *et al.*, J. Immunol. Methods 35:1-21, 1980). Any animal (mouse, rabbit, and the like) which is known to produce antibodies can be immunized with the selected polypeptide. Methods for immunization are well known in the art. Such methods include subcutaneous or intraperitoneal injection of the polypeptide. One skilled in the art will recognize that the amount of polypeptide used for immunization will vary based on the animal that is immunized, the antigenicity of the polypeptide and the site of injection.

The polypeptide may be modified or administered in an adjuvant in order to increase the peptide antigenicity. Methods of increasing the antigenicity of a polypeptide are well known in the art. Such procedures include coupling the antigen with a heterologous protein (such as globulin or β -galactosidase) or through the inclusion of an adjuvant during immunization.

For monoclonal antibodies, spleen cells from the immunized animals are removed, fused with myeloma cells, such as SP2/0-Agl4 myeloma cells, and allowed to become monoclonal antibody producing hybridoma cells. Any one of a number of methods well known in the art can be used to identify the hybridoma cell that produces an antibody with the desired characteristics. These include screening the hybridomas with an ELISA assay, western blot analysis, or radioimmunoassay (Lutz *et al.*, Exp. Cell Res. 175:109-124, 1988). Hybridomas secreting the desired antibodies are cloned and the class and subclass are determined using procedures known in the art (Campbell, "Monoclonal Antibody Technology: Laboratory Techniques in Biochemistry and Molecular Biology", *supra*, 1984).

For polyclonal antibodies, antibody-containing antisera is isolated from the immunized animal and is screened for the presence of antibodies with the desired specificity using one of the above-described procedures. The above-described antibodies may be detectably labeled. Antibodies can be detectably labeled through the use of radioisotopes, affinity labels (such as biotin, avidin, and the like), enzymatic labels (such as horse radish peroxidase, alkaline phosphatase, and the like) fluorescent labels (such as FITC or rhodamine, and the like), paramagnetic atoms, and the like. Procedures for accomplishing such labeling are well-known in the art, for example, *see* Stemberger *et al.*, J. Histochem. Cytochem. 18:315, 1970; Bayer *et al.*, Meth. Enzym. 62:308-, 1979; Engval *et al.*, Immunol. 109:129-, 1972; Goding, J. Immunol. Meth. 13:215-, 1976. The labeled antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays to identify cells or tissues that express a specific peptide.

The above-described antibodies may also be immobilized on a solid support. Examples of such solid supports include plastics such as polycarbonate, complex carbohydrates such as agarose and sepharose, acrylic resins and such as polyacrylamide and latex beads. Techniques for coupling antibodies to such solid supports are well known in the art (Weir *et al.*, "Handbook of Experimental Immunology" 4th Ed., Blackwell Scientific Publications, Oxford, England, Chapter 10, 1986; Jacoby *et al.*, Meth. Enzym. 34, Academic Press, N.Y., 1974). The immobilized antibodies of the present invention can be used for *in vitro*, *in vivo*, and *in situ* assays as well as in immunochromatography.

Furthermore, one skilled in the art can readily adapt currently available procedures, as well as the techniques, methods and kits disclosed herein with regard to antibodies, to generate peptides capable of binding to a specific peptide sequence in order to generate rationally designed anti-peptide peptides (Hurby *et al.*, "Application of Synthetic Peptides: Antisense Peptides", In Synthetic Peptides, A User's Guide, W.H. Freeman, NY, pp. 289-307, 1992; Kaspczak *et al.*, Biochemistry 28:9230-9238, 1989).

Anti-peptide peptides can be generated by replacing the basic amino acid residues found in the peptide sequences of the kinases of the invention with acidic residues, while maintaining hydrophobic and uncharged polar groups. For example, lysine, arginine, and/or histidine residues are replaced with aspartic acid or glutamic acid and glutamic acid residues are replaced by lysine, arginine or histidine.

The present invention also encompasses a method of detecting a kinase polypeptide in a sample, comprising: (a) contacting the sample with an above-described antibody, under conditions such that immunocomplexes form, and (b) detecting the presence of said antibody bound to the polypeptide. In detail, the methods comprise incubating a test sample with one or more of the antibodies of the present invention and assaying whether the antibody binds to the test sample. Altered levels of a kinase of the invention in a sample as compared to normal levels may indicate disease.

Conditions for incubating an antibody with a test sample vary. Incubation conditions depend on the format employed in the assay, the detection methods employed, and the type and nature of the antibody used in the assay. One skilled in the art will recognize that any one of the commonly available immunological assay formats (such as radioimmunoassays, enzyme-linked immunosorbent assays, diffusion based Ouchterlony, or rocket immunofluorescent assays) can readily be adapted to employ the antibodies of the present invention. Examples of such assays can be found in Chard ("An Introduction to Radioimmunoassay and Related Techniques" Elsevier Science Publishers, Amsterdam, The Netherlands, 1986), Bullock *et al.* ("Techniques in Immunocytochemistry," Academic Press, Orlando, FL Vol. 1, 1982; Vol. 2, 1983; Vol. 3, 1985), Tijssen ("Practice and Theory of Enzyme Immunoassays: Laboratory Techniques in Biochemistry and Molecular Biology," Elsevier Science Publishers, Amsterdam, The Netherlands, 1985).

The immunological assay test samples of the present invention include cells, protein or membrane extracts of cells, or biological fluids such as blood, serum, plasma, or urine. The test samples used in the above-described method will vary based on the assay format, nature of the detection method and the tissues, cells or extracts used as the sample to be assayed. Methods for preparing protein extracts or membrane extracts of cells are well known in the art and can be readily be adapted in order to obtain a sample which is testable with the system utilized.

A kit contains all the necessary reagents to carry out the previously described methods of detection. The kit may comprise: (i) a first container means containing an above-described antibody, and (ii) second container means containing a conjugate comprising a binding partner of the antibody and a label. In another preferred embodiment, the kit further comprises one or more other containers comprising one or more of the following: wash reagents and reagents capable of detecting the presence of bound antibodies.

Examples of detection reagents include, but are not limited to, labeled secondary antibodies, or in the alternative, if the primary antibody is labeled, the chromophoric, enzymatic, or antibody binding reagents that are capable of reacting with the labeled antibody. The compartmentalized kit may be as described above for nucleic acid probe kits. One skilled in the art will readily recognize that the antibodies described in the present invention can readily be incorporated into one of the established kit formats that are well known in the art.

VI. Isolation of Compounds That Interact With Protein Kinases

The present invention also relates to a method of detecting a compound capable of binding to a protein kinase of the invention, comprising incubating the compound with a kinase of the invention and detecting the presence of the compound bound to the kinase. The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts.

The present invention also relates to a method of detecting an agonist or antagonist of kinase activity or kinase binding partner activity comprising incubating cells that produce a kinase of the invention in the presence of a compound and detecting changes in the level of kinase activity or kinase binding partner activity. The compounds thus identified would produce a change in activity indicative of the presence of the compound.

The compound may be present within a complex mixture, for example, serum, body fluid, or cell extracts. Once the compound is identified it can be isolated using techniques well known in the art.

5 The present invention also encompasses a method of agonizing (stimulating) or antagonizing kinase associated activity in a mammal comprising administering to said mammal an agonist or antagonist to a kinase of the invention in an amount sufficient to effect said agonism or antagonism. A method of treating diseases in a mammal with an agonist or antagonist of kinase activity comprising administering the agonist or antagonist to a mammal in an amount sufficient to agonize or antagonize kinase associated functions
10 is also encompassed in the present application.

In an effort to discover novel treatments for diseases, biomedical researchers and chemists have designed, synthesized, and tested molecules that inhibit the function of protein kinases. Some small organic molecules form a class of compounds that modulate the function of protein kinases. Examples of molecules that have been reported to inhibit
15 the function of protein kinases include, but are not limited to, bis monocyclic, bicyclic or heterocyclic aryl compounds (PCT WO 92/20642, published November 26, 1992 by Maguire *et al.*), vinylene-azaindole derivatives (PCT WO 94/14808, published July 7, 1994 by Ballinari *et al.*), 1-cyclopropyl-4-pyridyl-quinolones (U.S. Patent No. 5,330,992), styryl compounds (U.S. Patent No. 5,217,999), styryl-substituted pyridyl compounds (U.S. Patent No. 5,302,606), certain quinazoline derivatives (EP Application No. 0 566 266 A1),
20 seleoindoles and selenides (PCT WO 94/03427, published February 17, 1994 by Denny *et al.*), tricyclic polyhydroxylic compounds (PCT WO 92/21660, published December 10, 1992 by Dow), and benzylphosphonic acid compounds (PCT WO 91/15495, published October 17, 1991 by Dow *et al.*).

25 Compounds that can traverse cell membranes and are resistant to acid hydrolysis are potentially advantageous as therapeutics as they can become highly bioavailable after being administered orally to patients. However, many of these protein kinase inhibitors only weakly inhibit the function of protein kinases. In addition, many inhibit a variety of protein kinases and will cause multiple side-effects as therapeutics for diseases.

30 Some indolinone compounds, however, form classes of acid resistant and membrane permeable organic molecules. WO 96/22976 (published August 1, 1996 by Ballinari *et al.*) describes hydrosoluble indolinone compounds that harbor tetralin,

naphthalene, quinoline, and indole substituents fused to the oxindole ring. These bicyclic substituents are in turn substituted with polar moieties including hydroxylated alkyl, phosphate, and ether moieties. U.S. Patent Application Serial Nos. 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187) and 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298) and International Patent Publication WO 96/22976, published August 1, 1996 by Ballinari *et al.*, all of which are incorporated herein by reference in their entirety, including any drawings, describe indolinone chemical libraries of indolinone compounds harboring other bicyclic moieties as well as monocyclic moieties fused to the oxindole ring. Applications 08/702,232, filed August 23, 1996, entitled "Indolinone Combinatorial Libraries and Related Products and Methods for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 221/187), 08/485,323, filed June 7, 1995, entitled "Benzylidene-Z-Indoline Compounds for the Treatment of Disease" by Tang *et al.* (Lyon & Lyon Docket No. 223/298), and WO 96/22976, published August 1, 1996 by Ballinari *et al.* teach methods of indolinone synthesis, methods of testing the biological activity of indolinone compounds in cells, and inhibition patterns of indolinone derivatives.

Other examples of substances capable of modulating kinase activity include, but are not limited to, tyrphostins, quinazolines, quinoxolines, and quinolines. The quinazolines, tyrphostins, quinolines, and quinoxolines referred to above include well known compounds such as those described in the literature. For example, representative publications describing quinazolines include Barker *et al.*, EPO Publication No. 0 520 722 A1; Jones *et al.*, U.S. Patent No. 4,447,608; Kabbe *et al.*, U.S. Patent No. 4,757,072; Kaul and Vougioukas, U.S. Patent No. 5, 316,553; Kreighbaum and Comer, U.S. Patent No. 4,343,940; Pegg and Wardleworth, EPO Publication No. 0 562 734 A1; Barker *et al.*, Proc. of Am. Assoc. for Cancer Research 32:327 (1991); Bertino, J.R., Cancer Research 3:293-304 (1979); Bertino, J.R., Cancer Research 9(2 part 1):293-304 (1979); Curtin *et al.*, Br. J. Cancer 53:361-368 (1986); Fernandes *et al.*, Cancer Research 43:1117-1123 (1983); Ferris *et al.*, J. Org. Chem. 44(2):173-178; Fry *et al.*, Science 265:1093-1095 (1994); Jackman *et al.*, Cancer Research 51:5579-5586 (1981); Jones *et al.*, J. Med. Chem. 29(6):1114-1118; Lee and Skibo, Biochemistry 26(23):7355-7362 (1987); Lemus *et al.*, J.

Org. Chem. 54:3511-3518 (1989); Ley and Seng, Synthesis 1975:415-522 (1975); Maxwell *et al.*, Magnetic Resonance in Medicine 17:189-196 (1991); Mini *et al.*, Cancer Research 45:325-330 (1985); Phillips and Castle, J. Heterocyclic Chem. 17(19):1489-1596 (1980); Reece *et al.*, Cancer Research 47(11):2996-2999 (1977); Sculier *et al.*, Cancer Immunol. and Immunother. 23:A65 (1986); Sikora *et al.*, Cancer Letters 23:289-295 (1984); Sikora *et al.*, Analytical Biochem. 172:344-355 (1988); all of which are incorporated herein by reference in their entirety, including any drawings.

Quinoxaline is described in Kaul and Vougioukas, U.S. Patent No. 5,316,553, incorporated herein by reference in its entirety, including any drawings.

Quinolines are described in Dolle *et al.*, J. Med. Chem. 37:2627-2629 (1994); MaGuire, J. Med. Chem. 37:2129-2131 (1994); Burke *et al.*, J. Med. Chem. 36:425-432 (1993); and Burke *et al.*, BioOrganic Med. Chem. Letters 2:1771-1774 (1992), all of which are incorporated by reference in their entirety, including any drawings.

Tyrphostins are described in Allen *et al.*, Clin. Exp. Immunol. 91:141-156 (1993); Anafi *et al.*, Blood 82:12:3524-3529 (1993); Baker *et al.*, J. Cell Sci. 102:543-555 (1992); Bilder *et al.*, Amer. Physiol. Soc. pp. 6363-6143:C721-C730 (1991); Brunton *et al.*, Proceedings of Amer. Assoc. Cancer Rsch. 33:558 (1992); Bryckaert *et al.*, Experimental Cell Research 199:255-261 (1992); Dong *et al.*, J. Leukocyte Biology 53:53-60 (1993); Dong *et al.*, J. Immunol. 151(5):2717-2724 (1993); Gazit *et al.*, J. Med. Chem. 32:2344-2352 (1989); Gazit *et al.*, " J. Med. Chem. 36:3556-3564 (1993); Kaur *et al.*, Anti-Cancer Drugs 5:213-222 (1994); Kaur *et al.*, King *et al.*, Biochem. J. 275:413-418 (1991); Kuo *et al.*, Cancer Letters 74:197-202 (1993); Levitzki, A., The FASEB J. 6:3275-3282 (1992); Lyall *et al.*, J. Biol. Chem. 264:14503-14509 (1989); Peterson *et al.*, The Prostate 22:335-345 (1993); Pillemer *et al.*, Int. J. Cancer 50:80-85 (1992); Posner *et al.*, Molecular Pharmacology 45:673-683 (1993); Rendu *et al.*, Biol. Pharmacology 44(5):881-888 (1992); Sauro and Thomas, Life Sciences 53:371-376 (1993); Sauro and Thomas, J. Pharm. and Experimental Therapeutics 267(3):119-1125 (1993); Wolbring *et al.*, J. Biol. Chem. 269(36):22470-22472 (1994); and Yoneda *et al.*, Cancer Research 51:4430-4435 (1991); all of which are incorporated herein by reference in their entirety, including any drawings.

Other compounds that could be used as modulators include oxindolinones such as those described in U.S. patent application Serial No. 08/702,232 filed August 23, 1996, incorporated herein by reference in its entirety, including any drawings.

VII. Biological Significance, Applications and Clinical Relevance of Novel Protein
5 Kinases

For each protein kinase in this application, we provide a classification of the protein class and family to which it belongs, a summary of non-catalytic protein motifs, a profile of its expression in several hundred tissue and cell sources, and a chromosomal location. This information can be used to suggest potential function, regulation or
10 therapeutic utility for each of the proteins.

The kinase classification and protein domains often reflect pathways, cellular roles, or mechanisms of up- or down-stream regulation. Also disease-relevant genes often occur in families of related genes. For example if one member of a kinase family functions as an oncogene, a tumor suppressor, or has been found to be disrupted in an immune,
15 neurologic, cardiovascular, or metabolic disorder, frequently other family members may play a related role.

The expression analysis organizes kinases into groups that are transcriptionally upregulated in tumors and those that are more restricted to specific tumor types such as melanoma or prostate. This analysis also identifies genes that are regulated in a cell cycle
20 dependent manner, and are therefore likely to be involved in maintaining cell cycle checkpoints, entry, progression, or exit from mitosis, oversee DNA repair, or are involved in cell proliferation and genome stability. Expression data also can identify genes expressed in endothelial sources or other tissues that suggest a role in angiogenesis, thereby implicating them as targets for control of diseases that have an angiogenic
25 component, such as cancer, endometriosis, retinopathy and macular degeneration, and various ischemic or vascular pathologies. A proteins' role in cell survival can also be suggested based on restricted expression in cells subjected to external stress such as oxidative damage, hypoxia, drugs such as cisplatinum, or irradiation. Metastases-associated genes can be implicated when expression is restricted to invading regions of a
30 tumor, or is only seen in local or distant metastases compared to the primary tumor, or when a gene is upregulated during cell culture models of invasion, migration, or motility.

Chromosomal location can identify candidate targets for a tumor amplicon or a tumor-suppressor locus. Summaries of prevalent tumor amplicons are available in the literature, and can identify tumor types to experimentally be confirmed to contain amplified copies of a kinase gene which localizes to an adjacent region.

5 Based on these criteria several kinases immediately stand out as being of potential therapeutic relevance. The protein kinases can be divided into the following disease-relevant categories (nucleotide Seq ID #s in parentheses):

Tumor associated: Mok (SEQ ID NO:57), EPK2, AA316804 (SEQ ID NO:11), AA435956 (SEQ ID NO:48), AA278842 (SEQ ID NO:88), AA599286 (SEQ ID NO:89), AA826850 (SEQ ID NO:3), HRI (SEQ ID NO:73), MLK4 AA232253 (SEQ ID NO:82), AA883975 SGK 235 (SEQ ID NO:95), AA311714 (SEQ ID NO:101), MPSK1 (SEQ ID NO:110), R19609 (Seq ID111), AA383293 (SEQ ID NO:26).

Prostate-specific: AA234451 (SEQ ID NO:47), TSK4 (SEQ ID NO:93), RIP4 (SEQ ID NO:84), KIAA0965 (SEQ ID NO:8).

15 Oncogenic or proliferation associated: KIAA0781 (SEQ ID NO:38), AA789239 (SEQ ID NO:52), CCRK (SEQ ID NO:54), CLK4 (SEQ ID NO:55), H85389 (SEQ ID NO:97).

Neuronal restricted: CAMKKB (SEQ ID NO:66)

Hematopoietic expressed: PTK9L (SEQ ID NO:22), DRAK2 (SEQ ID NO:29), AI025291 (SEQ ID NO:94)

20 Angiogenic or endothelial expressed: DRAK1 (SEQ ID NO:31), MAK-V (SEQ ID NO:40), TRAD (SEQ ID NO:44), MOK (SEQ ID NO:57), AA08847 (SEQ ID NO:78), HGP_66444466 (SEQ ID NO:79), RSK4 (SEQ ID NO:16).

Cell cycle regulated: AA454060 (SEQ ID NO:45), KIAA0999 (Mitotic – SEQ ID NO:32), AA579641 (Mitotic – SEQ ID NO:60), AA305176 (Mitotic – SEQ ID NO:6), AA018361 (S1 phase – SEQ ID NO:100).

VIII. Transgenic Animals.

A variety of methods are available for the production of transgenic animals associated with this invention. DNA can be injected into the pronucleus of a fertilized egg before fusion of the male and female pronuclei, or injected into the nucleus of an embryonic cell (e.g., the nucleus of a two-cell embryo) following the initiation of cell division (Brinster *et al.*, Proc. Nat. Acad. Sci. USA 82: 4438-4442, 1985). Embryos can

be infected with viruses, especially retroviruses, modified to carry inorganic-ion receptor nucleotide sequences of the invention.

Pluripotent stem cells derived from the inner cell mass of the embryo and stabilized in culture can be manipulated in culture to incorporate nucleotide sequences of the invention. A transgenic animal can be produced from such cells through implantation into a blastocyst that is implanted into a foster mother and allowed to come to term. Animals suitable for transgenic experiments can be obtained from standard commercial sources such as Charles River (Wilmington, MA), Taconic (Germantown, NY), Harlan Sprague Dawley (Indianapolis, IN), etc.

The procedures for manipulation of the rodent embryo and for microinjection of DNA into the pronucleus of the zygote are well known to those of ordinary skill in the art (Hogan *et al.*, *supra*). Microinjection procedures for fish, amphibian eggs and birds are detailed in Houdebine and Chourrout (Experientia 47: 897-905, 1991). Other procedures for introduction of DNA into tissues of animals are described in U.S. Patent No., 4,945,050 (Sanford *et al.*, July 30, 1990).

By way of example only, to prepare a transgenic mouse, female mice are induced to superovulate. Females are placed with males, and the mated females are sacrificed by CO₂ asphyxiation or cervical dislocation and embryos are recovered from excised oviducts. Surrounding cumulus cells are removed. Pronuclear embryos are then washed and stored until the time of injection. Randomly cycling adult female mice are paired with vasectomized males. Recipient females are mated at the same time as donor females. Embryos then are transferred surgically. The procedure for generating transgenic rats is similar to that of mice (Hammer *et al.*, Cell 63:1099-1112, 1990).

Methods for the culturing of embryonic stem (ES) cells and the subsequent production of transgenic animals by the introduction of DNA into ES cells using methods such as electroporation, calcium phosphate/DNA precipitation and direct injection also are well known to those of ordinary skill in the art (Teratocarcinomas and Embryonic Stem Cells, A Practical Approach, E.J. Robertson, ed., IRL Press, 1987).

In cases involving random gene integration, a clone containing the sequence(s) of the invention is co-transfected with a gene encoding resistance. Alternatively, the gene encoding neomycin resistance is physically linked to the sequence(s) of the invention.

Transfection and isolation of desired clones are carried out by any one of several methods well known to those of ordinary skill in the art (E.J. Robertson, *supra*).

DNA molecules introduced into ES cells can also be integrated into the chromosome through the process of homologous recombination (Capecchi, Science 244: 1288-1292, 1989). Methods for positive selection of the recombination event (*i.e.*, neo resistance) and dual positive-negative selection (*i.e.*, neo resistance and gancyclovir resistance) and the subsequent identification of the desired clones by PCR have been described by Capecchi, *supra* and Joyner *et al.* (Nature 338: 153-156, 1989), the teachings of which are incorporated herein in their entirety including any drawings. The final phase of the procedure is to inject targeted ES cells into blastocysts and to transfer the blastocysts into pseudopregnant females. The resulting chimeric animals are bred and the offspring are analyzed by Southern blotting to identify individuals that carry the transgene. Procedures for the production of non-rodent mammals and other animals have been discussed by others (Houdebine and Chourrout, *supra*; Pursel *et al.*, Science 244:1281-1288, 1989; and Simms *et al.*, Bio/Technology 6:179-183, 1988).

Thus, the invention provides transgenic, nonhuman mammals containing a transgene encoding a kinase of the invention or a gene effecting the expression of the kinase. Such transgenic nonhuman mammals are particularly useful as an *in vivo* test system for studying the effects of introduction of a kinase, or regulating the expression of a kinase (*i.e.*, through the introduction of additional genes, antisense nucleic acids, or ribozymes).

A "transgenic animal" is an animal having cells that contain DNA which has been artificially inserted into a cell, which DNA becomes part of the genome of the animal which develops from that cell. Preferred transgenic animals are primates, mice, rats, cows, pigs, horses, goats, sheep, dogs and cats. The transgenic DNA may encode human STE20-related kinases. Native expression in an animal may be reduced by providing an amount of anti-sense RNA or DNA effective to reduce expression of the receptor.

IX. Gene Therapy

Protein kinases of the invention, or their genetic sequences will also be useful in gene therapy (reviewed in Miller, Nature 357:455-460, 1992). Miller states that advances have resulted in practical approaches to human gene therapy that have demonstrated

positive initial results. The basic science of gene therapy is described in Mulligan (Science 260:926-931, 1993).

In one preferred embodiment, an expression vector containing protein kinase coding sequence is inserted into cells, the cells are grown *in vitro*, and then are infused in large numbers into patients. In another preferred embodiment, a DNA segment containing a promoter of choice (for example a strong promoter) is transferred into cells containing an endogenous gene encoding kinases of the invention in such a manner that the promoter segment enhances expression of the endogenous kinase gene (for example, the promoter segment is transferred to the cell such that it becomes directly linked to the endogenous kinase gene).

The gene therapy may involve the use of an adenovirus containing kinase cDNA targeted to a tumor, systemic kinase increase by implantation of engineered cells, injection with kinase-encoding virus, or injection of naked kinase DNA into appropriate tissues.

Target cell populations may be modified by introducing altered forms of one or more components of the protein complexes in order to modulate the activity of such complexes. For example, by reducing or inhibiting a complex component activity within target cells, an abnormal signal transduction event(s) leading to a condition may be decreased, inhibited, or reversed. Deletion or missense mutants of a component, that retain the ability to interact with other components of the protein complexes but cannot function in signal transduction may be used to inhibit an abnormal, deleterious signal transduction event.

Expression vectors derived from viruses such as retroviruses, vaccinia virus, adenovirus, adeno-associated virus, herpes viruses, several RNA viruses, or bovine papilloma virus, may be used for delivery of nucleotide sequences (*e.g.*, cDNA) encoding recombinant kinase of the invention protein into the targeted cell population (*e.g.*, tumor cells). Methods which are well known to those skilled in the art can be used to construct recombinant viral vectors containing coding sequences (Maniatis *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory, N.Y., 1989; Ausubel *et al.*, Current Protocols in Molecular Biology, Greene Publishing Associates and Wiley Interscience, N.Y., 1989). Alternatively, recombinant nucleic acid molecules encoding protein sequences can be used as naked DNA or in a reconstituted system *e.g.*, liposomes or other lipid systems for delivery to target cells (*e.g.*, Felgner *et al.*, Nature 337:387-8,

1989). Several other methods for the direct transfer of plasmid DNA into cells exist for use in human gene therapy and involve targeting the DNA to receptors on cells by complexing the plasmid DNA to proteins (Miller, *supra*).

5 In its simplest form, gene transfer can be performed by simply injecting minute amounts of DNA into the nucleus of a cell, through a process of microinjection (Capecchi, Cell 22:479-88, 1980). Once recombinant genes are introduced into a cell, they can be recognized by the cell's normal mechanisms for transcription and translation, and a gene product will be expressed. Other methods have also been attempted for introducing DNA into larger numbers of cells. These methods include: transfection, wherein DNA is
10 precipitated with CaPO_4 and taken into cells by pinocytosis (Chen *et al.*, Mol. Cell Biol. 7:2745-52, 1987); electroporation, wherein cells are exposed to large voltage pulses to introduce holes into the membrane (Chu *et al.*, Nucleic Acids Res. 15:1311-26, 1987); lipofection/liposome fusion, wherein DNA is packaged into lipophilic vesicles which fuse with a target cell (Felgner *et al.*, Proc. Natl. Acad. Sci. USA. 84:7413-7417, 1987); and
15 particle bombardment using DNA bound to small projectiles (Yang *et al.*, Proc. Natl. Acad. Sci. 87:9568-9572, 1990). Another method for introducing DNA into cells is to couple the DNA to chemically modified proteins.

It has also been shown that adenovirus proteins are capable of destabilizing endosomes and enhancing the uptake of DNA into cells. The admixture of adenovirus to
20 solutions containing DNA complexes, or the binding of DNA to polylysine covalently attached to adenovirus using protein crosslinking agents substantially improves the uptake and expression of the recombinant gene (Curiel *et al.*, Am. J. Respir. Cell. Mol. Biol., 6:247-52, 1992).

As used herein "gene transfer" means the process of introducing a foreign nucleic
25 acid molecule into a cell. Gene transfer is commonly performed to enable the expression of a particular product encoded by the gene. The product may include a protein, polypeptide, anti-sense DNA or RNA, or enzymatically active RNA. Gene transfer can be performed in cultured cells or by direct administration into animals. Generally gene transfer involves the process of nucleic acid contact with a target cell by non-specific or
30 receptor mediated interactions, uptake of nucleic acid into the cell through the membrane or by endocytosis, and release of nucleic acid into the cytoplasm from the plasma membrane or endosome. Expression may require, in addition, movement of the nucleic

acid into the nucleus of the cell and binding to appropriate nuclear factors for transcription.

As used herein "gene therapy" is a form of gene transfer and is included within the definition of gene transfer as used herein and specifically refers to gene transfer to express a therapeutic product from a cell *in vivo* or *in vitro*. Gene transfer can be performed *ex vivo* on cells which are then transplanted into a patient, or can be performed by direct administration of the nucleic acid or nucleic acid-protein complex into the patient.

In another preferred embodiment, a vector having nucleic acid sequences encoding a protein kinase polypeptide of the invention is provided in which the nucleic acid sequence is expressed only in specific tissue. Methods of achieving tissue-specific gene expression are set forth in International Publication No. WO 93/09236, filed November 3, 1992 and published May 13, 1993.

In all of the preceding vectors set forth above, a further aspect of the invention is that the nucleic acid sequence contained in the vector may include additions, deletions or modifications to some or all of the sequence of the nucleic acid, as defined above.

In another preferred embodiment, a method of gene replacement is set forth. "Gene replacement" as used herein means supplying a nucleic acid sequence which is capable of being expressed *in vivo* in an animal and thereby providing or augmenting the function of an endogenous gene that is missing or defective in the animal.

X. Administration of Substances

Methods of determining the dosages of compounds to be administered to a patient and modes of administering compounds to an organism are disclosed in U.S. Application Serial No. 08/702,282, filed August 23, 1996 and International patent publication number WO 96/22976, published August 1 1996, both of which are incorporated herein by reference in their entirety, including any drawings, figures, or tables. Those skilled in the art will appreciate that such descriptions are applicable to the present invention and can be easily adapted to it.

The proper dosage depends on various factors such as the type of disease being treated, the particular composition being used, and the size and physiological condition of the patient. Therapeutically effective doses for the compounds described herein can be estimated initially from cell culture and animal models. For example, a dose can be formulated in animal models to achieve a circulating concentration range that initially

takes into account the IC_{50} as determined in cell culture assays. The animal model data can be used to more accurately determine useful doses in humans.

Plasma half-life and biodistribution of the drug and metabolites in the plasma, tumors, and major organs can be also be determined to facilitate the selection of drugs most appropriate to inhibit a disorder. Such measurements can be carried out. For example, HPLC analysis can be performed on the plasma of animals treated with the drug and the location of radiolabeled compounds can be determined using detection methods such as X-ray, CAT scan, and MRI. Compounds that show potent inhibitory activity in the screening assays, but have poor pharmacokinetic characteristics, can be optimized by altering the chemical structure and retesting. In this regard, compounds displaying good pharmacokinetic characteristics can be used as a model.

Toxicity studies can also be carried out by measuring the blood cell composition. For example, toxicity studies can be carried out in a suitable animal model as follows: 1) the compound is administered to mice (an untreated control mouse should also be used); 2) blood samples are periodically obtained via the tail vein from one mouse in each treatment group; and 3) the samples are analyzed for red and white blood cell counts, blood cell composition, and the percent of lymphocytes versus polymorphonuclear cells. A comparison of results for each dosing regime with the controls indicates if toxicity is present.

At the termination of each toxicity study, further studies can be carried out by sacrificing the animals (preferably, in accordance with the American Veterinary Medical Association guidelines Report of the American Veterinary Medical Assoc. Panel on Euthanasia, *Journal of American Veterinary Medical Assoc.*, 202:229-249, 1993). Representative animals from each treatment group can then be examined by gross necropsy for immediate evidence of metastasis, unusual illness, or toxicity. Gross abnormalities in tissue are noted, and tissues are examined histologically. Compounds causing a reduction in body weight or blood components are less preferred, as are compounds having an adverse effect on major organs. In general, the greater the adverse effect the less preferred the compound.

For the treatment of cancers the expected daily dose of a hydrophobic pharmaceutical agent is between 1 to 500 mg/day, preferably 1 to 250 mg/day, and most preferably 1 to 50 mg/day. Drugs can be delivered less frequently provided plasma levels of the active moiety are sufficient to maintain therapeutic effectiveness.

5 Plasma levels should reflect the potency of the drug. Generally, the more potent the compound the lower the plasma levels necessary to achieve efficacy.

EXAMPLES

10 The examples below are not limiting and are merely representative of various aspects and features of the present invention. The examples below demonstrate the isolation and characterization of the protein kinases of the invention.

EXAMPLE 1: Isolation of cDNA clones Encoding Novel Mammalian Protein Kinases Materials and Methods Identification from cDNA databases and isolation of clones encoding novel protein kinases

15 Novel kinases were identified from the public EST databases using a Hidden Markov model, abbreviated HMM (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. 1994. Hidden Markov models in computational biology: Applications to protein modeling. *J. Mol. Biol.*, 235:1501-1531). The model was built with 70 mammalian and yeast kinase catalytic domain sequences. These sequences were chosen from a comprehensive collection of kinases such that no two sequences had more than 50% sequence identity. ESTs were translated in six open reading frames and were searched against the model. ESTs that had a score of at least 10 against the HMM were
25 then masked for repetitive sequences and vectors and were clustered using MSA. The resulting contigs were searched against known kinases to identify EST clones that encode novel kinases.

30 Approximately 40% of the ESTs encoding potentially novel kinases did not correspond to the correct EST upon sequence analysis. Most of these discrepancies were resolved by ordering additional clones, however, 14 remained unavailable. These 14 ESTs were amplified from a variety of single-stranded cDNA sources with primers derived from the corresponding EST entry as shown on Table 5. The PCR product was subcloned into a bluescript vector, digested to confirm the presence of a correct size insert and sequenced. Full sequencing of EST and PCR was carried out using a cycle sequencing Big-dye kit

with AmpliTaq DNA Polymerase, FS (ABI, Foster City, CA). Sequencing reaction products were run on an ABI Prism 377 DNA Sequencer.

Table 5: Primers used to clone PCR products corresponding to novel kinases

	ID#	ID#	Parent	5' primer	3' primer
sp	na	aa	Sequence	Sequence*	Sequence*
H	33	153	2R22-5-11	GAGATCGRNTTYAARGA RTTYGA	TGTCACNCCNAGNSWCCAN AYRTT
M	81	200	5R57_10_2_ m TESK2_m	GCTGCTGGACAGTGACT TGTATTT	GAAAGCAAAGCCTTCACAC CTT
H	67	187	5R69_17_2_h	CTCTCACCTCAGGAACT GG	GCTTGCGGATCTTCTCA
H	46	166	SGK309_h	GACATCCTGCCGGCCAA CTACG	CGGCCCTGGAGCTGCATCA CTA
M	67	228	5R72_16_2_h	TGCGCGACACCATTGAC CAG	CTCAGGGCTTACATACAGA G
H	45	165	5R72_8_2_h	AAAGGAGAACTACATT TGAAAAT	CTTCATCATCTCTAATACAT TGTTGG
H	41	161	Z36720	CAAATTAAGATCATTGA CTTTGGG	GGAAACAAAGTCCTTGGCC TC
H	115	234	AL031652 - Pak6	GTGGACATCTGGTCCCT CG	GTAGGTCCTTCACTCTTGG AG

- degenerate oligonucleotide residue designation:

5 N= A,C,G or T

R= A or G

Y= C or T

S = C or G

W= A or T

10

Full-length sequence extension of protein kinases using cDNA and genomic databases

Extension of partial cDNA sequences to encompass the full-length open-reading frame was carried out by iterative blastn searching of the cDNA databases listed in Table 6. All blastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1. The gapped blast algorithm is described in: (Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schaffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and

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PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402).

Table 6. Databases used for cDNA-based sequence extensions

Database	Database Date
LifeGold templates	Feb 2000
LifeGold compseqs	Feb 2000
LifeGold compseqs	Mar 2000
LifeGold compseqs	Apr 2000
LifeGold fl	Feb 2000
LifeGold flft	Apr 2000
NCBI human Ests	May 2000
NCBI murine Ests	May 2000
NCBI nonredundant	May 2000

5

Extension of partial cDNA sequences to encompass the full-length open-reading frame was also carried out by iterative searches of genomic databases. Three methods were used. The first method made use of the Smith-Waterman algorithm to carry out protein-protein searches of the closest homologue or orthologue to the partial kinase. The target databases consisted of Genescan and open-reading frame (ORF) predictions of all human genomic sequence derived from the human genome project (HGP) as well as from Celera. The complete set of genomic databases searched is shown in Table 7 below. Genomic sequences encoding potential extensions were further assessed by blastp analysis against the NCBI nonredundant to confirm the novelty of the hit. The extending genomic sequences were incorporated into the cDNA sequence after removal of potential introns using the Seqman program from DNASTar. The default parameters used for Smith-Waterman searches were as shown next. Matrix: blosum 62; gap-opening penalty: 12; gap extension penalty: 2. Genescan predictions were made using the Genescan program as detailed in (Chris Burge and Sam Karlin "Prediction of Complete Gene Structures in Human Genomic DNA", JMB (1997) 268(1):78-94). ORF predictions from genomic DNA were made using a standard 6-frame translation.

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The second method for genomic sequence-based extensions made use of tBlastn searches of the homologue or orthologue to the partial kinase against the cDNA databases listed in Table 7. The recognition of significant hits in these databases made possible to identify bridging partial cDNA clones. The iterative application of the two methods made possible the assemblage of the virtual full-length sequence for a large number of the kinases presented in this application. All tblastn searches were conducted using a blosum62 matrix, a penalty for a nucleotide mismatch of -3 and reward for a nucleotide match of 1.

The last method for defining cDNA extensions from genomic sequence used iterative searches of genomic databases through the Genescan program to predict exon splicing and the Genewise program (<http://www.sanger.ac.uk/Software/Wise2/>) to predict potential ORFs based on homology to the closest orthologue/homologue.

Table 7. Databases used for genomic-based sequence extensions

Database	Number of entries	Database Date
Celera v. 1-5	5,306,158	Jan 19/00
Celera v. 6-10	4,209,980	Mar 24/00
Celera v. 11-14	7,222,425	Apr 24/00
Celera v. 15	243,044	May 14/00
HGP all Genescan	25,885	Apr 04/00
HGP; Phase 0	4,944	May 04/00
HGP; Phase 1	28,478	May 05/00
HGP; Phase 2	1,508	May 04/00
HGP; Phase 3	9,971	May 05/00

Virtual Extensions

Human AA826850 (SEQ ID NO: 3, SEQ ID NO:124)

Blastn analysis of the partial AA826850 sequence revealed an extension to encompass the complete ORF in the Incyte EST 238299.1. A frame-shift correction at position 595 of this EST (marked by X in NA sequence) generated an uninterrupted ORF.

Human AA960957 (SEQ ID NO: 4, SEQ ID NO:125)

Since the initial filing of this application, the partial AA960957 sequence appeared in the public database as the full-length gene for a protein kinase encoded by a gene that maps adjacent to the evc (AJ250839) (ellis-van creveld syndrome and weyers acrodermal dysostosis) gene from 4p16.1.

5 Human 5R79-46-1_h (SEQ ID NO: 5, SEQ ID NO:126)

Blastn analysis of the partial 5R79-46-1 sequence revealed an extension to encompass the complete ORF in the Incyte EST 463894.6. Since the initial filing of this application, the full-length virtual 5R79-46-1 appeared in the public database as the full-length gene for the TANK-binding kinase (TBK1) (Pomerantz, J.L. and Baltimore, D.
10 (1999) EMBO J. 18 (23), 6694-6704). TBK1 participates in NF- κ B activation through the formation of a signaling complex with TRAF2 and TANK.

Human AA305176 (SEQ ID NO: 6, SEQ ID NO:127)

Blastn analysis of the partial AA305176 sequence revealed an extension to encompass the complete ORF in the Incyte EST 220937.1.

15 Human AA256100 (SEQ ID NO: 8, SEQ ID NO:129)

Blastn analysis of the partial AA256100 sequence revealed an extension to encompass the complete ORF through the assembly of three partial clones: Incyte EST 480815.6, KIAA0965 (BAA76809) and AA256100.

Human AA210825 (SEQ ID NO: 9, SEQ ID NO: 130)

20 Blastn analysis of the partial AA210825 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte EST 014721.7, and the NCBI EST's AW01158 and AA210825. An insertion of two "N's" at positions 1915 and 1916 generated an uninterrupted ORF. Blastx analysis indicated the possibility of a start Met in the range of 400-450 nucleotides (i.e. compared to the closest
25 homolog, human PKCmu (CAA53384.1). However, no Met was found in this region; rather ORF ends in an in-frame stop preceded by the sequence "RGL LAPGDPPCPPNPAPATPPSSRLPTLFSNFCDS". It is possible that part of the sequence covered by nucleotide positions 1-400 derived from AW01158 comes from an intron, explaining the absence of a start Met.

30 Human AA127299 (SEQ ID NO:10, SEQ ID NO:131)

No entries in the database extended this sequence. The 1684 bp insert of this EST contains a 1369 bp intron at the 3' end. Blastx and SW analysis of the 315 bp coding

region revealed homology to the extracatalytic C2 domain of PKC. This EST, may or may not encode a kinase.

Human AA316804 (SEQ ID NO:11, SEQ ID NO:132)

5 Since the initial filing of this application, the partial AA316804 sequence appeared in the public database as the full-length gene for the PKC family protein kinase EPK2 or PKCnu (AB015982).

Human H19102 (SEQ ID NO:14, SEQ ID NO:135)

10 Genewise and Genescan analyses of the partial H19102 sequence revealed an extension from the HGP phase 3 contig 3810672 to encompass the complete catalytic domain of this EST. Blastn analysis against the non-redundant database revealed that this gene is found in the cosmid AC005726 from chromosome 17. H19102 may encode a dual catalytic kinase given the homology to S6 kinase. Analysis of genomic sequence upstream of the 5' end of H19102 revealed a non-kinase gene oriented in the same polarity as H19102 suggestive of the start Met for H19102 being close to the 5' end of the H19102
15 sequence. From this analysis it is deduced that the second catalytic domain of H19102, if present, is most likely located within the 47334-185,215 bp region of the genomic sequence of AC005726.

Human AA476563 (SEQ ID NO:15, SEQ ID NO:136)

20 Since the initial filing of this application, the partial AA476563 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KC1 (NM_012424) (Zhang, H. et al Genomics (1999) 61, 314-318), which is an S6 kinase mapping to 12q12-q13.1.

Human AA626690 (SEQ ID NO:16, SEQ ID NO:137)

25 Since the initial filing of this application, the partial AA626690 sequence appeared in the public database as the full-length gene for the protein kinase RPS6KA6 (AF184965) (Yntema, H.G et al (1999) Genomics 62, 332-343), an S6 kinase commonly deleted in patients with complex X-linked (Xq21.1) mental retardation.

Human AI215680 (SEQ ID NO: 17, SEQ ID NO:138)

30 Since the initial filing of this application, the partial AI215680 sequence appeared in the public database as the full-length gene encoding a hypothetical protein (AAD30182) from the locus AC006530.4 from chromosome 14.

Human AA887783 (SEQ ID NO:21, SEQ ID NO:142)

Blastn analysis of the partial AA887783 sequence revealed an extension to encompass the nearly complete ORF through the assembly of three partial clones: Incyte 415390R6 and the NCBI EST's AA887783 and N94726. Since the initial filing of this application, the nearly full-length virtual AA887783 sequence appeared in the public database as the full-length gene encoding SGK3 (AF169035), a serum- and glucocorticoid-induced protein kinase (Kobayashi, T. et al (1999) Biochemical J. 344, 189-197.

Human R47805 (SEQ ID NO:22, SEQ ID NO:143)

A cDNA clone encoding the full-length ORF of R47805 was isolated using R47805 as a screening probe. A full-length form for R47805 has also appeared in the public database as

PTK9L (NM_007284), an A6-related protein kinase.

Human H60215 (SEQ ID NO:23, SEQ ID NO:144)

Blastn analysis of the partial H60215 sequence revealed an extension to encompass the complete ORF in the public EST AI275726. This was confirmed through the full insert sequencing of this EST (2,310 bp) which corresponds to the sequence under SEQ ID NO:144.

A different stop codon was predicted for AI275726 compared to H60215 due to a single nucleotide insertion at position 1586 in AI275726. Evidence for the extra nucleotide comes from EST AI191922.

SGK324_h orthologue of W30246_m (SEQ ID NO:24, SEQ ID NO:145)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding to the human orthologue of murine W30246. Exons predicted from the following sequences were used for contig construction: Celera 17000189645083, 17000057549105 and 11000501939981; Incyte142404.1, HGP_7249119, Incyte 7196489H1, Celera 11000501939981, 17000028165594; Incyte 7249119_3, Celera 17000035772368, 11000502081575 and 17000140274329. The latter Celera sequence provides the N-terminus.

Human AA383293 (SEQ ID NO:26, SEQ ID NO:147)

Blastn, blastx and Smith-Waterman analyses of genomic databases revealed an extension to encompass the complete ORF corresponding for AA383293. Exons predicted from the following sequences were used for contig construction: (numbers in parenthesis

refer to the aa sequence of the closest homolog (RU2S, NP_057440) used for the Smith-Waterman query): N-term from Incyte 6010175_2 (14-97), Incyte 6981981 (134-184) 7596749 (186-232) Celera 17000020789545 (243-301) CAB75619.1 (310-341)--(56-145 DCX homology) 6010175_2 , Celera 17000030058129 (241-262 DCX homology).

5 Human AA021445 (SEQ ID NO:32, SEQ ID NO:152)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. Contig reconstruction was as follows: nucleotides 1-802 from KIAA0999 (AB023216); nucleotides 803-4321 from full-insert sequence of AA021445. A pairwise alignment between the AA021445 and KIAA0999 revealed three
10 inserts in the extracatalytic C-terminus of 48, 48 and 161 aminoacids. In addition, both AA021445 and KIAA0999 have 15 copies of a CAG repeat. Trinucleotide repeats are often found in genes that linked to neurodegenerative diseases.

Human 2R22-55-1 (SEQ ID NO:33, SEQ ID NO:153)

15 Blastn analysis revealed an extension in the Incyte EST clone 321074.1 to encompass the complete ORF corresponding to 2R22-55-1.

Human orthologue of AA544838_m (SEQ ID NO:36, SEQ ID NO:156)

tBlastn analysis identified the partial human KIAA0135 (U79240) clone as the human orthologue of murine AA544838. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from
20 Incyte406786.5, KFZp430051 and KIAA0135 (U79240).

Human orthologue of AI785735_m (SEQ ID NO:38, SEQ ID NO:158)

tBlastn analysis identified the partial human KIAA0781 (AB018324) clone as the human orthologue of murine AI785735. Blastn revealed an extension KIAA0135_h (U79240) to encompass the complete ORF. The full ORF was reconstructed from Incyte
25 986123.37 KIAA0781 (AB018324).

Human AA207220 (SEQ ID NO: 39, SEQ ID NO:159)

Blastn analysis revealed an extension to encompass the nearly complete ORF corresponding for AA021445. The full ORF was reconstructed from Incyte 402740.1 and AA207220. Frame corrections: deletion of 441 and 595 over Inc402740.1 seq based on
30 blastx to keep frame open; two n insertions 940, 941 over AA207220 to keep frame open.

Human AA426580 (SEQ ID NO:40, SEQ ID NO:160)

Since the initial filing of this application, the partial AA426580 sequence appeared in the public database as the full-length gene encoding MAK-V (AJ271722) from chromosome 21q22.1.

Human 5R79-54-1 (SEQ ID NO: 41, SEQ ID NO:161)

Genewise and Genescan analyses of the partial 5R79-54-1 sequence revealed an extension from genomic sequence to encode the full ORF for 5R79-54-1.

Human orthologue of AA542015_m (SEQ ID NO: 42, SEQ ID NO:162)

tBlastn analysis identified KIAA1297 (AB037718). Blastn extended the KIAA1297 sequence to provide the C-terminus through the Incyte 224074.1 EST. The partial ORF consists of a dual catalytic domain flanked by 6 Ig domains and 2 fibronectin repeats. Based on homology to the bt drosophila protein (AAF59316.1), the human form of AA542015 is expected to be missing 16 Ig domains.

Human R19772 (SEQ ID NO:44, SEQ ID NO:164)

The full-length ORF for R19772 was isolated by screening a cDNA library using a probe derived from R19772. Since the initial filing of this application, the R19772 sequence appeared in the public database as the full-length gene encoding Trio (Duet) (AB011422). CDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 8. Isoforms for R19772

Kestrl Name	Kestrl AA Acc #	Isoform type	Source	Description*
Trad (Duet)	R19772	B	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762
		C	Skeletal muscle	Deletion of K at 124
				Deletion of Q at 616
				Substitution of E for G at 762

				Deletion of 32 aa (160-191)
		D	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)
		E	Lung tumor	Deletion of Q at 616
				Deletion of 32 aa (160-191)

* reference amino acid position are with respect to sequence of Trad (AB011422)

Human AA435956 (SEQ ID NO:48, SEQ ID NO:168)

5 Blastn analysis revealed an extension to encompass the nearly complete catalytic region of AA435956. 5' end sequence extension was provided by genomic locus AC007242.3_h (range 44880-43801). Based on blastx analysis, the extended sequence encodes is full-length at the C-terminus.

Human AA397553 (SEQ ID NO: 51, SEQ ID NO:171)

10 Since the initial filing of this application, the partial AA397553 sequence appeared in the public database as the full-length gene encoding CRK7 (AF227198), a novel CDC2-related protein kinase that colocalizes with interchromatin granule clusters.

Human AA789239 (SEQ ID NO: 52, SEQ ID NO:172)

15 Since the initial filing of this application, the partial AA789239 sequence appeared in the public database as the full-length gene encoding NKIAMRE (AF130372), a novel kinase deleted in human leukemia.

Human AA631990 (SEQ ID NO:55, SEQ ID NO:175)

20 Blastn analysis revealed an extension to encompass the full-length ORF for AA631990. The full ORF was reconstructed from 253847.5 and AA631990 and AA207220. Frame corrections: delete 1 C at 1380, delete 2N's at 2033/2034.

Human AA557536 (SEQ ID NO:56, SEQ ID NO:176)

25 Blastn analysis revealed an extension to encompass full-length ORF for AA557536. The full ORF was reconstructed from AA557536, celera 11000504061899 and the Incyte 097089.1 EST. An 85bp intron was removed from AA557536.

Human N34132 (SEQ ID NO: 63, SEQ ID NO:183)

Full sequencing of EST N34132 (1.3 kb) confirmed that this cDNA encodes a novel NEK-subfamily kinase. Blast analysis against the EST database showed that four

EST sequences (AA283140, AA283140, AA282911 and N53011) extended the sequence of N34132 at the 3' end to form a 2.31 kb contig. Blast analysis of the new contig against the nonredundant public database showed that the N34132 extended contig overlapped (100% identity) over 228 bp at its 3' end with human KIAA0344 (AB002342), a 5,787 bp cDNA encoding a 1246 aa polypeptide. The 5' 790 bp of the KIAA0344 cDNA (encoding the 58 N-terminal protein sequence) were found to be divergent with respect to the extended 2.32 kb N34132 contig. Evidence that the extended N34132 contig (2.31 kb) and KIAA0344 (AB002342) belong to the same gene is the following. First, blast analysis of the nucleotide sequences for N34132 and KIAA0344 against the NR database confirmed that these cDNA's are transcribed from the same genomic locus defined by two overlapping BACs (AC004765 and AC004803) from chromosome 12p13.3. Second, full sequence determination of a PCR fragment amplified from single-stranded cDNA confirmed the junction between the extended N34132 contig and KIAA0344_h (AB002342). The 462 PCR product was amplified with primers CTCCTCAACAGACAGTGCAG (5' primer) and GACATTCTACTACTCGGTCTC (3' primer) designed from the N34132 extended contig and KIAA0344 sequences, respectively. The region of N34132 containing the start Met was isolated by PCR from a testis cDNA library (Clontech).

Human 5R69-17-2 (SEQ ID NO:67, SEQ ID NO:187)

The full-length ORF for 5R69-17-2 was isolated by screening a cDNA library using a probe derived from 5R69-17-2.

Human H85811 (SEQ ID NO:68, SEQ ID NO:188)

Tblastn, Smith-Waterman and blastn analyses using cDNA databases revealed an extension to encompass full-length ORF for H85811. The full ORF was reconstructed from Incyte ESTs 202971.8, 034583.3 and 034583.1 and public ESTs H85811 and AI570599.

Human R43524 (SEQ ID NO:73, SEQ ID NO:192)

Blastn analysis revealed an extension to encompass the complete catalytic region and the C-terminus of R43524. Since the initial filing of this application, the partial R43524 sequence appeared in the public database as the full-length gene encoding the heme-regulated initiation factor 2-alpha kinase (HRI) (AF181071).

Human AA088547 (SEQ ID NO:78, SEQ ID NO:197)

Genewise and Genescan analyses of genomic databases revealed an extension to encompass the complete ORF for AA088547.

Human orthologue of AA139478_m (SEQ ID NO:80, SEQ ID NO:199)

Tblastn identified the Incyte 211475.1 as the potential full-length human orthologue of murine AA139478

Human AA232253 (SEQ ID NO:82, SEQ ID NO:201)

The full-length ORF for AA232253 was isolated by screening a cDNA library using a probe derived from AA232253. Since the initial filing of this application, the AA232253 sequence appeared in the public database as the full-length gene encoding SLK (AB011422). SLK is a stress-regulated mixed lineage kinase-like protein that activation of Rac and induction of apoptosis. cDNA library screening revealed multiple isoforms for this gene which are summarized in the Table below.

Table 9. Isoforms for AA232253

Kestrl Name	Kestrl AA Acc #	Isoform type	Description*
MLK4	AA232253	MLK4	Substitution of C for W at 346
		MLK4B	Different Cterm (332-800); seq in MLK4B is as shown in *

* C-terminus specific to MLK4B

LPLAARMSEESYFESKTEESNSAEMSCQITATSN GEGHGMNPSLQAMMLMGFGDI
FSMNKAGAVMHSGMQINMQAKQNSS
KTTSKRRGKKVNMA LGFSDFDLSEGDDDDDDDGEEEDNDMDNSE

Human H97685 (SEQ ID NO:84, SEQ ID NO:203)

Blastn analysis revealed an extension to encompass the full-length ORF for H97685. The full ORF was reconstructed from Incyte 474824.1 and the public ESTs H97685 and M62021.

Human AI052250 (SEQ ID NO:87, SEQ ID NO:206)

Blastn analysis revealed an extension to encompass the full-length ORF for AI052250. The full ORF was reconstructed from Incyte 396868.1, the public partial cDNA FLJ10074 (minus intron) and the public ESTs and the public ESTs AI052250 and H97685, AI499220 and M62021.

5 Human AA278842 (SEQ ID NO:88, SEQ ID NO:206)

A nearly full-length cDNA (FL4F12) for AA278842 was isolated by screening a cDNA library using a probe derived from AA278842. A full-length virtual ORF was generated using FL4F12 and AA278842.

Human AA599286 (SEQ ID NO:89, SEQ ID NO:208)

10 Since the initial filing of this application, the partial AA599286 sequence appeared in the public database as a full-length ORF (AK000342).

Human AA425725 (SEQ ID NO:90, SEQ ID NO:209)

Since the initial filing of this application, the partial AA425725 sequence appeared in the public database as MSSK1, a serine kinase gene located from human chromosome Xq28.

15

Human SGK022 orthologue of AA060026_m (SEQ ID NO:91, SEQ ID NO:210)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed a potential human orthologue for murine AA060026. The full-length ORF for SGK022 was reconstructed from genomic locus AC022307.

20

Human AA399669 (SEQ ID NO:93, SEQ ID NO:212)

Blastn analysis revealed an extension to encompass the full-length ORF for AA399669. The full ORF was reconstructed as follows: sequence 1-1007 from AL136295.2; sequence1008-2319 from AA399669 and Incyte 428177.1.

Human AA883975 (SEQ ID NO:95, SEQ ID NO:214)

25

Genescan and Genewise analyses of the genomic databases revealed an extension for AA883975 to encompass the full-length ORF

Human AA905446 (SEQ ID NO:96, SEQ ID NO:215)

Tblastn, Smith-Waterman and blastn analyses of cDNA and genomic databases revealed an extension for AA905446 to encompass the full-length ORF. For the Smith-Waterman analysis murine STK22 (NP_033462) was used as the closest orthologue. Contig formation: range 162133-163687 from HGP_h 6921333_9; removed intron (146-893) predicted from blastx analysis.

30

Human H29974 (SEQ ID NO: 97 SEQ ID NO:216)

Blastn analysis revealed an extension to encompass a complete catalytic ORF for AA399669. The nearly full-length ORF was reconstructed using Incyte 213829.1 and H29974.

5 Human AA215311 (SEQ ID NO:99, SEQ ID NO:218)

Blastn analysis revealed an extension to encompass the full-length ORF for AA21531. The full ORF was reconstructed from Incyte 067584.1, 022456.1, AA215311 and the reverse complement of CPG_043208.

Human AA018361 (SEQ ID NO:100, SEQ ID NO:219)

10 The full-length ORF for AA018361 was isolated by screening a cDNA library using a probe derived from AA018361. This yielded clone Sug4-30. Clone Sug4-30, like multiple, independent cDNA clones contained a 181bp intron. The existence of intron-less RNA's was confirmed by a PCR reaction that generated a product that upon sequence analysis skipped the intron region. The full-length virtual ORF for AA018361 was
15 generated through a contig between AL117482 (seq 1-367) and the sequence for clone Sug4-30.

Human orthologue of AA396601_m (SEQ ID NO:106, SEQ ID NO:225)

tBlastn and Smith-Waterman analyses of genomic sequence revealed an extension to encompass the full catalytic region for the human orthologue of AA396601. The ORF
20 was reconstructed from Incyte 018653.9 (7261449H1, 6891740J1) and genomic sequence CPG_040010.

Human orthologue of AA671275_m (SEQ ID NO:108, SEQ ID NO:227)

Since the initial filing of this application, a potential human orthologue for murine AA671275 appeared in the public database as the full-length ORF for vaccinia related
25 kinase 3 (BAA90769).

Human H05721 (SEQ ID NO:111, SEQ ID NO:230)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for H05721.

Human AI086865 (SEQ ID NO:112, SEQ ID NO:231)

30 Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AI086865. The full-length ORF was reconstructed from Celera 17000102901516, Incyte 243269.1 and public AL1377531.

Human AA836348 (SEQ ID NO:113, SEQ ID NO:232)

Genescan and Genewise analyses of genomic sequence revealed an extension to encompass the full-length ORF for AA836348.

Human R86668 (SEQ ID NO:14, SEQ ID NO:233)

5 The full-length ORF for R86668 was isolated by screening a cDNA library using a probe derived from R86668. Since the initial filing of this application, the R8668 sequence appeared in the public database as the full-length gene mitogen-activated protein kinase kinase kinase 6 (MAP3K6) (NM_00467).

Human 2R41-9-4 (SEQ ID NO: 16, SEQ ID NO:235)

10 The full-length virtual ORF for 2R41-9-4 was generated using genomic sequence to provide the Nterminus for the partial ORF predicted from clone 2R41-9-4

Table 10. Sequences deleted from the provisional patent due to duplication with other genes in the patent

Prov. SEQ ID NO: (na)	Prov. SEQ ID NO: (aa)
160	196
213	214
215	216
122	126
119	123
148	184
4	20
7	23
205	206
14	30
15	31
35	56
42	63
51	72
44	65
77	91

78	92
79	93
80	94
157	193

Results

Table 1 documents the results from the analysis of the nucleic acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "ORF Start", "ORF End", "ORF Length" refer to the open reading frame range and length as calculated by standard nucleic acid translation programs such as MapDraw (DNASStar). "DNA Repeats" refers to regions of low complexity sequence or repetitive elements such as Alu, LINE, SINE, and LTR sequences. The chromosomal location (CHR localization) for 37 of the 110 novel protein kinases is shown on Table 1 (NA, not available). The methods for determining chromosomal position are outlined below, in Example 2.

Table 2 documents the results from the analysis of the amino acid sequence data. From left to right the data presented is as follows. "Gene name" refers to the EST or PCR fragment that defined the novel kinase. "Species" refers to the organism the sequence was derived from. "ID#" refers to the nucleic acid and amino acid sequence ID number designation from this patent. "Kinase family" and "Kinase group" refers to the protein kinase classification defined by sequence homology and based on previously established phylogenetic analysis [Hardie, G. and Hanks S. The Protein Kinase Book, Academic Press (1995) and Hunter T. and Plowman, G. Trends in Biochemical Sciences (1977) 22:18-22 and Plowman G.D. *et al.* (1999) Proc. Natl. Acad. Sci. 96:13603-13610)]. "nraa Score", "ID match aa", "Identity", "Similar", "nraa Match Acc#", "Description" refer to the data obtained using a Smith-Waterman search of the amino acid sequence against the non-

redundant protein database (Matrix: Pam100; gap open/extension penalties 14/1). "Kinase Domain Start", "Kinase Domain End", "Profile Start" and "Profile End" refer to data obtained using a Hidden-Markov Model to define catalytic range boundaries. The profile has a length of 261 amino acids, corresponding to the complete protein kinase catalytic domain. Proteins in which the profile recognizes a full length catalytic domain have a "Profile Start" of 1 and a "Profile End" of 261. The boundaries of the catalytic domain within the overall protein are noted in the "Kinase Domain Start" and "Kinase Domain End" columns.

The following abbreviations were used for kinases:

ASK	Apoptosis signal-regulating kinase
CaMK	Ca ²⁺ /calmodulin-dependent protein kinase
CCRK	Cell cycle-related kinase
CDK	Cyclin-dependent kinase
CK	Casein kinase
DAPK	Death-associated protein kinase
DM	myotonic dystrophy kinase
Dyrk	dual-specificity-tyrosine phosphorylating-regulated kinase
GAK	Cyclin G-associated kinase
GRK	G-protein coupled receptor
GuC	Guanylate cyclase
HIPK	Homeodomain-interacting protein
IRAK	Interleukin-1 receptor-associated kin
MAPK	Mitogen activated protein kinase
MAST	Micotubule-associated STK
MLCK	Myosin-light chain kinase
MLK	Mixed lineage kinase
NIMA	NimA-related protein kinase
PKA	cAMP-dependent protein kinase
RSK	Ribosomal protein S6 kinase
RTK	Receptor tyrosine kinase

SGK	Serum and glucocorticoid-regulated kinase
STK	serine threonine kinase
ULK	UNC-51-like kinase

The following abbreviations were used for species

H	Human
M	Murine
R	Rat
FV	Fowlpox virus
MT	<i>M. thermoautotrophicum</i>
CE	<i>Caenorhabditis elegans</i>
DM	<i>Drosophila melanogaster</i>
OS	<i>Oryza sativa</i>
SP	<i>Schizosaccharomyces pombe</i>
TP	<i>Tetrahymena pyriformis</i>
PI	<i>Petunia inflata</i>
NC	<i>Neurospora crassa</i>
MSV	<i>Medicago sativa</i>
MSV	Moloney murine sarcoma virus
SA	<i>Squalus acanthias</i>
CS	<i>Cucumis sativus</i>
GM	<i>Glycine max</i>
LL	<i>Lilium longiflorum</i>
TV	<i>Trichomonas vaginalis</i>
MP	<i>Mycoplasma pneumoniae</i>
DD	<i>Dictyostelium discoideum</i>
SC	<i>Saccharomyces cerevisiae</i>
MT	<i>Methanobacterium thermoautotrophicum</i>

Domain and Motif Identification

A Hidden Markov model (HMM) (Krogh, A., Brown, M., Mian, I. S., Sjolander, K., and Haussler, D. (1994). Hidden Markov models in computational biology: Applications to protein modeling. J. Mol. Biol., 235:1501-1531) was used to identify, both catalytic and extracatalytic domains. Table 4 shows extra-catalytic domains that were identified using the HMM program. Other domains such as coiled-coil and pest motifs were identified as described next.

Potential coiled-coil domains were identified using the COILS program (www.ch.embnet.org/software/COILS_form.html). The matrix used was MTIDK with windows of 14, 21, 28 amino acids. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region.

Protein sequences containing potential pest motifs were identified using the program PESTfind (www.at.embnet.org/embnet/tools/bio/PESTfind/). PEST regions in proteins are by definition sequences that tend to be rich in proline, glutamic or aspartic acid, arginine and histidine; they have been associated with increased protein turnover rates (Rogers S. *et al.* (1986) Science 234, 364-368. The algorithm defines PEST sequences as hydrophilic stretches of amino acids greater than or equal to 12 residues in length. Such regions contain at least one P, one E or D and one S or T. They are flanked by lysine (K), arginine (R) or histidine (H) residues, but positively charged residues are disallowed within the PEST sequence. PESTfind produces a score ranging from about -50 to +50. By definition, a score above zero denotes a possible PEST region; a value greater than +5 defines a high probability that there is a PEST domain.

Identification of potential coiled-coil domains and PEST domains in N34132

Potential coiled-coil domains were identified in N34132 (SEQ ID NO:183) using the COILS program. Only regions scoring 0.5 or higher were considered to have potential coiled-coil domain region. The amino acid positions within N34231 scoring for potential coil-coil regions are shown below.

Table 11 coiled-coil domains predicted for N34132

Coiled-coil Region	Amino acid range	Length (aa)
1	124-147	24
2	437-451	15
3	495-526	32
4	1,723-1,749	27

Potential PEST domains were identified in N34132 using PESTfind, a value greater than +5 defines a high probability that there is a PEST domain. The amino acid positions within N34132 scoring for potential PEST regions are shown below.

Table 12 Potential Pest domains identified in N34132

PEST Region	Score	Amino acid range	Amino Acid Length
1	+ 4.91	54-95	42
2	+11.4	537-570	34
3	+31.08	1293-1304	12
4	+10.15	1543-1565	23
5	+ 6.17	1698-1732	35

EXAMPLE 2. Chromosomal Localization of Novel Mammalian Protein Kinases

Materials and Methods

Several sources were used to find information about the chromosomal localization of each of the genes described in this patent. First, the accession number for the nucleic acid sequence was used to query the Unigene database. The site containing the Unigene search engine is: <http://www.ncbi.nlm.nih.gov/UniGene/Hs.Home.html>. Information on map position within the Unigene database is imported from several sources, including the Online Mendelian Inheritance in Man (OMIM, <http://www.ncbi.nlm.nih.gov/Omim/searchomim.html>), The Genome Database (<http://gdb.infobiogen.fr/gdb/simpleSearch.html>), and the Whitehead Institute human physical map (http://carbon.wi.mit.edu:8000/cgi-bin/contig/sts_info?database=release). For example, searching Unigene with W56561, an EST for a MAK-like kinase, the

following information is retrieved: Chr.14, D14S65-qTEL. The location of this gene on an "ideogram" of the cytogenetic map of chromosome 14 is also provided, showing that W56561 maps to the bottom of chromosome 14, between 14q31 and 14qTel. If Unigene has not mapped the EST, then the nucleic acid for the gene of interest is used as a query against databases, such as dbsts and htgs (described at http://www.ncbi.nlm.nih.gov/BLAST/blast_databases.html) containing sequences that have been mapped already. The nucleic acid sequence is searched using BLAST-2 at NCBI (<http://www.ncbi.nlm.nih.gov/cgi-bin/BLAST/nph-newblast>) and is used to query either dbsts or htgs. In addition to the Whitehead and GDB sites mentioned above, Stanford University maintains a useful site for chromosomal mapping from STS data (<http://www-shgc.stanford.edu/RH/rhserverformnew.html>). Matches in htgs are often resolved immediately because the genomic region hit is annotated in the htgs entry. If an exact match match is found (defined roughly as 99% identity over a region of about 100 base pairs or longer, excluding any repetitive sequence), then the mapped position of the entry in the database is assigned to the original kinase query. Once a cytogenetic region has been identified by one of these approaches, disease association is established by searching OMIM (see above for URL) with the cytogenetic location. OMIM maintains a searchable catalog of cytogenetic map locations organized by disease. A thorough search of available literature for the cytogenetic region is also made using Medline (<http://www.ncbi.nlm.nih.gov/PubMed/medline.html>). References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123.

Results

The chromosomal location for 37 of the 110 novel protein kinases is shown on Table 1. Three of the novel protein kinases were mapped to regions associated with cancer amplicons, as shown on this table. The regions were also cross-checked with the Mendelian Inheritance in Man database, which tracks genetic information for many human diseases, including cancer. References for association of the mapped sites with chromosomal abnormalities found in human cancer can be found in: Knuutila, *et al.*, Am J Pathol, 1998, 152:1107-1123. Association of these mapped regions with other diseases is

documented in the Online Mendelian Inheritance in Man (OMIM)
(<http://www.ncbi.nlm.nih.gov/htbin-post/Omim>).

EXAMPLE 3: Generation of Specific Immunoreagents

5 Materials and Methods

Peptide sequences to extra-catalytic regions of novel kinases are chosen which are not homologous to other known kinases based on a Smith Waterman homology search against the non-redundant protein database and predicted to be antigenic based on the DNASTar Protean program. These peptides are conjugated to KLH using Glutaraldehyde.

10 Rabbits are immunized with the KLH-peptide conjugates by four injections three weeks apart. The rabbits are bled ten and fourteen days following the third injection and bled out ten days after the fourth. The serum is checked against the peptide by ELISA.

Table 13. Peptides to be used as immunogens for raising antibodies

Clone Name	SEQ ID NO (aa)	Peptide Sequence	Amino Location
AA8256850	124	KSRDNSRDSSQSEND	339-353
		TEKLKRSQDLPRELP	372-386
		RGWRPYDIHS	223-232
5R79-46-1	126	FEGPRRNKEVMYK	224-236
		KDDYNETVHKKTE	451-463
		GTHPKDRNVEKLQ	541-553
		EVSKYQEYTNELQET	643-657
AA256100	129	IDDTSNFDDFPESDI	405-419
		TEPDYKSKDWVFL	427-439
		EEKKLRRSQHARKET	61-75
AA210825	130	SNKDTLRKRHYWRLD	507-521
		RHTTRKSSTTLRE	488-500
		FQNNTTNRYYYKEIPL	528-542
		GKHRKTGRDVAVK	668-680
		FPTKQESQLRNE	687-698

AA316804	132	ESHVHQEPSKRIPS	239-252
		HTKRKSSTMVKEGW	409-422
		PSDLDERDEEAVK	375-388
		SPGQGKDHKDLSTSI	543-557
R47805	143	EPVGRWDQDYDRAVL	44-58
		KPKGPGGKRGHKRLI	325-339
		PTDVAQLPSRVPRDA	219-233
AA234451	167	DPFDWEKTGNDGSLT	293-307
		HPRPQEKDVWEE	374-385
		RENTDEVFPDEQLSD	340-354
		RSEITQPDRDIPLVR	427-441
AA460132	180	LKSYSTSSKKARPVL	222-236
		KKLDEVRLRGRKRSM	237-251
		ETEKTAQGLSNLAKT	131-145
N34132	183	SGRRRRPTKSKGSKS	1848-1862
		PGTAPSKPPLTKAPV	1474-1488
		VSDTQPKAPGIDD	1365-1378
		AHSLDKTSHSSTTGL	1253-1267
5R69-17-2	187	GTTREKTDRVKST	178-190
		HSEAPELHGKIRSSN	138-152
		DETVTPPQFSIV	87-98
		QYDVKSEIYS	204-213
AA278842	206	TVDPEKSVRDQAFKA	515-529
		DSSTADRWDDEDWGS	637-651
		SVSEDPTQLEEVEKD	539-553
AA836348	232	NAPTKRPRSSTVTEA	323-337
		LDSEEDYYTPQKVDV	514-528
		GDKASYRQPKHVEKL	409-423

EXAMPLE 4. Expression analysis of Novel Mammalian Protein KinasesGENE EXPRESSION ANALYSIS

Tissue Arrays

“cDNA libraries” derived from a variety of sources were immobilized onto nylon
5 membranes and probed with ³²P-labeled cDNA fragments derived from the gene(s) of
interest.

Total RNA or mRNA was used as template in a reverse transcription reaction to
generate single-stranded cDNAs (ss cDNA) that were tagged with specific sequences at
each end. An oligo dT primer containing a specific sequence (CDS:

10 AAGCAGTGGTAACAACGCAGAGTACT30VN (V=A,G,C N=A,G,C,T)) anneals at
the polyA track at the 3' end of the mRNA and the reverse transcriptase (MMLV
RnaseH-) transcribes the antisense strand until it reaches the end of the RNA strand when
it adds additional C residues. If a primer (SMII:

AAGCAGTGGTAACAACGCAGAGTACGCGGG or ML2G:

15 AAGTGGCAACAGAGATAACGCGTACGCGGG) ending with 3 Gs is added, it anneals
to the added Cs and the MMLV recognizes the rest of the primer sequence as template and
continues transcription. As a result, the synthesized cDNAs contain specific sequence tags
at both the 5' and the 3' end. When the 5' and the 3' ends are tagged with the same
sequence (CDS and SMII) it is referred to as “symmetric.” When the 5' end is tagged
20 with a different sequence than the 3' end (CDS and ML2G) is referred to as “asymmetric”
A double-stranded “cDNA library “ is then generated by PCR amplification using the
3'PCR and ML2 primers (3' PCR: AAGCAGTGGTAACAACGCAGAGT and ML2:
AAGTGGCAACAGAGATAACGCGT) that anneal to the added sequence tags.

The amplified “cDNA libraries” were manually arrayed onto nylon membranes
25 with a 384 pin replicator. The DNA was denatured by alkali treatment, neutralized and
cross-linked by UV light. The arrays were pre-hybridized with Express Hyb (Clontech)
and hybridized with ³²P labeled probes generated by random hexamer priming of cDNA
fragments corresponding to the genes of interest. After washing, the blots were exposed to
phosphorimaging cassettes and the intensity of the signal was quantified. The amount of
30 the DNA on the arrays was also quantified by treating non-denatured or denatured arrays
with Syber Green I or Syber Green II respectively (1:100,000 in 50mM Tris, pH8.0) for 2
minutes. After washing with 50mM Tris, pH8.0, the fluorescent emission was detected

with a phosphorimager (Molecular Dynamics) and quantified. The amount of the arrayed DNA was used to normalize the hybridization signal and the corrected values are tabulated in Table 3.

5 Results

The results of the microarray expression analysis of the protein kinases presented in this application is shown in Table 3. Data presentation from left to right is as follows: "Tissue": tissue type of the cDNA; "Tumor sym", indicates that the tissue is derived from a tumor, "sym" refers to the fact that the 5' and 3' primers used to make the sample are the same; "Normal Sym", indicates normal tissue was used to make the sample, with symmetric primers as described above; "Tumor 1o", indicates that primary tumor tissue was used to make the cDNA; "Tumor cells", indicates that these cDNA samples were made from cultured tumor cells; "Normal", indicates that these samples are derived from normal tissue or cell lines; "Endos", indicates that these samples are derived from endothelium-related tissue sources; "p53" refers to the status, mutant or wild-type, of the p53 gene in the source samples. Normalized expression values are presented for each gene referred to by its SEQ ID# on the subsequent columns. Genes represented in expression Table 3 are: SEQ ID NO:3 (AA826850), SEQ ID NO:5 (TBK1), SEQ ID NO:6 (AA305176), SEQ ID NO:8 (AA256100), SEQ ID NO:9 (CAB43292), SEQ ID NO:11 (EPK2), SEQ ID NO:12 (PKNbeta), SEQ ID NO:14 (H19102), SEQ ID NO:16 (RSK4), SEQ ID NO:17 (AAD30182), SEQ ID NO:20 (SGK2), SEQ ID NO:22 (PTK9L), SEQ ID NO:26 (AA383293), SEQ ID NO:29 (DRAK2), SEQ ID NO:31 (DRAK1), SEQ ID NO:032 (AA015726), SEQ ID NO:40 (MAK-V), SEQ ID NO:044 (TRAD), SEQ ID NO:044 (TRAD), SEQ ID NO:45 (AA454060), SEQ ID NO:47 (AA234451), SEQ ID NO:48 (AA436054), SEQ ID NO:49 (AA626859), SEQ ID NO:51 (KIAA0904), SEQ ID NO:52 (AA789239), SEQ ID NO:54 (CCRK), SEQ ID NO:55 (CLK4), SEQ ID NO:56 (AA557536), SEQ ID NO:57 (W56561), SEQ ID NO:60 (AA579641), SEQ ID NO:63 (NEK7), SEQ ID NO:66 (CAMKKB), SEQ ID NO:68 (HIPK2), SEQ ID NO:72 (R19609), SEQ ID NO:73 (HRI), SEQ ID NO:78 (AA088547), SEQ ID NO:79 (AA449542), SEQ ID NO:082a (MLK4), SEQ ID NO:82 (MLK4b), SEQ ID NO:84 (RIP4), SEQ ID NO:88 (AA278842), SEQ ID NO:89 (AA195964), SEQ ID NO:90 (MSSK1), SEQ ID NO:93 (TSK4), SEQ ID NO:94 (AI025291), SEQ ID NO:95

(AA948538), SEQ ID NO:96 (AA905446), SEQ ID NO:97 (H85389), SEQ ID NO:100 (AA018361), SEQ ID NO:101 (AA311714), SEQ ID NO:110 (AA452647), SEQ ID NO:111 (AA310219), SEQ ID NO:112 (AI086865), SEQ ID NO:114 (MEKK6), and SEQ ID NO:116 (SuRTK106).

5

EXAMPLE 5. Kinase assays for Erk, JNK1 and p38 MAP kinases

293T cells were transiently transfected with HA- p38 or co-transfected with Flag-tagged wt MLK4A, kinase-dead MLK4A, wild-type MLK4B or kinase-dead MLK4B using Lipofectamine 2000 (Lifetech). Cells were lysed 36 hr post-transfection. Cell lysates normalized to contain equivalent amounts of HA-p38 were immunoprecipitated with anti-HA antibody (Mab HA-11, Babco). Immunoprecipitates were split in two portions, one portion was Western-blotted with anti- HA antibody and the other with a phospho-specific p38 antibody (Promega) to detect activated levels of p38. Activation of Erk1 and Jnk1 was measured similarly. (This example applies to AA232253 (SEQ ID NO:82, SEQ ID NO:201).)

15

Results:

In transient assays wild-type MLK4A and MLK4B (but not kinase-inactive MLK4A(K45M) or MLK4B(K45M)) activate Erk, JNK1 and p38 MAP kinases.

20

EXAMPLE 6. RAC1 guanine-exchange factor assay

293T cells were transiently transfected with HA-Rac1 or co-transfected with Flag-tagged Duet C, Duet E, Dbl and HA-Tiam-1. Cells were lysed 36 hour post-transfection. Cell lysates normalized to contain equivalent amounts of Rac1 were affinity precipitated with immobilized GST-PBD (p21-binding domain of Pak3). Bound proteins were Western blotted and probed with anti-HA antibody to detect levels of activated Rac1. ((This example applies to R199772 (Trad/Duet)(SEQ ID NO:44, SEQ ID NO:164).)

25

Results:

Duet C and Duet E both act as guanine nucleotide exchange factors on Rac1.

CONCLUSION

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The molecular complexes and the methods, procedures, treatments, molecules, specific compounds described herein are presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention.

All patents and publications mentioned in the specification are indicative of the levels of those skilled in the art to which the invention pertains.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms “comprising”, “consisting essentially of” and “consisting of” may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed.

In particular, although some formulations described herein have been identified by the excipients added to the formulations, the invention is meant to also cover the final formulation formed by the combination of these excipients. Specifically, the invention includes formulations in which one to all of the added excipients undergo a reaction during formulation and are no longer present in the final formulation, or are present in modified forms.

In addition, where features or aspects of the invention are described in terms of Markush groups, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush

group. For example, if X is described as selected from the group consisting of bromine, chlorine, and iodine, claims for X being bromine and claims for X being bromine and chlorine are fully described.

Other embodiments are within the following claims.

What is claimed is:

CLAIMS

1. An isolated, enriched, or purified nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ
5 ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ
ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ
ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ
ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ
ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ
10 ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ
ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ
ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ
ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ
ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ
15 ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ
ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ
ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ
ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ
ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ
20 ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ
ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ
ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ
ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ
ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ
25 ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ
ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ
ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ
ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

2. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule comprises a nucleotide sequence that:

(a) encodes a polypeptide comprising the amino acid sequence set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID
5 NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID
NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID
NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID
NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID
NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID
10 NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID
NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID
NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID
NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID
NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID
15 NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID
NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID
NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
20 NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
25 NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242;

(b) is the complement of the nucleotide sequence of (a);

30 (c) hybridizes under highly stringent conditions to the nucleotide molecule of (a) and encodes a naturally occurring kinase polypeptide;

(d) encodes a kinase polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of a domain selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(e) is the complement of the nucleotide sequence of (d);

(f) encodes a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, wherein said domain is selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a coiled-coil structure region, a proline-rich region, a spacer region, an insert, and a C-terminal tail;

(g) is the complement of the nucleotide sequence of (f);

(h) encodes a polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID

NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID
NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID
NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID
NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID
5 NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID
NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID
NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID
NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID
NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID
10 NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID
NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID
NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID
NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID
NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID
15 NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID
NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID
NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID
NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID
NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID
20 NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID
NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID
NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID
NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not
all, of the domains selected from the group consisting of an N-terminal domain, a catalytic
25 domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure
region, and a C-terminal tail; or

(i) is the complement of the nucleotide sequence of (h).

3. The nucleic acid molecule of claim 1, further comprising a vector or
promoter effective to initiate transcription in a host cell.

4. The nucleic acid molecule of claim 1, wherein said nucleic acid molecule is isolated, enriched, or purified from a mammal.

5. The nucleic acid molecule of claim 4, wherein said mammal is a human.

6. A nucleic acid probe for the detection of nucleic acid encoding a kinase polypeptide in a sample, wherein said polypeptide is selected from the group consisting of
5 SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
10 SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

7. The probe of claim 6, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

8. A recombinant cell comprising a nucleic acid molecule encoding a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

9. The cell of claim 8, wherein said polypeptide is a fragment of a protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

10. An isolated, enriched, or purified kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

11. The polypeptide of claim 10, wherein said polypeptide is a fragment of the protein encoded by an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

12. The polypeptide of claim 10, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all of the domains selected from the group consisting of an N-terminal domain, a catalytic domain, a C-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

13. The kinase polypeptide of claim 10, wherein said polypeptide is isolated, purified, or enriched from a mammal.

14. The kinase polypeptide of claim 13, wherein said mammal is a human.

15. The kinase polypeptide of claim 10, wherein said polypeptide is a AA144574, AA116841, AA256100, AA305176, AA210825, AA316804, AA980090, N42050, AA476563, AA626690, AA960957, H19102, AA045601, AA107515, AA109508 or AA887783 polypeptide.

16. The kinase polypeptide of claim 10, wherein said polypeptide is a H60215, AA197883, AA297313, W30246, AA172300, AA383293, AA542015, H01248, N23936, W44160, 2R22-5-11, 5R72-18-1, AA021445, AA207220, AA426580, AA544838, W90839, 5R79-54-1, AA839940, R19772 or 5R72-8-2 polypeptide.

17. The kinase polypeptide of claim 10, wherein said polypeptide is a AA234451 polypeptide.

18. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R65-16-1, AA061797, AA065538, AA124976, AA397553, AA435956, AA575635, AA626859, AA789239, AI086865, H17727, H29974, AA557536 or N28606 polypeptide.

19. The kinase polypeptide of claim 10, wherein said polypeptide is a AA631990 or W08549 polypeptide.

20. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R72-16-2, R19927 or R43524 polypeptide.

21. The kinase polypeptide of claim 10, wherein said polypeptide is a 5R57-10-2 polypeptide.

5 22. The kinase polypeptide of claim 10, wherein said polypeptide is a AA232253 polypeptide.

23. The kinase polypeptide of claim 10, wherein said polypeptide is a AA430250, AA836348, R86668 or N34132 polypeptide.

10 24. The kinase polypeptide of claim 10, wherein said polypeptide is a AA098024 or SuRTK106 polypeptide.

25. The kinase polypeptide of claim 10, wherein said polypeptide is a R47805, AA099102, AA589241, H85811, AA013524, AA452647, AA840598, AA088547, AA139478, AA826850, R87679, W65887, H97685, W20810, AA599286, AA425725, AA103218, AA711829, AA060026, AA399669, AA758539, AA883975, AA948538, 15 AA018361, AA215311, AA311714, AA498104, 5R69-17-2, 5R69-23-3, 5R69-26-2, AA118352, AA396601, AA671275, AA278842, AA460132 or H05721 polypeptide.

26. An antibody or antibody fragment having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

27. The antibody or antibody fragment of claim 26, wherein said polypeptide comprises:

(a) an amino acid sequence selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ

5 ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
10 ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ
ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ
ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ
ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ
15 ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ
ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ
ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ
ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ
ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ
20 ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ
ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ
ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ
ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ
ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ
ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ
ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and
SEQ ID NO:242;

(b) an amino acid sequence selected from the group consisting of SEQ
ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ
25 ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ
ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ
ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ
ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ
ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ
30 ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ
ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ
ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ

ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, except that it lacks one or more, but not all, of the domains selected from the group consisting of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a proline-rich region, a coiled-coil structure region, and a C-terminal tail.

(c) a domain of an amino acid sequence selected from the group set forth in SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID

NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID
NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID
NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID
NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID
5 NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID
NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID
NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID
NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID
NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID
10 NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID
NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID
NO:241, and SEQ ID NO:242 wherein said domain is selected from the group consisting
of a C-terminal domain, a catalytic domain, an N-terminal domain, a spacer region, a
proline-rich region, a coiled-coil structure region, and a C-terminal tail.

28. A hybridoma which produces an antibody having specific binding affinity to a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

29. A method for identifying a substance that modulates kinase activity comprising:

(a) contacting a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136,

SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141,
SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146,
SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151,
SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156,
5 SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161,
SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166,
SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171,
SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176,
SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181,
10 SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186,
SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191,
SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196,
SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201,
SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206,
15 SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211,
SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216,
SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221,
SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226,
SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231,
20 SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236,
SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241,
and SEQ ID NO:242 with a test substance;

(b) measuring the activity of said polypeptide; and

(c) determining whether said substance modulates the activity of said
25 polypeptide.

30. A method for identifying a substance that modulates kinase activity in a
cell comprising:

(a) expressing a kinase polypeptide in a cell, wherein said polypeptide
is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID
30 NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID
NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID
NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID

NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242;

- (b) adding a test substance to said cell; and
- (c) monitoring a change in cell phenotype or the interaction between said polypeptide and a natural binding partner.

31. A method for treating a disease or disorder by administering to a patient in need of such treatment a substance that modulates the activity of a kinase selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242.

32. The method of claim 31, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

33. The method of claim 31, wherein said substance modulates kinase activity *in vitro*.

34. The method of claim 33, wherein said substance is a kinase inhibitor.

35. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) contacting said sample with a nucleic acid probe which hybridizes under hybridization assay conditions to a nucleic acid target region of a kinase polypeptide selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:199, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, said probe comprising the nucleic acid sequence encoding said polypeptide, fragments thereof, or the complements of said sequences and fragments; and

(b) detecting the presence or amount of the probe:target region hybrid as an indication of said disease.

36. The method of claim 35, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

37. A method for detection of a kinase polypeptide in a sample as a diagnostic tool for a disease or disorder, wherein said method comprises:

(a) comparing a nucleic acid target region encoding said kinase polypeptide in a sample, wherein said kinase polypeptide is selected from the group consisting of SEQ ID NO:122, SEQ ID NO:123, SEQ ID NO:124, SEQ ID NO:125, SEQ ID NO:126, SEQ ID NO:127, SEQ ID NO:128, SEQ ID NO:129, SEQ ID NO:130, SEQ ID NO:131, SEQ ID NO:132, SEQ ID NO:133, SEQ ID NO:134, SEQ ID NO:135, SEQ ID NO:136, SEQ ID NO:137, SEQ ID NO:138, SEQ ID NO:139, SEQ ID NO:140, SEQ ID NO:141, SEQ ID NO:142, SEQ ID NO:143, SEQ ID NO:144, SEQ ID NO:145, SEQ ID NO:146, SEQ ID NO:147, SEQ ID NO:148, SEQ ID NO:149, SEQ ID NO:150, SEQ ID NO:151, SEQ ID NO:152, SEQ ID NO:153, SEQ ID NO:154, SEQ ID NO:155, SEQ ID NO:156, SEQ ID NO:157, SEQ ID NO:158, SEQ ID NO:159, SEQ ID NO:160, SEQ ID NO:161, SEQ ID NO:162, SEQ ID NO:163, SEQ ID NO:164, SEQ ID NO:165, SEQ ID NO:166, SEQ ID NO:167, SEQ ID NO:168, SEQ ID NO:169, SEQ ID NO:170, SEQ ID NO:171, SEQ ID NO:172, SEQ ID NO:173, SEQ ID NO:174, SEQ ID NO:175, SEQ ID NO:176, SEQ ID NO:177, SEQ ID NO:178, SEQ ID NO:179, SEQ ID NO:180, SEQ ID NO:181, SEQ ID NO:182, SEQ ID NO:183, SEQ ID NO:184, SEQ ID NO:185, SEQ ID NO:186, SEQ ID NO:187, SEQ ID NO:188, SEQ ID NO:189, SEQ ID NO:190, SEQ ID NO:191, SEQ ID NO:192, SEQ ID NO:193, SEQ ID NO:194, SEQ ID NO:195, SEQ ID NO:196, SEQ ID NO:197, SEQ ID NO:198, SEQ ID NO:199, SEQ ID NO:200, SEQ ID NO:201, SEQ ID NO:202, SEQ ID NO:203, SEQ ID NO:204, SEQ ID NO:205, SEQ ID NO:206, SEQ ID NO:207, SEQ ID NO:208, SEQ ID NO:209, SEQ ID NO:210, SEQ ID NO:211, SEQ ID NO:212, SEQ ID NO:213, SEQ ID NO:214, SEQ ID NO:215, SEQ ID NO:216, SEQ ID NO:217, SEQ ID NO:218, SEQ ID NO:219, SEQ ID NO:220, SEQ ID NO:221, SEQ ID NO:222, SEQ ID NO:223, SEQ ID NO:224, SEQ ID NO:225, SEQ ID NO:226, SEQ ID NO:227, SEQ ID NO:228, SEQ ID NO:229, SEQ ID NO:230, SEQ ID NO:231, SEQ ID NO:232, SEQ ID NO:233, SEQ ID NO:234, SEQ ID NO:235, SEQ

ID NO:236, SEQ ID NO:237, SEQ ID NO:238, SEQ ID NO:239, SEQ ID NO:240, SEQ ID NO:241, and SEQ ID NO:242, or one or more fragments thereof, with a control nucleic acid target region encoding said kinase polypeptide, or one or more fragments thereof; and

5 (b) detecting differences in sequence or amount between said target region and said control target region, as an indication of said disease or disorder.

38. The method of claim 37, wherein said disease or disorder is selected from the group consisting of immune-related diseases and disorders, cardiovascular disease, neurodegenerative disorders, and cancer.

Table 1

Gene Name	SP	Prov	Seq ID	NA	Prov	Seq ID	AA	SEQ ID # na	SEQ ID # aa	Family	Group	Length NA	Length AA	ORF Start	ORF end	ORF Length	DNA Repeats	CHR localization
X09117 h BARX2 h	H	1	1	1	1	1	1	1	1	AGC	GRK	267	689	1	264	264	x	2q11
AA144574 m BARX2 m	M	1	1	1	1	1	1	1	1	AGC	GRK	267	689	1	264	264	x	2q11
AA029850 h	H	140	176	3	123	123	123	123	123	AGC	GRK	1368	378	2	1135	1134	x	NA
AA080957 h	H	11	27	4	124	124	124	124	124	AGC	GRK	1788	419	8	1264	1257	285-304	4p16.1
SR79-46.1 h TBK1 h	H	207	208	5	125	125	125	125	125	AGC	GRK	3274	414	65	1306	1242	x	NA
AA305176 h	H	42	1820	6	126	126	126	126	126	AGC	GRK	3013	729	93	2279	2167	x	NA
AA116841 m	M	42	1820	7	127	127	127	127	127	AGC	GRK	1421	329	53	1039	867	x	10p11.2
AA210825 h	H	3	19	8	128	128	128	128	128	AGC	GRK	552	88	3	268	264	x	NA
AA210825 h	H	5	19	9	129	129	129	129	129	AGC	GRK	4983	464	86	1477	1382	x	12q11
AA127299 h	H	203	204	10	130	130	130	130	130	AGC	GRK	978	978	117	3050	2034	x	19q13-q13.3
AA316804 h EPK2	H	6	22	11	131	131	131	131	131	AGC	GRK	315	105	1	315	315	x	NA
NA2050 h PKNbeta	H	8	24	12	132	132	132	132	132	AGC	GRK	2673	890	1	2870	2870	x	2p21
AA021023 m PKNbeta m	M	8	24	12	133	133	133	133	133	AGC	GRK	2670	889	1	2867	2867	2221-2280	NA
HA19102 h	H	12	28	13	134	134	134	134	134	AGC	GRK	929	205	2	616	615	x	NA
AA476563 h RPS8K1	H	9	25	14	135	135	135	135	135	AGC	GRK	1155	384	1	1152	1152	596-639	CHR17
AA626890 h RSK4	H	10	26	15	136	136	136	136	136	AGC	GRK	1410	469	1	1407	1407	x	12q12-q13.1
AA215680 h	H	227	228	17	137	137	137	137	137	AGC	GRK	2238	745	1	2235	2235	x	Xq21.1
SGK h	H	18	3	18	138	138	138	138	138	AGC	GRK	1650	549	1	1647	1647	787-788	14q24.3
AA107515 m	M	13	28	19	139	139	139	139	139	AGC	GRK	1258	431	1	1253	1253	656-683	8q21-q22
AA109508 m	M	13	28	20	140	140	140	140	140	AGC	GRK	2432	430	75	1364	1280	1804-1830	NA
AA087783 h SGK3, SGK	H	16	32	21	141	141	141	141	141	AGC	GRK	1346	244	2	733	732	x	NA
RA7805 h PTRSL	H	131	167	22	142	142	142	142	142	AGC	GRK	1050	349	1	1047	1047	x	3p14.3
H0215 h	H	33	54	23	143	143	143	143	143	AGC	GRK	1050	349	1	1047	1047	x	3p14.3
SGK324 h	H	33	54	23	144	144	144	144	144	AGC	GRK	1050	349	1	1047	1047	x	3p14.3
W07246 m SGK324 m	M	36	57	24	145	145	145	145	145	AGC	GRK	1050	349	1	1047	1047	x	3p14.3
AA333293 h	H	36	57	25	146	146	146	146	146	AGC	GRK	1246	297	1	801	801	208-227	NA
AA197883 m	M	34	55	26	147	147	147	147	147	AGC	GRK	1246	297	1	801	801	208-227	NA
AA172300 h DRAX2	H	37	58	27	148	148	148	148	148	AGC	GRK	1246	297	1	801	801	208-227	NA
W41160 m DRAX2 m	M	40	61	28	149	149	149	149	149	AGC	GRK	1246	297	1	801	801	208-227	NA
H01248 h DRAX1 h	H	40	61	29	150	150	150	150	150	AGC	GRK	1246	297	1	801	801	208-227	NA
AA021445 h	H	45	68	30	151	151	151	151	151	AGC	GRK	1246	297	1	801	801	208-227	NA
RA22-511 h, AAC33487	H	43	64	31	152	152	152	152	152	AGC	GRK	1246	297	1	801	801	208-227	NA
R1237 h, AAC33487	H	43	64	32	153	153	153	153	153	AGC	GRK	1246	297	1	801	801	208-227	NA
W09039 m	M	49	70	33	154	154	154	154	154	AGC	GRK	1246	297	1	801	801	208-227	NA
W09039 m	M	49	70	34	155	155	155	155	155	AGC	GRK	1246	297	1	801	801	208-227	NA
W09039 m	M	49	70	35	156	156	156	156	156	AGC	GRK	1246	297	1	801	801	208-227	NA
W09039 m	M	49	70	36	157	157	157	157	157	AGC	GRK	1246	297	1	801	801	208-227	NA
AA544838 m, 406766 m	M	48	69	37	158	158	158	158	158	AGC	GRK	1246	297	1	801	801	208-227	NA
AA785135 h	H	48	69	38	159	159	159	159	159	AGC	GRK	1246	297	1	801	801	208-227	NA
AA207220 h	H	46	67	39	160	160	160	160	160	AGC	GRK	1246	297	1	801	801	208-227	NA
AA426580 h, MAK V h	H	47	68	40	161	161	161	161	161	AGC	GRK	1246	297	1	801	801	208-227	NA
Z36720 h	H	50	71	41	162	162	162	162	162	AGC	GRK	1246	297	1	801	801	208-227	NA
SGK088 h	H	39	60	42	163	163	163	163	163	AGC	GRK	1246	297	1	801	801	208-227	NA
AA542015 m, SGK088 m	M	39	60	43	164	164	164	164	164	AGC	GRK	1246	297	1	801	801	208-227	NA
R1972 h	H	52	73	44	165	165	165	165	165	AGC	GRK	1246	297	1	801	801	208-227	NA
SR72 h, 2 h	H	53	74	45	166	166	166	166	166	AGC	GRK	1246	297	1	801	801	208-227	NA
SGK309 h	H	139	185	46	167	167	167	167	167	AGC	GRK	1246	297	1	801	801	208-227	NA
AA234451 h	H	75	76	47	168	168	168	168	168	AGC	GRK	1246	297	1	801	801	208-227	NA
AA435956 h	H	82	78	48	169	169	169	169	169	AGC	GRK	1246	297	1	801	801	208-227	NA
AA626659 h	H	84	78	49	170	170	170	170	170	AGC	GRK	1246	297	1	801	801	208-227	NA
AA081197 m	M	81	65	50	171	171	171	171	171	AGC	GRK	1246	297	1	801	801	208-227	NA
AA397553 h, CRK7	H	81	65	51	172	172	172	172	172	AGC	GRK	1246	297	1	801	801	208-227	NA
AA789239 h	H	85	99	52	173	173	173	173	173	AGC	GRK	1246	297	1	801	801	208-227	NA
AA124978 m	M	85	99	53	174	174	174	174	174	AGC	GRK	1246	297	1	801	801	208-227	NA
AA575635 m, CCRK m	M	85	99	54	175	175	175	175	175	AGC	GRK	1246	297	1	801	801	208-227	NA
AA631980 h, CLK4	H	105	107	55	176	176	176	176	176	AGC	GRK	1246	297	1	801	801	208-227	NA
AA57536 h	H	89	103	56	177	177	177	177	177	AGC	GRK	1246	297	1	801	801	208-227	NA
N26606 h, MOK	H	90	104	57	178	178	178	178	178	AGC	GRK	1246	297	1	801	801	208-227	NA
AB02153 h, IOK	H	90	104	58	179	179	179	179	179	AGC	GRK	1246	297	1	801	801	208-227	NA
AA089940 m	M	90	104	59	180	180	180	180	180	AGC	GRK	1246	297	1	801	801	208-227	NA
AA460132 h	H	165	201	60	181	181	181	181	181	AGC	GRK	1246	297	1	801	801	208-227	NA
SGK034 h	H	147	183	61	182	182	182	182	182	AGC	GRK	1246	297	1	801	801	208-227	NA
AA103218 m, SGK034 m	M	147	183	62	183	183	183	183	183	AGC	GRK	1246	297	1	801	801	208-227	NA
NEK7 h, N34132 h	H	122	126	63	184	184	184	184	184	AGC	GRK	1246	297	1	801	801	208-227	NA

Table 1 (cont'd)

Gene Name	SP	Prov Seq ID NA	Prov Seq ID AA	SEQ ID # na	SEQ ID # aa	Family	Group	Length NA	Length AA	ORF Start	ORF End	ORF Length	DNA Repeat	CHR localization
BCDN3 h	H	x	x	84	184	Other	C26C2_c2	2164	538	113	1717	1608	245-267	NA
AA711829 m	M	148	184	65	185	Other	C26C2_c2	1568	378	1	1134	1134	x	NA
AA009102 h CalkXB	H	132	188	66	186	Other	CAMKX	1787	588	1	1764	1764	65-84	12p23-q14
5RE9.17.2 h	H	158	194	67	187	Other	CTRI	3387	241	1850	2572	723	489-521	NA
165811 h	H	134	170	68	188	Other	DYRK	3993	1171	183	3895	3513	1328-1348	CHR7
AA02163 h DYRK3	H	x	x	69	189	Other	DYRK	2141	553	253	1911	1659	x	NA
AA588241 m DYRK3 m	M	133	169	70	190	Other	DYRK	741	168	3	568	504	x	NA
5R72.16.2 h R19827 h	H	109	112	71	191	Other	EPK	5163	1849	20	4968	4947	x	NA
R43524 h HR1 h R19809	H	111	114	72	192	Other	EPK	1963	630	1	1880	1890	x	NA
1700057519457 h	H	111	114	73	193	Other	Endop	3055	253	219	877	759	2283-2365	NA
AA013524 m	M	135	171	74	194	Other	Endop	928	216	1	646	648	x	NA
17000139801197 h IRAKM	M	135	171	75	195	Other	IRAK	2243	580	1	1788	1788	x	NA
AA040598 m IRAKM m	M	137	173	76	196	Other	IRAK	2243	580	1	1788	1788	x	NA
AA088547 h	H	139	174	77	197	Other	IRE	2768	922	1	1175	1176	x	NA
HGP 6844466	H	x	x	78	198	Other	KYR2_did	1857	322	178	1144	968	x	NA
AA449542 m	M	138	175	79	199	Other	KYR2_did	1251	260	2	841	840	602-621	NA
5R37.10.2 m TESK2 m	M	115	118	80	200	Other	LMK	140	41	2	124	123	x	NA
AA232253 h	H	117	118	81	201	Other	LMK	2403	800	1	2400	2400	x	NA
H97685 h	H	143	178	82	202	Other	MLK	2508	835	1	2565	2565	2218-2238	NA
AA744236 h	H	144	180	83	203	Other	RIP	2354	634	161	2062	1902	x	1q31
AA052250 h	H	225	212	84	204	Other	RIP	1073	289	3	869	867	x	NA
AA278642 h	H	184	200	85	205	Other	SCY1_sc	2067	688	1	2084	2084	x	1q23
AA598286 h	H	145	181	86	206	Other	SCY1_sc	1739	505	174	1888	1515	x	NA
AA425725 h	H	146	182	87	207	Other	SCY1_sc	2888	808	105	2528	2424	1764-1783	11q12-q13 Amplicon
SGK022 h	H	x	x	88	208	Other	SLOB1	1949	648	1	1849	1949	x	NA
AA060206 m SGK022 m	M	146	185	89	209	Other	SRPK	1802	533	1	1599	1599	x	NA
AA399689 h	H	150	196	90	210	Other	STR22A	1028	268	184	987	804	x	NA
AA083975 h	H	151	197	91	211	Other	STR22A	1004	268	147	950	804	x	NA
AA050446 h	H	153	199	92	212	Other	STR22A	1537	282	372	1244	876	x	14p11-q11
H29974 h	H	223	224	93	213	Other	STR22A	1322	358	101	1174	1074	x	NA
AA408104 m H29974 m	M	x	x	94	214	Other	TSK	822	273	1	819	818	x	NA
AA215311 h	H	155	191	95	215	Other	TSK	1066	216	385	1012	848	x	NA
AA018361 h	H	154	190	96	216	Other	UNC	1938	333	2	1000	999	x	NA
AA311714 h	H	156	192	97	217	Other	UNC	1490	412	1	1238	1238	701-728	NA
SGK384 h	H	x	x	98	218	Other	UNC	2011	341	199	1221	1023	x	NA
AA210451 m SGK384 m	M	108	108	99	219	Other	UNC	2759	461	113	1555	1443	x	15q23
SGK071.2 h	H	x	x	100	220	Other	UNC	1876	565	138	1833	1685	x	NA
AA118352 m SGK071 m	M	161	187	101	221	Other	UNC	117	38	1	117	117	x	NA
018853.9 h	H	162	188	102	222	Other	UNC	2721	349	222	1288	1047	235-2286	NA
AA396601 m	M	163	189	103	223	Other	UNC	2115	704	1	2112	2112	57-76, 318-337	NA
AA671275 h VRK3	H	183	199	104	224	Other	UNC	1729	540	3	1622	1620	x	NA
S71575 m VRK3 m	M	x	x	105	225	Other	UNC	2461	540	1	1620	1620	240-259	NA
AA452647 h MPSK1	M	138	172	106	226	Other	VRK	1888	365	3	1087	1095	x	NA
H05721 h	H	166	202	107	227	Other	VRK	1425	474	1	1422	1422	x	18q13
AA088895 h	H	88	100	108	228	Other	YPL239_sc	1008	234	3	704	702	937-957	NA
R86668 h MKK8	H	120	124	109	229	Other	YPL239_sc	918	305	1	915	915	x	3cen-3q21
PAK6 h SR95-20-11	H	121	125	110	230	Other	YPL239_sc	2688	581	95	1837	1743	x	1p12.3-3.1 Amplicon
SGK106 h SR95-20-11	H	128,127	130	111	231	Other	STE	2463	698	7	2100	2094	x	NA
AA089022 m	M	128,127	130	112	232	Other	STE	2511	638	1	2508	2508	x	NA
H08950 h CORK	H	67	101	113	233	Other	STE11	3038	1011	1	3033	3033	x	1p2.3-p3.1
NM 007170 h TESK2	H	x	x	114	234	Other	STE11	2160	719	1	2157	2157	x	20p12
				115	235	Other	STE20-02	2460	495	1	1485	1485	x	12p12.3
				116	236	Other	TK	1793	387	1	1485	1485	1302-1382	NA
				117	237	Other	TK	1812	387	88	1188	1101	x	NA
				118	238	Other	SGK	1359	452	1	1356	1356	x	9q21.1-q21.3
				119	239	Other	CDK	3016	555	398	2060	1885	x	NA

Table 2

Patent Seq ID# na	Patent Seq ID# aa	Family	Group	nraa Pscore	Length aa	ID match	% Identity	% Similar	nraa Match ACG#	Description	Kinase Domain(s) start	Kinase Domain (s) end	Profile start	Profile end
H 1	122	AGC	GRK	2.7e-314	688	687	100	100	CAB45857.1	BAR22 [Homo sapiens]	191	453	1	261
M 2	123	AGC	GRK	1.30E-180	378	371	98	89	NP 037029.1	Adrenergic receptor kinase, beta 2 (G-protein-linked receptor kit)	3	143	121	261
M 3	124	AGC	03C11.1 c	5.80E-108	419	262	71	86	CAB7647.1	Serine/threonine protein kinase [Homo sapiens]	26	286	1	261
H 4	125	AGC	03C11.1 c	1.40E-137	414	262	71	100	CAB7647.1	Serine/threonine protein kinase [Homo sapiens]	23	283	1	261
H 5	126	AGC	03C11.1 c	0	729	728	100	100	NP 037386.1	TANK-binding kinase 1 [Homo sapiens]	9	304	1	261
M 6	127	AGC	NDR	1.20E-09	329	73	48	68	BAA76817.1	KIAA0973 protein [Homo sapiens]	35	310	1	261
M 7	128	AGC	NDR	1.30E-19	88	42	49	71	AAF55594.1	CG7719 gene product [Drosophila melanogaster]	24	44	242	261
H 8	129	AGC	NDR	6.10E-181	464	463	100	100	BAA76809.1	KIAA0965 protein [Homo sapiens]	90	383	1	261
H 9	130	AGC	PKC	8.60E-160	978	815	67	80	NP 002733.1	Protein kinase C, mu [Homo sapiens]	651	907	1	261
H 10	131	AGC	PKC	1.10E-10	105	42	42	57	P05127	Protein kinase C, BETA-II TYPE (PKC-BETA-2) [Homo sapiens]	19	24	256	261
H 11	132	AGC	PKC	0	890	890	100	100	NP 005804.1	Protein kinase C, nu [Homo sapiens]	578	832	1	261
H 12	133	AGC	PKC	9.4e-319	889	889	100	100	NP 037487.1	Protein kinase N beta [Homo sapiens]	559	818	1	261
M 13	134	AGC	PKC	1.20E-106	205	204	100	100	JC708.3	Protein kinase N beta [Homo sapiens]	1	134	126	261
H 14	135	AGC	S6K	3.60E-12	384	94	38	55	AAC02495.1	Ribosomal protein S6 kinase 3 [Homo sapiens]	81	333	1	261
H 15	136	AGC	S6K	2.90E-257	469	468	100	100	NP 036556.1	Ribosomal protein S6 kinase, 52kD, polypeptide 1 [Homo sapiens]	225	459	1	261
H 16	137	AGC	S6K	7.00E-178	745	745	100	100	NP 055311.1	Ribosomal protein S6 kinase, 90kD, polypeptide 6 [Homo sapiens]	73 & 428	330 & 683	1	261
H 17	138	AGC	S6K	9.60E-222	549	549	100	100	AAD30182.1	Unknown [Homo sapiens]	153	539	1	261
H 18	139	AGC	SGK	9.20E-103	431	430	100	100	AAA41091.1	SGK [Homo sapiens]	98	355	1	261
M 19	140	AGC	SGK	2.90E-157	430	426	99	99	NP 035491.1	Serum/glucocorticoid regulated kinase [Mus musculus]	98	354	1	261
M 20	141	AGC	SGK	2.00E-76	244	244	100	100	AAF12757.1	Protein kinase [Homo sapiens]	1	169	24	261
H 21	142	AGC	SGK	4.10E-211	446	375	88	88	AAF27051.1	SGK-like protein SGK [Homo sapiens]	162	369	1	261
H 22	143	Atypical	A6	5.60E-216	349	349	100	100	NP 009215.1	Protein tyrosine kinase 9-like (A6-related protein) [Homo sapiens]	10	17	253	261
H 23	144	CAMK	AMPK	1.40E-19	440	68	39	61	CAA04119.1	Phosphoprotein [Homo sapiens]	40	333	1	261
H 24	145	CAMK	CAMK	1.50E-165	699	468	65	77	O15075	DCAMK1 DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1	368	625	1	261
M 25	146	CAMK	CAMK	1.60E-62	297	199	67	83	AAF26675.1	CPG16 [Mus musculus]	59	297	1	261
M 26	147	CAMK	CAMK	2.80E-48	708	181	44	60	O15075	DCAMK1 [DOUBLECORTIN-LIKE AND CAM KINASE-LIKE 1]	415	673	1	261
M 28	148	CAMK	CAMK	2.60E-31	806	147	55	73	AAF26675.1	CPG16 [Mus musculus]	514	771	1	261
H 29	149	CAMK	DAPK	3.10E-121	372	372	100	100	NP 004217.1	Death-associated protein kinase-related 2	33	293	1	261
M 30	150	CAMK	DAPK	7.90E-93	372	340	81	95	NP 004217.1	Death-associated protein kinase-related 2	32	293	1	261
H 31	151	CAMK	DAPK	1.20E-113	414	414	100	100	NP 004751.1	Death-associated protein kinase-related 1	61	321	1	261
H 32	152	CAMK	EMK	5.90E-185	1311	1053	80	80	BAA76843.1	KIAA0999 protein [Homo sapiens]	8	259	1	261
H 33	153	CAMK	EMK	1.20E-45	436	153	51	70	T22427	Hypothetical protein F49C5.4 - [Caenorhabditis elegans]	74	325	1	261
H 34	154	CAMK	EMK	1.40E-32	436	122	46	65	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	56	307	1	261
M 35	155	CAMK	EMK	1.30E-184	729	729	100	100	AAC15093.1	Cdc25C associated protein kinase C-TAK1 [Homo sapiens]	59	340	1	261
H 36	156	CAMK	EMK	3.50E-126	462	462	100	100	AAC33487.1	R31237 1, partial CDS [Homo sapiens]	999	1258	1	261
M 37	157	CAMK	EMK	5.10E-59	230	183	79	85	BAA09484.1	KIAA0135 gene, related to p1n-1 oncogene, [Homo sapiens]	1	158	23	261
H 38	158	CAMK	EMK	3.00E-111	926	636	100	100	BAA34501.1	KIAA0781 protein [Homo sapiens]	20	271	1	261
H 39	159	CAMK	EMK	7.30E-80	629	367	57	69	NP 058655.1	KIAA0537 gene product [Homo sapiens]	53	304	1	261
H 40	160	CAMK	EMK	1.40E-244	714	714	100	100	NP 055401.1	Homologously upregulated neu tumor-associated kinase [Homo sapiens]	61	320	1	261
H 41	161	CAMK	MLCK	8.20E-76	874	211	63	80	AAAT73168.1	Skeletal muscle myosin light chain kinase [Gallus gallus]	570	825	1	261
H 42	162	CAMK	Trio	0	2266	227	100	100	BAA92535.1	KIAA1297 protein [Homo sapiens]	620 & 1086	873 & 1356	1	261
M 43	163	CAMK	Trio	7.80E-37	127	67	99	99	BAA92535.1	KIAA1297 protein [Homo sapiens]	3	78	186	261
H 44	164	CAMK	Trio	0	1287	1284	100	100	NP 008995.1	STK with Dbl- and pleckstrin homology domains [Homo sapiens]	985	1239	1	261
H 45	165	CAMK	Uniqye	5.00E-20	514	114	41	63	P25323	MLCK [Drosophila discoidium]	116	361	1	261
H 46	166	CKI	CKI	3.30E-89	508	181	53	65	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	34	313	1	261
H 47	167	CKI	CKI	8.60E-98	478	188	57	68	AAF59340.1	CG11533 gene product [Drosophila melanogaster]	21	471	1	261
H 48	168	CMGC	CDK	9.60E-39	268	138	62	79	NP 036527.1	PFTAIRE protein kinase [Homo sapiens]	1	218	23	261
H 49	169	CMGC	CDK	7.10E-48	247	146	59	75	NP 004187.1	Cyclin-dependent kinase-like 1 [CDC2-related kinase] [Homo sapiens]	1	191	23	261

Table 2 (cont'd)

M 50	170	CMGC	CDK	2.90E-64	298	193	65	78	NP_004187.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	1	240	24	261
H 51	171	CMGC	CDK	1.10E-284	1490	1480	100	100	AAF38401.1	CDC2-related protein kinase 7 [Homo sapiens]	21	1020	1	261
H 52	172	CMGC	CDK	9.20E-101	534	377	82	82	AAF38509.1	NKIATRE [Homo sapiens]	4	365	1	261
M 53	173	CMGC	CDK	1.40E-128	337	225	92	96	AAF34871.1	NKIATRE alpha [Rattus norvegicus]	1	28	235	261
M 54	174	CMGC	CDK	3.00E-68	211	159	79	84	NP_036251.1	Cell cycle related kinase [Homo sapiens]	1	153	134	261
H 55	175	CMGC	CLK	1.50E-242	499	438	91	93	NP_031740.1	Cyclin-dependent kinase-like 1 (CDC2-related kinase) [Homo sapiens]	177	483	1	261
H 56	176	CMGC	RCK	9.10E-89	544	343	57	64	AAD12719.1	Extracellular signal-regulated kinase 7, ERK7 [Rattus norvegicus]	13	305	1	261
H 57	177	CMGC	RCK	2.30E-188	419	419	100	100	NP_055041.1	Renal tumor antigen [Homo sapiens]	4	285	1	261
H 58	178	CMGC	RCK	1.50E-180	632	632	100	100	AAF37278.1	Intestinal cell kinase [Homo sapiens]	4	284	1	261
M 59	179	CMGC	RCK	1.60E-78	413	198	60	77	P20689	MLCK [Rattus norvegicus]	109	364	1	261
H 60	180	Microbial PK	YGR262 sc	2.50E-45	253	102	46	67	AAF50789.1	CG10873 gene product [Drosophila melanogaster]	101	187	65	147
H 61	181	Other	C26C2 ce	2.30E-158	509	258	100	100	CAB70864.1	Hypothetical protein [Homo sapiens]	2	267	1	261
M 62	182	Other	C26C2 ce	1.80E-152	281	243	94	98	CAB70864.1	Hypothetical protein [Homo sapiens]	59	86	235	261
H 63	183	Other	C26C2 ce	8.70E-300	1852	1193	99	99	NP_055638.1	KIAA0344 gene product [Homo sapiens]	221	478	1	261
H 64	184	Other	C26C2 ce	1.10E-254	535	535	100	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	73	327	1	261
M 65	185	Other	C26C2 ce	2.50E-208	378	372	98	100	NP_037524.1	Nuclear receptor binding protein [Homo sapiens]	1	170	85	261
H 66	186	Other	CAMKK	3.80E-148	588	588	100	100	AAD31507.1	Ca2+/calmodulin-dependent protein kinase kinase beta [Homo sapiens]	165	446	1	261
H 67	187	Other	CTRI	9.90E-24	287	87	33	52	QJ1743	Hypothetical 33.8K protein - rabbit fibroblast virus	24	285	1	261
H 68	188	Other	DYRK	0	1171	1137	97	99	AAD52566.1	Nuclear body associated kinase 1a [Mus musculus]	199	527	1	261
H 69	189	Other	DYRK	2.10E-280	553	553	100	100	NP_003573.1	Dual-specific tyrosine-(Y)-phosphorylation regulated kinase 3	174	487	1	261
M 70	190	Other	DYRK	2.30E-95	168	149	90	96	NP_003573.1	Dual-specific tyrosine-(Y)-phosphorylation regulated kinase 3	76	103	235	261
H 71	191	Other	EIFK	0	1649	1493	90	96	NP_038747.1	GCN2 alpha kinase [Mus musculus]	280 & 590	539 & 1001	1	261
H 72	192	Other	EIFK	1.50E-220	630	630	100	100	NP_055228.1	Heme-regulated initiation factor 2-alpha kinase [Homo sapiens]	167	563	1	261
H 73	193	Other	Endop	2.50E-45	253	102	46	67	AAF50789.1	CG10873 gene product [Drosophila melanogaster]	101	187	65	147
M 74	194	Other	Endop	3.70E-45	216	100	45	64	AAF50789.1	(AE003567) CG10673 gene product [Drosophila melanogaster]	118	150	116	147
H 75	195	Other	IRAK	0	596	596	100	100	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	165	443	1	261
M 76	196	Other	IRAK	1.20E-170	392	293	75	85	NP_009130.1	Interleukin-1 receptor-associated kinase M [Homo sapiens]	1	239	19	261
H 77	197	Other	IRE	1.5e-323	922	746	82	89	NP_036148.1	Irf1, nuclear-require 1 gene [Mus musculus]	516	777	1	261
H 78	198	Other	KYK2 dd	8.70E-40	225	102	45	62	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	32	318	1	261
M 80	199	Other	KYK2 dd	5.90E-32	280	109	32	50	AAF48758.1	CG8173 gene product [Drosophila melanogaster]	12	266	1	261
M 81	200	Other	LMK	2.60E-17	41	37	92	95	NP_009101.1	testis-specific kinase 2 [Homo sapiens]	12	39	101	128
H 82	201	Other	MLK	2.50E-282	800	799	100	100	AAF63490.1	Mixed lineage kinase [Homo sapiens]	16	259	1	261
H 83	202	Other	MLK	8.60E-251	835	835	100	100	AAD29632.1	Putative protein-tyrosine kinase [Homo sapiens]	463	723	1	261
H 84	203	Other	RIP	2.20E-158	634	365	100	100	BAA32317.1	KIAA0472 protein [Homo sapiens]	357	620	1	261
M 85	204	Other	RIP	5.50E-158	289	288	100	100	AAF03133.1	Receptor interacting protein 3 [Mus musculus]	7	27	181	202
H 86	205	Other	SCY1 sc	0	688	688	100	100	CAB55300.1	Hypothetical protein [Homo sapiens]	57	83	50	78
H 87	206	Other	SCY1 sc	1.70E-209	505	354	98	98	BAA92598.1	KIAA1360 protein [Homo sapiens]	32	327	1	261
H 88	207	Other	SLOB7	2.20E-157	808	396	45	61	AAF56933.1	CG1973 gene product [Drosophila melanogaster]	65	131	47	116
H 89	208	Other	SLOB7	7.40E-196	649	649	100	100	BAA91097.1	Unnamed protein product [Homo sapiens]	230	305	81	143
H 90	209	Other	SRPK	5.80E-252	533	533	100	100	NP_055185.1	Serine/threonine kinase 23 [Homo sapiens]	79	531	1	261
M 92	211	Other	STK22A	3.80E-53	268	122	46	70	NP_033461.1	Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus]	10	265	1	261
H 93	212	Other	STK22	2.70E-52	268	127	48	68	NP_033462.1	Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus]	10	265	1	261
H 94	213	Other	STK22A	4.80E-16	292	112	45	64	NP_033461.1	Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus]	25	280	1	261
H 95	214	Other	TSK	5.10E-123	358	322	90	96	NP_033462.1	Serine/threonine kinase 22B (spERMogenesis associated) [Mus musculus]	12	272	1	261
H 96	215	Other	TSK	2.10E-33	273	122	46	62	NP_033461.1	Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus]	12	267	1	261
H 97	216	Other	UNC	2.50E-32	216	93	41	58	NP_033462.1	Serine/threonine kinase 22A (spERMogenesis associated) [Mus musculus]	1	213	7	261
M 98	217	Other	UNC	0.000062	333	57	36	56	AAD32787.1	Putative protein kinase [Arabidopsis thaliana]	1	329	1	261
H 99	218	Other	UNC	0.002492	412	53	37	52	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	80	408	1	261
H 100	219	Other	UNC	0.001096	34	50	36	56	BAA77341.1	UNC-51-like kinase (ULK) 2 [Mus musculus]	8	340	1	261
H 101	220	Other	UNC	1.90E-48	480	247	100	100	T17265	Hypothetical protein DKFZp434C131.1 - human (fragment)	57	313	1	261
H 102	221	Other	Unique	1.60E-208	565	468	96	96	BAA91270.1	Unnamed protein product [Homo sapiens]	4	265	1	261
				6.70E-10	39	27	69	90	AAD00575.1	Serum-inducible kinase [Homo sapiens]	1	39	84	124

Table 2 (cont'd)

M 103	222	Other	Unique	0.000022	349	38	30	50	CAA18118.1	Serine/threonine protein kinase like protein [Arabidopsis thaliana]	80	159	1	88
H 104	223	Other	Unique	0.000126	704	54	30	45	BAA86578.1	KIAA1284 protein [Homo sapiens]	1	246	25	261
M 105	224	Other	Unique	0.007385	540	25	42	61	AAF47916.1	Tie gene product [Drosophila melanogaster]	9	104	168	261
H 106	225	Other	Unique	0.31334	540	52	30	42	P10182	SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [Homo sapiens]	1	272	18	73
M 107	226	Other	Unique	0.022948	365	25	34	57	NP_006276.1	Testis-specific kinase 1 [Homo sapiens]	68	86	42	71
H 108	227	Other	VRK	3.10E-263	474	474	100	100	BAA80769.1	Vaccinia related kinase 3 [Homo sapiens]	247	318	63	136
M 109	228	Other	VRK	1.20E-111	234	191	82	80	BAA80769.1	(AB031052) vaccinia related kinase 3 [Homo sapiens]	7	76	63	136
H 110	229	Other	YPL236.sc	7.40E-144	305	304	100	100	AAC28337.1	MPKX [Homo sapiens]	20	290	1	261
H 111	230	Other	YQ09.ce	5.10E-49	581	135	43	63	AAF46188.1	CG4523 gene product [Drosophila melanogaster]	156	507	1	261
H 112	231	STE	NEK	3.30E-30	698	122	48	67	P51954	NEK1 (NIMA-RELATED PROTEIN KINASE 1) [Mus musculus]	4	251	1	261
H 113	232	STE	NEK	2.70E-119	836	357	86	86	AAD31839.1	(AC007055) unknown [Homo sapiens]	52	308	1	261
H 114	233	STE	STE11	1.10E-291	1011	1011	100	100	NP_004663.1	mitogen-activated protein kinase kinase kinase 6 [Homo sapiens]	376	629	8	261
H 115	234	STE	STE20-02	7.70E-177	719	719	100	100	BAA84184.1	(AB040812) protein kinase PAK5 [Homo sapiens]	449	700	1	261
H 116	235	TK	RTK-20	4.90E-24	495	77	38	56	AAA88465.1	(U40827) protein tyrosine kinase [Mus musculus]	187	453	1	261
M 117	236	TK	RTK-20	5.30E-18	183	53	39	57	NP_032038.1	fibroblast growth factor receptor 3 [Mus musculus]	8	143	123	261
H 118	237	AGC	SGK	6.30E-112	367	367	100	100	AAF12757.2	SGK2alpha protein kinase [Homo sapiens]	35	292	1	261
H 120	238	CMGC	CDK	2.80E-137	452	452	100	100	NP_036251.1	Cell cycle related kinase [Homo sapiens]	4	287	1	261
H 121	239	Other	LMNK	6.50E-233	555	555	100	100	NP_009101.1	Testis-specific kinase 2 [Homo sapiens]	62	293	5	261

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Table 3

Tissue	Tumor-sym	Normal-sym	Tumor - to	Tumor code	Normal	Endos	p53	ISEQ	003	AREQ	3	TBM	SEQ	006	AREQ	004	AREQ	0	CAR	SEQ	11	EP	SEQ	17	PU	SEQ	14	HY	SEQ	16	RS
adrenal gland - h		1						7480	13841	563727	29846	34705	56360	11054	45820	13165															
lymph node - h		2						8151	32265	1202484	118257	105118	55339	19997	94629	18246															
bone marrow - h		3						4465	9236	1477586	35387	32237	33850	13151	82024	12109															
pancreatic gland - h		4						954	378	105057	4031	4318	1884	1985	24739	2503															
breast - h		5						9889	5023	259763	52622	21860	7861	7736	54153	7107															
pancreas - h		6						5433	3574	334665	50925	32390	8831	11839	71540	12794															
carotid artery - h		7						6350	19704	787223	84606	35692	16370	29250	82436	13345															
pancreatic gland - h		8						5542	7688	712184	82497	35569	18473	11010	87365	12186															
testis - h		9						15719	6046	867041	65401	30146	23343	13741	103274	8907															
placenta - h		10						6783	15458	1232178	48305	45070	24271	13887	80242	10501															
testis - h		11						47077	10839	837527	81089	87946	31175	19968	65084	10689															
prostate, h		12						3477	1784	120258	60269	48912	11799	9664	74834	11164															
testis - h		13						3307	5284	1546113	28106	35129	17029	10418	58677	9440															
adipose gl. - h		14						2725	3638	429781	37047	37750	11433	13806	80763	14403															
testis - h		15						8215	8481	1305487	78578	88484	31811	34594	82518	15435															
ovoid muscle - h		16						5482	3765	167682	81053	12318	10889	11874	57531	8296															
heart - h		17						3012	1915	227634	27479	22973	6357	11717	43881	7763															
arterial intima - h		18						3920	5561	833318	78567	28583	11720	12220	42979	11051															
kidney - h		19						2588	9455	412001	41491	24102	7829	8696	48325	12062															
epididym - h		20						5186	2789	224006	21586	12872	12298	4648	34755	8788															
breast - h		21						3763	4479	334587	34563	15261	11556	6365	40332	6300															
spleen - h		22						3364	1519	208605	46111	29975	10799	8169	44868	8681															
lung - h		23						4121	1921	488627	35513	26347	10800	4418	37827	7084															
colon - h		24						2829	418	312852	33891	12206	5670	3999	18010	5109															
testis - h		25						1542	1263	1546113	18148	11784	10861	8666	44868	11194															
thymus - h		26						7654	4986	1874062	122906	80848	46509	31139	85252	13780															
HPAEC		27						7304	0	88668	34171	26274	2919	14479	67087	9110															
pancreatic gland - h		28						5670	193	136311	42836	25861	8827	8143	34767	8992															
RTPEC		29						24571	1923	80362	131	1054	1054	1054	47340	7144															
trachea - h		30						6724	3092	807783	59948	49813	15260	16042	78666	11787															
HPAEC		31						7791	1355	138606	24824	15301	4715	11713	85184	3638															
ovary - h		32						5388	4649	534257	34433	33931	14725	15085	66678	8640															
HPAEC		33						1878	0	6784	6784	12123	28435	11717	8203																
pancreas - h		34						11668	519	41843	19592	15818	6140	6513	66433	7464															
lymph node - h		35						6132	371	47839	15781	20735	8420	3812	64078	7285															
ovoid muscle - h		36						8806	727	0	11060	5411	5264	2070	30349	3459															
testis - h		37						8806	2171	144983	18355	15066	3458	1447	64137	8164															
heart - h		38						7091	745	5019	15303	8552	2515	3920	47872	7275															
thymus - h		39						8710	2472	872200	40613	17473	10184	1502	70722	10210															
Ovarian - h		40						2879	0	28028	8776	14898	4049	8070	42191	6588															
testis - h		41						12295	3265	21478	20955	16311	1818	3563	86800	9323															
testis - h		42						4498	0	6814	17344	12177	4150	3293	35172	8985															
testis - h		43						8992	23869	33514	15562	14896	17932	4369	57094	8787															
HT12-normal		44						385	0	385	0	385	0	385	0	385															
HT12-normal		45						385	0	385	0	385	0	385	0	385															
HT15-normal		46						385	0	385	0	385	0	385	0	385															
HT15-normal		47						385	0	385	0	385	0	385	0	385															
HT15-normal		48						385	0	385	0	385	0	385	0	385															
HT15-normal		49						385	0	385	0	385	0	385	0	385															
HT15-normal		50						385	0	385	0	385	0	385	0	385															
HT15-normal		51						385	0	385	0	385	0	385	0	385															
HT15-normal		52						385	0	385	0	385	0	385	0	385															
HT15-normal		53						385	0	385	0	385	0	385	0	385															
HT15-normal		54						385	0	385	0	385	0	385	0	385															
HT15-normal		55						385	0	385	0	385	0	385	0	385															
HT15-normal		56						385	0	385	0	385	0	385	0	385															
HT15-normal		57						385	0	385	0	385	0	385	0	385															
HT15-normal		58						385	0	385	0	385	0	385	0	385															
HT15-normal		59						385	0	385	0	385	0	385	0	385															
HT15-normal		60						385	0	385	0	385	0	385	0	385															
HT15-normal		61						385	0	385	0	385	0	385	0	385															
HT15-normal		62						385	0	385	0	385	0	385	0	385															
HT15-normal		63						385	0	385	0	385	0	385	0	385															
HT15-normal		64						385	0	385	0	385	0	385	0	385															
HT15-normal		65						385	0	385	0	385	0	385	0	385															
HT15-normal		66																													

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor - 1a	Tumor cells	Normal	Endoc	p53	SEQ 003	ANEO 3	TBMSEQ 006	ANEO 006	ANEO 3	CARSEQ 11	EP1SEQ 12	PI/SEQ 14	MYSEQ 16	AS
Hs 578T	155							13571	0	186024	349411	18721	12712	90761	46243	5514	
MCF-7/ADR-RES	151							13420	1292	37520	352621	9797	5794	8870	45543	5180	
MCF-7	151							15237	1095	80387	52016	21779	19050	10782	53049	9415	
M14	149							5452	566	204414	17174	10734	78348	2544	63303	4830	
UACC-257	147							11456	0	159816	13607	10437	42807	4580	36208	6237	
SK-MEL-28	144							2456	123	56725	21571	11116	17584	1820	17441	4551	
UO-31	143							4479	0	350827	13751	7222	23647	2124	26951	5624	
SK-MEL-3	142							6387	0	247414	15138	8047	23533	4196	56230	8343	
KM-12	141							5444	690	436868	10465	4434	30762	7048	23051	5245	
SK-MEL-2	140							5633	377	43470	12208	4099	4523	2794	30992	3132	
HCT-15	139							2946	331	331883	18006	13917	13874	7005	30577	5799	
Matrnx-3M	139							1187	0	352055	14372	8250	17403	5478	54739	10741	
COLO 205	137							8596	0	403466	18970	8670	21327	8334	45060	7827	
LOX IMV	136							5349	0	384020	16795	8554	17481	4888	17736	10840	
SW-620	135							4200	204	1878684	23713	10725	23514	5599	26010	7615	
TK-10	134							11820	0	622856	16554	5952	16514	7213	38849	5702	
HCT 116	133							3536	1582	230533	21155	7532	9162	4091	43207	9030	
TML-0	132							3482	0	184816	13895	7380	8546	4085	37409	5317	
HCC-2998	131							3264	0	386264	17720	4892	13644	5047	34175	4877	
ACHN	130							6970	2297	300066	17568	5751	10030	3671	62362	9455	
PC-3	129							8652	177	84811	18456	10359	8438	4663	36560	5785	
ROP 303	128							12590	0	48624	14186	4879	6473	3508	35262	6853	
DU-145	127							5633	279	469833	21616	7110	11098	3324	40444	5886	
Gals-1	126							18928	138	305090	12131	3150	3840	4291	37777	2307	
SA	125							3046	722	712648	12748	8699	12345	4267	35257	6407	
A-18	124							3345	257	430381	13247	3620	10151	2542	37590	4327	
RPMI 8226	123							9123	0	64349	18090	41974	17229	4374	39104	6293	
SN12C	122							2278	0	272938	18399	9418	26799	1191	50455	5958	
HL-60	121							6285	217	203577	71182	14358	28787	5796	42578	5287	
MCA-14	120							11442	0	137022	68548	53291	224221	4164	36440	4569	
OVCA-3	119							4384	0	440040	12769	10231	15496	2986	28309	4478	
K-562	118							3930	369	1086525	16534	5752	41860	4117	25375	6636	
OVCA-3	117							2150	798	864733	14187	8845	24925	9340	54213	9030	
CCRF-CEM	116							3847	3587	4965333	18556	8040	112397	5681	27099	3201	
OVCA-3	115							4910	0	3589707	21767	9518	81643	9569	36120	4575	
SP-539	114							3371	0	551858	10974	7064	21926	5119	52017	5813	
HOP-62	113							4819	0	862870	13841	4718	16863	2604	34465	6113	
SP-295	112							2174	369	345760	5634	5102	11026	3780	19576	4413	
AS4B/ATCC	111							11905	716	68583	16107	8440	7164	2565	40830	7962	
SP-288	110							17217	598	378850	27272	12358	18617	5359	47439	6328	
NCI-H522	109							3084	1363	253241	16600	6551	11824	2278	36243	2718	
U251	108							4147	0	1128364	18115	12185	32962	3153	44511	6643	
NCI-H460	107							6539	373	230300	18786	8509	12059	5746	54078	6280	
SNB-75	106							6777	0	452393	13060	6839	18803	4436	28896	5244	
NCI-H022M	105							2579	630	71892	8638	223	6216	2822	41104	4518	
SNB-19	104							6471	921	590327	19449	14470	18523	3222	49937	6532	
NCI-H26	103							7350	0	219881	17548	7958	12434	3103	50554	5744	
SK-OV-3	102							32859	310	108338	20696	10726	24187	3054	61587	8993	
NCI-H23	101							9457	0	202789	15647	7470	11071	2287	33170	2884	
IGROV1	100							5614	371	109602	13255	8342	15724	2898	39481	3518	
EXV2	99							18803	768	313545	14157	9518	9579	2981	41869	3318	
OVCA-8	98							5228	1110	358618	18612	8432	21788	2010	25017	2624	
HOP-62	97							12781	614	18774	10361	4718	16863	2604	34465	6113	
n.su8i SMC 10/21/82 #17	47							7808	0	317849	22815	4248	38600	3261	33500	3980	
n.hemocytes 27/25/82 #10	48							11086	0	177631	18183	6067	4047	3678	32090	4127	
TCGP	26							4478	137	8072	14410	12890	3096	588	30937	5335	
AS49-1								13802	240	159425	22184	6858	14419	3871	26128	5742	
AS49-3								8008	0	558454	15245	19296	19157	3430	22553	6471	
AS49-4								1491	5421	44905	11719	0	0	0	0	0	
AS49-5								139	4212	26336	6707	0	0	0	0	0	
AS49-6								278	5323	38473	10836	0	0	0	0	0	
AS49-7								488	2872	28588	10727	0	0	0	0	0	
EXV2-1								148	162	15733	8786	0	0	0	0	0	
EXV2-4								846	1343	88024	18784	0	0	0	0	0	
EXV2-5								1480	4260	78383	25018	0	0	0	0	0	
EXV2-7								635	834	22887	12511	0	0	0	0	0	
EXV2-8								0	0	58803	7740	0	0	0	0	0	
EXV2-9								732	1878	29892	11042	0	0	0	0	0	
MCF-7-1								840	718	50119	10820	0	0	0	0	0	
MCF-7-2								507	5245	68350	7883	0	0	0	0	0	
MCF-7-3								639	1155	140711	14817	0	0	0	0	0	
MCF-7-4								224	1050	81146	11019	0	0	0	0	0	
MCF-7-5								0	1337	10167	8726	0	0	0	0	0	
MCF-7-6								0	3885	91125	19485	0	0	0	0	0	
ADR-RES-1								425	525	27534	8062	0	0	0	0	0	
ADR-RES-2								0	361	15870	4449	0	0	0	0	0	
ADR-RES-3								268	472	33606	7549	0	0	0	0	0	
ADR-RES-4								650	7502	12923	13062	0	0	0	0	0	
ADR-RES-5								619	0	41827	24067	0	0	0	0	0	
ADR-RES-6								508	717	40970	18523	0	0	0	0	0	
WI-38-1								843	751	32710	9317	0	0	0	0	0	
WI-38-2								1151	3721	17091	11387	0	0	0	0	0	
WI-38-3								218	46177	84191	12284	0	0	0	0	0	
WI-38-4								532	12621	16493	13319	0	0	0	0	0	
WI-38-5								460	543	51837	17033	0	0	0	0	0	
WI-38-6								902	3311	48289	7885	0	0	0	0	0	
WI-38-7								213	1168	40254	16027	0	0	0	0	0	
WI-38-8								0	1048	37585	9575	0	0	0	0	0	
WI-38-9								84	0	68067	14723	0	0	0	0	0	
H1299-1								336	0	80284	14722	0	0	0	0	0	
H1299-2								338	2070	78789	25033	0	0	0	0	0	
H1299-3								204	1806	33235	10427	0	0	0	0	0	
H1299-4								440	0	41846	10384	0	0	0	0	0	
H1299-5								184	4270	37307	9382	0	0	0	0	0	
H1299-6								539	2003	23382	15628	0	0	0	0	0	
H1299-7								408	5597	36339	9134	0	0	0	0	0	
AS49-2								1123	3766	49630	21130	0	0	0	0	0	
EXV2-2								681	1380	43251	13827	0	0	0	0	0	
SF539-1								0	1849	19607	13005	0					

Table 3 (cont'd)

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Table 3 (cont'd)

Tissue	Tumor-adj	Normal-adj	Tumor - 10	Tumor cells	Normal	Endos	p53	SEQ 17	ANSEQ 20	SEQ 22	PTMSEQ 28	ANSEQ 29	DRSEQ 31	DRSEQ 32	ANSEQ 40	MASEQ 54	T	
adrenal gland - h								46825	13421	187762	8031	11409	2483	96250	599	4349		
lymph node - h								84639	1004	373107	14301	80824	15392	135195	338	2671		
bone marrow - h								82024	345	117789	11397	51933	6446	73538	0	294		
mammary gland - h								24799	0	18667	1710	2723	266	3276	154	306		
brain - h								54253	1826	188461	6870	929	1184	70030	2190	2311		
pancreas - h								71540	2036	48828	7425	7287	2972	31495	4955	1246		
coracoclavicular - h								82436	104	298725	10723	2745	2858	136678	6036	274		
ovary gland - h								87365	232	110587	15043	7314	2404	74870	3056	3472		
testis - h								103271	0	187092	22074	3038	1150	63217	1424	8838		
prostate - h								80242	894	105483	8213	8436	6569	126694	1506	4165		
renal artery - h								85084	5028	152975	10990	12234	2383	56346	5950	4517		
prostate - h								74934	1446	84243	10984	17733	1143	20480	979	86		
testis - h								59677	3153	88695	11342	15732	2410	32064	279	2130		
testis - h								80782	0	122833	3802	18767	1080	12009	0	223		
renal artery - h								82518	1478	187083	8127	18242	4178	87490	1544	3405		
testis - h								57531	171	575843	2744	1837	505	46874	1077	2017		
small intestine - h								43961	0	298349	865	4858	2245	31333	1102	2124		
kidney - h								42979	1357	80561	3331	14338	2021	21878	632	1632		
kidney - h								48325	8757	77677	1796	3202	1359	26570	2144	1494		
apical cord - h								54755	1315	53517	21224	5273	1063	21487	787	716		
testis - h								40332	3539	53033	4414	2272	1224	34138	947	413		
Spleen - h								44668	0	129409	2539	30444	4982	17845	0	622		
testis - h								37827	577	103801	818	25788	5316	33759	0	452		
intestine - h								18010	953	37850	1810	8695	1998	11833	665	331		
testis - h								44800	98	44543	13224	4547	33739	1802	1333			
thymus - h								85232	63	422519	10162	38950	6722	120548	1733	317		
HPAEC								67087	0	3134	3984	2437	1015	0	728	0		
thyroid gland - h								43670	542	181029	9252	4819	826	37702	0	755		
RPTEC								42248	30	42248	3372	3367	3367	418	0	0		
trachea - h								78966	303	144782	8232	30484	3321	42097	602	2352		
HPAEC								65184	650	21473	3421	0	2872	7056	397	0		
intestine - h								86678	354	142065	3371	8755	1003	37845	2648	3631		
HPAEC								51171	37	22364	2178	118	580	199	26	0		
Pancreas - h								46443	0	0	5314	13335	0	2589	0	1082		
lymph node - h								64018	0	0	5899	83785	2110	2825	208	0		
Shamless muscle - h								30349	418	26839	4136	26	219	2005	812	0		
testis - h								56177	64	3012	9198	1008	745	947	256	0		
testis - h								47872	0	2818	4886	1134	0	4386	492	0		
thymus - h								70722	0	0	3341	57019	1466	2672	220	0		
Duodenum - h								42191	145	0	4383	4470	560	2529	0	3081		
False brain - h								46080	570	0	6154	1108	205	1081	384	385		
Salivary gl. - h								35172	48	827	1319	17131	0	1205	0	0		
testis - h								57094	129	294	2689	13574	462	3483	326	0		
HT218-normal								12858	0	0	2058	91	37	0	356	0		
HT213-normal								8245	77	245	272	347	327	327	584	0		
HT157-normal								16329	0	0	248	163	0	542	0	0		
Bov-13								82144	1094	0	23735	8795	7232	5309	1480	12		
Bov-12								354	354	59857	59	0	42866	4027	1119	422	476	0
coracoclavicular - h								27729	0	0	229	829	50	0	0	0	0	
brain - h								31402	290	0	0	98	78	0	0	0	0	
RPTEC								71803	0	0	8004	8509	61	479	113	0		
lymph node - h								39786	277	335	2991	52657	283	367	0	0	0	
in situ SAC 102/182 #17								47280	22	0	788	41	0	273	54	0	0	
False brain - h								70908	0	6377	29585	10509	83	2749	1212	0	0	
HT388-normal								50974	0	399	0	10838	356	202	1110	0	0	
thymus - h								70826	0	634	42378	28110	721	750	526	115	0	
HT149 - normal								41371	416	0	0	43	166	325	0	0	0	
HEPM 3d untreated								61910	0	10739	6705	2892	225	3880	232	0	0	
intestine - h								69453	444	2041	24806	188533	8035	4242	12977	166	0	
trachea - h								48848	874	0	23053	128636	7113	2740	893	440	0	
thyroid gland - h								44846	0	1464	15691	64886	5240	1896	0	566	0	
Salivary gl. - h								61587	0	0	2684	38362	1045	347	0	0	0	
prostate - h								47809	525	0	280	29418	895	178	535	0	0	
ovary gland - h								30749	118	0	1592	18211	575	376	883	157	0	
Pancreas - h								44811	0	0	13038	1321	530	128	128	686	0	
mammary gland - h								86451	1168	0	8443	102692	7874	407	323	0	0	
breast - h								72421	667	3702	3722	10239	184	4728	1088	59	0	
testis - h								83188	444	0	3552	93342	6342	2616	1714	0	0	
test - h								83794	0	1047	11177	9023	1482	3474	1159	81	0	
Spleen - h								53225	0	138	2172	75586	8138	806	0	0	0	
apical cord - h								62962	454	0	23722	35430	3183	1843	1150	155	0	
small intestine - h								41822	38	0	2123	14058	2565	968	0	133	0	
coracoclavicular - h								60372	0	19	2079	62231	3802	2424	525	896	0	
bone marrow - h								50557	27	0	0	27722	358	0	0	0	0	
adrenal gland - h								84753	27	0	2305	5560	56	0	0	355	0	
HPAEC								27189	0	0	0	1157	0	432	0	0	0	
HT388-normal								38846	504	0	0	20358	0	741	506	0	0	
HT382-normal								44114	0	1370	0	3633	0	308	0	605	0	
Bov-11								239	239	73567	1154	0	1180	10288	1964	14	218	144
Bov-8								50453	281	0	108	22811	537	0	0	0	0	
HT372-normal								78287	0	1188	2687	13756	0	0	0	0	0	
Bov-7								71554	374	0	1052	1379	755	0	801	0	0	
Bov-6								52712	0	307	0	1671	1227	0	73	196	0	
Bov-2								45448	229	0	581	213	740	0	575	0	0	
Bov-1								41869	0	783	1630	942	0	0	0	0	0	
breast - h								33431	505	0	1299	6262	57	0	56	0	0	
testis - h								46488	0	2261	744	1154	0	0	139	0	0	
epididym - h								59011	0	767	69	839311	3007	323	579	0	0	
testis - h								33067	493	0	2248	353	43	339	131	0	0	
placenta - h								43829	0	0	0	11419	2776	0	397	0	0	
HCAEC								34737	290	38	16271	0	0	0	0	43	0	
testis - h								210	0	0	23	8938	226	0	449	0	0	
HPAEC								48678	155	87	1269	2433	39	1108	0	0	0	
Duodenum - h								39299	0	0	0	7396	35	322	335	120	0	
Shamless muscle - h								34158	0	0	562	34	0	0	323	295	0	
Pancreas - h								23307	0	148	0	13233	0	565	0	0	0	
testis - h								26853	0	0	179	8680	0	0	0	0	0	
Salivary gl. - h								30958	0	8020	566	15657	0	2026	83	0	0	
HEPM 3d TGFβ1 desargant-DHase								21310	326	546</								

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Table 3 (cont'd)

Tissue	Tumor - < ym	Normal - < ym	Tumor - to	Tumor cells	Normal	Endos	p53	SEQ 17	AA SEQ 20	SEQ 22	PT SEQ 25	AA SEQ 28	OR SEQ 31	OR SEQ 33	AA SEQ 40	MA SEQ 44
C-Met				165				25641								
T-470				166				43253	1415	1044	2482	2263	8374	109	0	89
Kan-3				169				52705	0	4622	638	771	1518	1109	0	124
CRL 1441 RNA B20				171				30045	47	218	900	0	88	0	0	0
FBT untreated + DNase				181				11955	0	486	1871	242	339	32	192	176
KB poly A+				183				21315	0	0	0	0	0	691	120	0
HOS poly A+				194				23563	194	0	1630	2000	1064	365	0	0
ACCH				196				39104	0	0	1150	3112	1662	145	46	30
LAOCC-42				198				32810	0	1874	1898	823	874	750	371	128
MCF-7ADP-RES				200				19120	130	99	1294	613	848	0	553	0
UTOS (Murchy) poly A+				202				12981	314	0	714	405	215	178	0	433
WISH (Cottarelli) poly A+				204				8408	0	0	1294	572	149	0	967	0
458 modulo mRNA				206				12990	0	0	14	0	82	0	209	0
CCL137 RNA 32105				208				83540	0	1041	3506	14092	411	0	411	0
W138 72h 0.5%FBS, 24h 10% FBS				218				21190	0	563	0	831	47	0	436	0
CRL 1441 + TPA (24h) B20				219				22063	0	0	0	3727	0	149	176	134
Kan-1				220				14725	0	133	0	0	355	862	0	0
Kan-2				221				28118	84	0	1468	338	447	157	0	0
Kan-4				223				32548	50	0	353	0	235	0	0	0
HOP-82				225				37530	43	904	194	0	22	0	887	0
MCL-4				241				22249	0	0	58	726	740	83	0	0
EXV2				242				18708	0	1383	142	22	394	636	0	56
HL-60				243				22457	367	303	1836	537	2757	371	0	0
HG-402				244				33149	0	0	0	0	4255	2003	0	0
RPMI 8226				245				28942	900	901	308	307	958	1115	1154	1434
AS49ATCC				246				34345	0	0	329	567	1814	14	222	60
SR				247				35516	0	0	865	0	153	0	401	0
OVCA-3				248				19586	0	1351	0	394	733	0	897	62
HCT-15				249				27443	30	500	669	852	1417	704	3625	266
OVCA-4				250				34518	0	5278	81	1086	2305	1074	0	0
UO-31				251				10333	478	1077	0	157	587	0	718	0
OVCA-5				252				13456	0	415	0	242	757	0	0	116
SH-12C				253				60297	0	3782	1757	564	7068	535	1034	271
OVCA-6				254				29550	119	0	3368	0	304	0	0	21
LOX BMV				255				16467	190	573	582	512	215	819	104	0
IGROV1				256				45485	0	18804	0	784	8133	0	278	890
SK-MEL-2				257				26126	121	290	740	373	1340	390	231	206
SK-OV-3				258				34725	0	0	0	0	0	0	0	0
SK-MEL-5				259				17172	262	0	0	312	584	0	157	118
SP-203				260				13827	212	505	0	141	339	0	54	0
SK-MEL-28				261				30531	856	1771	824	955	3468	0	658	408
K-562				262				34725	0	337	817	1130	2325	0	282	0
LAOCC-257				263				30125	190	11739	0	179	2690	590	55	336
W1				264				25143	184	0	606	210	817	97	612	0
MCF7				265				19129	48	0	0	176	34	278	0	0
MDA-MB-435				267				88523	0	2827	459	607	1109	2556	448	583
MDA-MB-435				268				26815	0	878	815	40	503	5	0	0
MDA-MB-435				269				26815	0	878	815	40	503	5	0	0
MDA-MB-435				270				26815	0	878	815	40	503	5	0	0
MDA-MB-435				271				26815	0	878	815	40	503	5	0	0
MDA-MB-435				272				26815	0	878	815	40	503	5	0	0
MDA-MB-435				273				26815	0	878	815	40	503	5	0	0
MDA-MB-435				274				26815	0	878	815	40	503	5	0	0
MDA-MB-435				275				26815	0	878	815	40	503	5	0	0
MDA-MB-435				276				26815	0	878	815	40	503	5	0	0
MDA-MB-435				277				26815	0	878	815	40	503	5	0	0
MDA-MB-435				278				26815	0	878	815	40	503	5	0	0
MDA-MB-435				279				26815	0	878	815	40	503	5	0	0
MDA-MB-435				280				26815	0	878	815	40	503	5	0	0
MDA-MB-435				281				26815	0	878	815	40	503	5	0	0
MDA-MB-435				282				26815	0	878	815	40	503	5	0	0
MDA-MB-435				283				26815	0	878	815	40	503	5	0	0
MDA-MB-435				284				26815	0	878	815	40	503	5	0	0
MDA-MB-435				285				26815	0	878	815	40	503	5	0	0
MDA-MB-435				286				26815	0	878	815	40	503	5	0	0
MDA-MB-435				287				26815	0	878	815	40	503	5	0	0
MDA-MB-435				288				26815	0	878	815	40	503	5	0	0
MDA-MB-435				289				26815	0	878	815	40	503	5	0	0
MDA-MB-435				290				26815	0	878	815	40	503	5	0	0
MDA-MB-435				291				26815	0	878	815	40	503	5	0	0
MDA-MB-435				292				26815	0	878	815	40	503	5	0	0
MDA-MB-435				293				26815	0	878	815	40	503	5	0	0
MDA-MB-435				294				26815	0	878	815	40	503	5	0	0
MDA-MB-435				295				26815	0	878	815	40	503	5	0	0
MDA-MB-435				296				26815	0	878	815	40	503	5	0	0
MDA-MB-435				297				26815	0	878	815	40	503	5	0	0
MDA-MB-435				298				26815	0	878	815	40	503	5	0	0
MDA-MB-435				299				26815	0	878	815	40	503	5	0	0
MDA-MB-435				300				26815	0	878	815	40	503	5	0	0
MDA-MB-435				301				26815	0	878	815	40	503	5	0	0
MDA-MB-435				302				26815	0	878	815	40	503	5	0	0
MDA-MB-435				303				26815	0	878	815	40	503	5	0	0
MDA-MB-435				304				26815	0	878	815	40	503	5	0	0
MDA-MB-435				305				26815	0	878	815	40	503	5	0	0
MDA-MB-435				306				26815	0	878	815	40	503	5	0	0
MDA-MB-435				307				26815	0	878	815	40	503	5	0	0
MDA-MB-435				308				26815	0	878	815	40	503	5	0	0
MDA-MB-435				309				26815	0	878	815	40	503	5	0	0
MDA-MB-435				310				26815	0	878	815	40	503	5	0	0
MDA-MB-435				311				26815	0	878	815	40	503	5	0	0
MDA-MB-435				312				26815	0	878	815	40	503	5	0	0
MDA-MB-435				313				26815	0	878	815	40	503	5	0	0
MDA-MB-435				314				26815	0	878	815	40	503	5	0	0
MDA-MB-435				315				26815	0	878	815	40	503	5	0	0
MDA-MB-435				316				26815	0	878	815	40	503	5	0	0
MDA-MB-435				317				26815	0	878	815	40	503	5	0	0
MDA-MB-435				318				26815	0	878	815	40	503	5	0	0
MDA-MB-435				319				26815	0	878	815	40	503	5	0	0
MDA-MB-435				320				26815	0	878	815	40	503	5	0	0
MDA-MB-435				321				26815	0	878	815	40	503	5	0	0
MDA-MB-435				322				26815	0	878	815	40	503	5	0	0
MDA-MB-435				323				26815	0	878	815	40	503	5	0	0
MDA-MB-435				324				26815	0	878	815	40	503	5	0	0
MDA-MB-435				325				26815	0	878	815	40	503	5	0	0
MDA-MB-435				326				26815	0	878						

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Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1a	Tumor calls	Normal	Enrich	p53	SEG 844	TRSD 43	AA SEQ 47	AA SEQ 44	AA SEQ 49	AA SEQ 51	KU SEQ 32	AA SEQ 34	CO SEQ 35	CL
DaPeng-7								85383	578	729	0	0	0	0	0	0	0
DaPeng-8								26490	248	374	0	0	0	0	0	0	0
DaPeng-9								44303	718	156	0	0	0	0	0	0	0
DaPeng-11								24987	0	628	0	0	0	0	0	0	0
DaPeng-12								95743	0	495	0	0	0	0	0	0	0
DaPeng-10								20110	294	211	0	0	0	0	0	0	0
DaPeng-1								7684	964	23	0	0	0	0	0	0	0
DaPeng-2								2129	281	38	0	0	0	0	0	0	0
DaPeng-3								688	1703	265	0	0	0	0	0	0	0
DaPeng-4								26552	324	0	0	0	0	0	0	0	0
DaPeng-5								49680	0	51	0	0	0	0	0	0	0
DaPeng-6								32900	20	0	0	0	0	0	0	0	0
AS49 - 8								1956	90	0	0	0	0	0	0	0	0
EOVX - 8								559	212	0	0	0	0	0	0	0	0
HCT-116 - 7								wt	0	722	0	0	0	0	0	0	0
HCT-116 - 8								wt	771	122	55	0	0	0	0	0	0
HT29 - 1								mutant	310	0	144	0	0	0	0	0	0
HT29 - 7								mutant	0	25	0	0	0	0	0	0	0
HT29 - 8								mutant	0	51	0	0	0	0	0	0	0
SF539 - 7								wt	1397	937	36	0	0	0	0	0	0
SF539 - 8								wt	3330	71	130	0	0	0	0	0	0
SF-268-7								mutant	17076	887	0	0	0	0	0	0	0
SF-268-8								mutant	15322	32	116	0	0	0	0	0	0
OVCAR-4 - 7								wt	1233	29	0	0	0	0	0	0	0
OVCAR-4 - 8								wt	12764	6	178	0	0	0	0	0	0
OVCAR-5 - 7								mutant	4732	0	0	0	0	0	0	0	0
OVCAR-5 - 8								mutant	3132	0	4	0	0	0	0	0	0
MCF-7 - 8								wt	3375	440	0	0	0	0	0	0	0
ADR-RES - 8								mutant	629	0	0	0	0	0	0	0	0
HeLa - 8								HPV E6	1027	89	0	0	0	0	0	0	0
SW480 - 7								mutant	1922	717	22	0	0	0	0	0	0
SW480 - 8								mutant	412	47	72	0	0	0	0	0	0
HT29 - 8								mutant	0	167	10	0	0	0	0	0	0
C33A - 7								mutant	0	235	4	0	0	0	0	0	0
C33A - 8								mutant	444	0	0	0	0	0	0	0	0
U2OS - 7								mutant	28519	148	84	0	0	0	0	0	0
U2OS - 8								mutant	4758	418	0	0	0	0	0	0	0
Hu68 - 7								wt	1303	0	0	0	0	0	0	0	0
Hu68 - 8								wt	512	324	0	0	0	0	0	0	0
WI 38 - 8								wt	1504	41	0	0	0	0	0	0	0
450 measles RNA																	
CRL 1572 3/17/88																	
Bov-4								84	642	0	0	189	5574	0	88	0	12425
HT368									0	0	0	5011	4675	0	0	7	16708
HT375									0	0	24	0	4412	215	0	0	2038
HT385									10732	0	0	0	5567	8257	81	158	6910
HT308									0	0	8	0	6143	168	0	0	24562
Bov-3								173	53	0	7	0	3031	498	328	297	1815
Bov-5								175	0	58	34	1425	843	264	0	0	53
Bov-9								177	0	0	17	2354	226	0	0	0	1299
h keratinocytes 2/25/92 #10									0	0	93	13	3875	9	112	0	186
Bov-10								237	0	0	18	123	4055	150	40	251	3522
HTB10									0	0	0	0	75311	0	421	550	1625
h fibroblasts 3/31/92 #12									0	0	30	23	4548	0	0	206	863
prostate h									0	0	0	81	2983	0	0	0	5650
MDMG-OS poly A+									916	0	0	0	2657	291	84	0	2243
SA-OS (Mundy) poly A+									0	0	0	56	1148	0	176	0	1566
BK poly A+									0	0	57	0	2520	0	257	0	5073
HCT-116 - 3									wt	298	22	3	0	0	0	0	0
HCT-116 - 4									wt	438	1211	0	0	0	0	0	0
HCT-116 - 5									wt	127	304	26	0	0	0	0	0
HCT-116 - 6									wt	1178	0	0	0	0	0	0	0
AS49 - 6									wt	0	0	4	0	0	0	0	0
HT29 - 3									mutant	18958	0	247	0	0	0	0	0
EOVX - 6									mutant	581	0	0	0	0	0	0	0
HT29 - 4									mutant	0	17	28	0	0	0	0	0
HT29 - 5									mutant	1078	0	244	0	0	0	0	0
HT29 - 6									wt	0	0	52	0	0	0	0	0
OVCAR-4 - 3									wt	5253	108	30	0	0	0	0	0
OVCAR-4 - 4									wt	0	0	0	0	0	0	0	0
OVCAR-4 - 5									wt	2869	271	0	0	0	0	0	0
OVCAR-4 - 6									wt	0	0	32	0	0	0	0	0
SF539 - 3									wt	4462	146	140	0	0	0	0	0
SF539 - 4									wt	3258	281	32	0	0	0	0	0
SF539 - 5									wt	591	0	30	0	0	0	0	0
SF539 - 6									wt	1280	312	0	0	0	0	0	0
OVCAR-5 - 3									mutant	2566	0	118	0	0	0	0	0
OVCAR-5 - 4									mutant	0	0	37	0	0	0	0	0
OVCAR-5 - 6									mutant	241	0	0	0	0	0	0	0
ADR-RES - 6									wt	629	646	60	0	0	0	0	0
MCF-7 - 6									wt	1297	1521	0	0	0	0	0	0
HeLa - 6									mutant	0	269	0	0	0	0	0	0
HT299 - 5									mutant	0	303	139	0	0	0	0	0
SW480 - 3									mutant	1137	629	67	0	0	0	0	0
SW480 - 4									mutant	3274	0	39	0	0	0	0	0
SW480 - 5									mutant	895	725	0	0	0	0	0	0
SW480 - 6									mutant	180	0	90	0	0	0	0	0
C33A - 3									mutant	4870	0	0	0	0	0	0	0
C33A - 4									mutant	0	678	80	0	0	0	0	0
C33A - 5									mutant	3086	0	0	0	0	0	0	0
Hu68 - 6									wt	0	0	69	0	0	0	0	0
U2OS - 3									mutant	71697	293	0	0	0	0	0	0
U2OS - 4									mutant	4526	0	0	0	0	0	0	0
U2OS - 5									mutant	7831	149	17	0	0	0	0	0
U2OS - 6									mutant	0	0	49	0	0	0	0	0
WI 38 - 6									wt	2111	0	242	0	0	0	0	0
Hu68 - 3									wt	2662	0	57	0	0	0	0	0
Hu68 - 4									wt	53108	1252	246	0	0	0	0	0
SF-268-3									mutant	123026	0	0	0	0	0	0	0
SF-268-4									mutant	70551	1540	0	0	0	0	0	0
SF-268-5									mutant	32295	292	0	0	0	0	0	0
SF-268-6									mutant	0	2127	0	0	0	0	0	0
DaPeng-13									mutant	43164	628	750	0	0	0	0	0
Michal - 20									wt	5219	5543	71	0	0	0	0	0
Michal - 21									wt	5250	3048	128	0	0	0	0	0
Michal - 22									wt	7053	9567	399	0	0	0	0	0
OVCAR-5 - 5									mutant	2940	763	112	0	0	0	0	0
Michal - 10									wt	2789	1330	113	0	0	0	0	0
Michal - 11									wt	2168	781	45	0	0	0	0	0
Michal - 12									wt	6365	81	286	0	0	0	0	0
Michal - 13									wt	4034	133	1023	0	0	0	0	0
Michal - 14																	

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Table 3 (contd)

Tissue	Tumor-ym	Normal-ym	Tumor-1a	Tumor calls	Normal	Endseq	p33	SEQ 56	ANSEQ 57	WSEQ 58	ANSEQ 59	WSEQ 60	ANSEQ 61	WSEQ 62	ANSEQ 63	WSEQ 64	ANSEQ 65	WSEQ 66	ANSEQ 67	WSEQ 68	ANSEQ 69	WSEQ 70	ANSEQ 71	WSEQ 72	ANSEQ 73	WSEQ 74	ANSEQ 75
adrenal gland - h	1							1179	4339	12721	10216	11127	16736	4756	24187	161827											
lymph node - h	2							1862	70208	24568	33524	13683	27483	7405	31327	144250											
bone marrow - h	3							57	50493	12341	24326	26128	21478	3999	86136	103964											
mammary gland - h	4							1027	5569	509	398	3128	2968	9641	4197	30763											
brain - h	5							1567	33741	2567	6870	113637	27644	36781	13512	88774											
pancreas - h	6							2734	38449	11763	2563	14284	19704	3671	27524	80255											
coracohum - h	7							2187	60537	2020	29667	80114	55613	7287	33350	150168											
parathyroid gland - h	8							2771	65207	14965	10920	5342	20661	5644	23788	126706											
testis - h	9							2102	65093	14224	9117	115508	32685	34780	23243	130701											
placenta - h	10							7934	50118	15882	8421	27503	31523	4144	28448	118921											
testis - h	11							2058	45761	9662	12231	27386	42058	4485	38782	202584											
prostate - h	12							2873	23487	15030	3127	8510	18409	4448	8670	180588											
testis - h	13							1862	21433	13743	10943	16727	24911	2114	47817	95705											
salivary gl. - h	14							1275	20668	9416	1854	18025	15078	2253	23301	188829											
testis - h	15							4578	50512	6396	6440	27133	27710	3092	32855	175336											
small intestine - h	16							3544	34674	86	5882	6633	12917	1781	9573	128486											
testis - h	17							1236	18128	3837	3249	17179	18472	2594	8412	108323											
testis - h	18							2013	18561	17299	1848	9510	17382	1878	15005	254953											
testis - h	19							1838	23780	6099	10680	7368	38048	2068	17635	150364											
testis - h	20							2970	15871	5250	6086	3857	29454	1869	7081	130873											
testis - h	21							4795	15711	8344	4517	3893	36372	2313	10324	110984											
testis - h	22							1065	20770	16369	2002	3127	20754	2057	4681	114233											
testis - h	23							464	22182	6232	5714	4273	38012	2183	6428	125666											
testis - h	24							1819	10425	12130	1652	4031	20680	2181	6584	387434											
testis - h	25							5462	103118	6356	10159	6356	10159	4776	20107	122359											
testis - h	26							1076	57864	40343	18133	17350	18556	1763	33446	115421											
testis - h	27							294	14420	0	896	4196	12372	3412	0	83109											
testis - h	28							2594	28474	2465	2102	11290	11291	3114	13597	80705											
testis - h	29							508	12744	0	129	1891	15156	3649	12263	88954											
testis - h	30							5137	74625	8278	3113	24729	22943	3340	21457	114300											
testis - h	31							18653	21362	28857	3353	0	25487	2697	9425	78553											
testis - h	32							1208	41825	3525	6655	34917	18410	2493	15360	68824											
testis - h	33							564	11765	750	0	435	17863	1892	4218	72812											
testis - h	34							10918	0	0	0	0	0	0	0	0											
testis - h	35							564	11765	750	0	435	17863	1892	4218	72812											
testis - h	36							1745	12072	5592	2849	638	7790	3831	3205	150364											
testis - h	37							621	3917	0	1071	2029	4530	805	2524	38353											
testis - h	38							8143	354	4517	1095	14398	2211	50874	76358												
testis - h	39							896	6677	0	8788	598	4578	688	1733	6881											
testis - h	40							1810	11513	1144	4500	53	5096	2118	8482	94284											
testis - h	41							827	6296	520	103	405	4145	1344	5178	56243											
testis - h	42							1670	16210	5843	551	6086	3645	8291	124700												
testis - h	43							1366	4890	0	2394	0	4275	3451	3676	81426											
testis - h	44							1658	17951	0	4560	0	13181	2101	10030	128683											
testis - h	45							365	0	7137	125	79	130	158	1614	5011	20873										
testis - h	46							0	6044	0	131	0	743	0	192	0	24933										
testis - h	47							361	451	2420	0	0	22	171	1861	336	30436										
testis - h	48							356	356	299	91127	404	1116	5137	10567	14131	14920	172785									
testis - h	49							354	354	1780	128946	0	21	3012	6067	7821	2525	95002									
testis - h	50							342	0	4508	73	83	228	478	2304	1611	30731										
testis - h	51							342	0	1387	715	175	0	129	2280	443	33272										
testis - h	52							334	334	1246	21042	10083	0	357	701	4284	274	165421									
testis - h	53							337	0	153	12413	0	1318	7	1559	3969	0	63500									
testis - h	54							337	0	5643	0	0	84	34	2860	0	43499										
testis - h	55							328	266	64197	537	825	1683	12083	8866	3780	99415										
testis - h	56							327	1215	4596	0	87	1	1803	1862	7794	38102										
testis - h	57							326	463	78773	0	287	5123	4822	8846	1169	89548										
testis - h	58							321	0	211	57	0	1	1316	2450	152	37063										
testis - h	59							320	1317	22630	0	848	214	5613	4217	2089	66214										
testis - h	60							318	0	85419	1050	1252	1531	15860	11203	30226	123075										
testis - h	61							316	0	40355	805	1959	2194	12222	8263	140783	104686										
testis - h	62							314	1	42897	0	1846	151	10232	6871	88001	147188										
testis - h	63							311	0	8659	0	0	0	2738	2519	4532	101244										
testis - h	64							309	0	6480	0	233	129	1622	2482	3056	70453										
testis - h	65							307	858	14108	0	114	235	1127	2496	2133	38646										
testis - h	66							305	0	6503	0	45	0	2636	2581	3386	55383										
testis - h	67							303	104	26215	589	467	220	667	4345	18318	88789										
testis - h	68							302	1973	18158	0	3240	507	9250	4496	7821	85038										
testis - h	69							297	1147	103861	7296	489	1602	19319	7297	28073	140418										
testis - h	70							296	2887	40917	2131	320	1898	8744	6235	131131	131980										

Table 3¹⁷¹ (cont'd)

Id	Tumor-gym	Normal-gym	Tumor - 1o	Tumor cells	Normal	Endos	p33	SEQ 17	AMSEQ 20	SGSEQ 22	PTSEQ 26	AMSEQ 28	DMSEQ 31	DMSEQ 33	AMSEQ 40	MASEQ 44	T	
Ms STET	155							48043	143	11814	7266	2356	897	12515	0	369		
MCF-7ADR-RES	153							48543	0	70411	0	0	15559	0	0	0		
MCF7	151							53849	804	30604	11924	2950	218	13420	0	0		
M14	149							65302	371	22226	15025	2725	257	4104	975	73		
UACC-257	147							38003	1993	72538	4018	1121	0	32363	0	311		
UACC-62	145							27441	0	7896	302	996	74	9020	306	20		
SK-MEL-28	144							20951	71	10249	1402	2016	634	4087	176	264		
UO-31	143							56230	0	12483	3319	844	1206	1827	1685	0		
SK-MEL-5	142							23301	0	13718	1082	110	260	18600	490	134		
KM-12	141							30992	297	8223	2928	5	85	1287	0	0		
HCT-MEL-2	140							30577	0	58294	2528	977	495	19663	0	189		
HCT-15	139							54739	445	25282	2789	1572	287	8966	526	0		
MDAMB-23	138							45066	1468	86498	4282	243	294	12794	242	451		
COLO 205	137							57736	0	18062	0	496	0	5746	0	17		
LOX IMVI	136							26010	0	161759	1512	680	562	26228	248	628		
SW-620	135							39849	437	29579	750	203	198	9406	375	166		
Tx-10	134							43207	69	10978	1719	963	262	7085	72	48		
HCT 116	133							37409	345	18778	1178	0	458	3812	721	0		
T86-0	132							34173	0	27523	0	534	157	6539	567	14		
HCC-T598	131							62362	734	17250	0	159	239	3661	0	54		
MDA-MB-231	130							36802	329	81729	1353	617	203	10449	275	22		
PC-3	129							35262	33	50087	1005	106	457	8255	519	0		
RDX 330	128							40444	305	82661	3148	2477	2041	26824	478	0		
DL-145	127							37777	0	8182	5153	140	400	15854	0	0		
484-1	126							33257	33	515153	9477	96	521	22266	596	190		
SR	125							37809	0	50238	5967	1172	551	26628	156	0		
A498	124							39104	0	106212	4214	0	1665	2925	423	668		
MDA-MB-226	123							50455	737	8134	2600	2182	525	13014	0	0		
HL-60	122							32575	95	44277	536	1473	590	23030	0	0		
MDA-MB-231	121							36440	968	2018	0	325	77	707	68	380		
MOLT-4	120							28309	782	17195	861	532	1023	4039	0	0		
OVCAR-5	119							25375	0	42226	1986	337	1595	6652	569	77		
U562	118							54713	562	181618	2732	367	223	10439	0	316		
OVCAR-4	117							42588	1500	108942	8320	2239	2583	525	1228	1170		
CCRF-CEM	116							38120	576	100622	2781	831	470	11560	0	0		
OVCAR-3	115							52017	548	47691	1242	969	303	10248	2443	0		
IF-33	114							34695	86	14022	2355	57	358	10263	0	250		
HOP-62	113							19576	0	64930	1645	1190	605	7729	0	0		
SF-295	112							40830	257	17808	700	708	1164	5386	417	637		
ASBMTCC	111							147439	0	78728	1610	498	303	17019	1514	672		
SF-268	110							30245	84	58487	1372	1834	1767	7347	482	0		
NCH-H22	109							44511	0	61028	565	813	278	8039	0	94		
U251	108							54076	433	48739	573	124	718	17977	806	0		
NCH-H20	107							26266	356	75718	436	405	803	17568	809	152		
SNB-75	106							41104	0	17012	407	456	365	4782	864	316		
NCH-H22M	105							49807	69	10250	3056	4827	461	26339	746	0		
SNB-19	104							90554	442	13625	1417	451	2644	37654	156	626		
NCH-H26	103							61587	833	8072	2208	1331	205	18328	743	69		
SK-OV-3	102							33170	0	18586	3441	522	18811	342	0	0		
NCH-H23	101							394811	0	5616	4702	140	203	26599	0	491		
ERUV1	100							11669	442	11790	3691	229	207	13118	0	0		
ERVX	99							25017	0	1457	1627	0	642	1177	0	0		
OVCAR-8	98							31129	0	1823	19	107	197	9397	17	0		
HOP-92	97							33300	0	18562	1074	364	465	12792	492	103		
B. Brachyotus 3/31/92 #12	48							32980	0	8173	1558	5270	141	401	200	184		
B. euk. SMC 10/21/92 #17	47							30537	0	1665	0	150	150	8623	203	122		
B. leucostictus 2/25/92 #10	46							29128	65	23461	1117	0	82	10270	344	0		
TGSP	26							22853	700	18108	7310	86	120	5277	1704	111		
A549 - 1	0						wt	0	0	0	349	1138	4388	413	5711	0		
A549 - 2	0						wt	0	0	0	631	124	4878	520	10333	0		
A549 - 3	0						wt	0	0	0	0	1294	7999	0	8902	0		
A549 - 4	0						wt	0	0	0	0	458	6066	143	0	0		
A549 - 5	0						wt	0	0	0	0	813	5874	787	0	0		
ERVX - 1	0						mutant	0	0	0	1340	3420	6820	475	2339	0		
ERVX - 4	0						mutant	0	0	0	2098	4210	10681	330	190	0		
ERVX - 3	0						mutant	0	0	0	1909	0	4661	0	705	0		
ERVX - 5	0						mutant	0	0	0	284	1113	5697	137	0	0		
ERVX - 7	0						mutant	0	0	0	37	7453	867	0	0	0		
MCF-7 - 1	0						wt	0	0	0	453	801	110	3344	155	0		
MCF-7 - 3	0						wt	0	0	0	16	1048	2097	0	482	0		
MCF-7 - 4	0						wt	0	0	0	875	827	1028	218	1366	0		
MCF-7 - 5	0						wt	0	0	0	1181	2631	6028	0	868	0		
MCF-7 - 7	0						wt	0	0	0	590	433	607	629	0	0		
ADR-RES - 1	0						mutant	0	0	0	0	2736	2787	4698	2088	0		
ADR-RES - 2	0						mutant	0	0	0	1148	3462	4639	1096	8	0		
ADR-RES - 3	0						mutant	0	0	0	112	0	2817	57	60	0		
ADR-RES - 5	0						mutant	0	0	0	403	2369	852	0	0	0		
ADR-RES - 7	0						mutant	0	0	0	0	2011	2698	1855	898	498	0	
WI 38 - 1	0						wt	0	0	0	776	3646	589	1631	0	0		
WI 38 - 3	0						wt	0	0	0	865	8906	8200	197	0	0		
WI 38 - 4	0						wt	0	0	0	1831	3066	6486	0	1593	0		
WI 38 - 5	0						wt	0	0	0	1300	7877	3292	563	597	0		
WI 38 - 7	0						wt	0	0	0	1456	3377	5628	312	0	0		
HLA-B - 1	0						wt	0	0	0	893	0	1918	0	60	0		
HLA-B - 3	0						HPV E6	0	0	0	842	849	4257	546	0	0		
HLA-B - 4	0						HPV E6	0	0	0	290	281	5658	335	650	0		
HLA-B - 5	0						HPV E6	0	0	0	1177	1708	4044	1260	173	0		
HLA-B - 7	0						HPV E6	0	0	0	1543	274	4769	0	0	0		
HI299 - 1	0						mutant	0	0	0	114	2065	2347	0	237	0		
HI299 - 2	0						mutant	0	0	0	0	431	2212	542	546	0		
HI299 - 4	0						mutant	0	0	0	267	123	4674	421	612	0		
HI299 - 5	0						mutant	0	0	0	0	1456	2279	26	0	0		
HI299 - 7	0						wt	0	0	0	458	1853	1167	10	0	0		
ASIF - 2	0						wt	0	0	0	334	756	2012	286	634	0		
BRVX - 2	0						mutant	0	0	0	1435	630	20773	0	0	0		
HCT-118 - 1	0						wt	0	0	0	1196	330	6649	1646	296	0		
HCT-118 - 2	0						wt	0	0	0	2960	2935	8264	148	811	0		
HI28 - 3	0						mutant	0	0	0	1014	29411	1846	496	0	0		
SF539 - 1	0						wt	0	0	0	313	2130	1019	0	5477	0		
SF539 - 2	0						wt	0	0	0	819	54471	744	780	179	0		
SF-268-1	0						mutant	0	0	0								

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Table 3 (cont'd)

Tissue	Tumor-eyn	Normal-eyn	Tumor - 1a	Tumor cells	Normal	Endoc	AS3	SEQ 17	AS SEQ 39	SD SEQ 21	PT SEQ 21	AS SEQ 29	DR SEQ 31	DR SEQ 632	AS SEQ 49	MA SEQ 644
DuPang-7								0	0	0	21691	8478	315861	2728	122	0
DuPang-8								0	0	0	10053	8543	17854	1590	1078	0
DuPang-9								0	0	0	9122	1508	25973	1318	684	0
DuPang-11								0	0	0	7501	8218	14351	1857	869	0
DuPang-12								0	0	0	3497	3208	16748	1028	0	0
DuPang-10								0	0	0	6432	286	19829	211	210	0
DuPang-2								0	0	0	3941	17336	8787	832	17852	0
DuPang-3								0	0	0	3679	10389	6327	148	69825	0
DuPang-4								0	0	0	4784	2948	2782	3207	4773	0
DuPang-5								0	0	0	1944	4731	97	4216	803	0
DuPang-6								0	0	0	1170	2020	327	1817	2183	0
AS3-8								0	0	0	12057	5346	0	2639	1453	0
EXV-8								0	0	0	1513	1484	3652	0	427	0
HCT-116-7								0	0	0	742	2507	3043	5499	619	0
HCT-116-8								0	0	0	614	6117	2307	761	0	0
HT29-1								0	0	0	420	3096	3122	691	0	0
HT29-7								0	0	0	444	150	8	0	151	0
HT29-8								0	0	0	1051	2006	2178	0	1148	0
SP339-7								0	0	0	0	6143	2843	1075	208	0
SP339-8								0	0	0	99	10246	2922	562	0	0
SP-208-7								0	0	0	771	6901	2712	1198	1054	0
SP-208-8								0	0	0	1169	8034	4622	394	0	0
OVCAR-4-7								0	0	0	0	1284	6363	0	0	0
OVCAR-4-8								0	0	0	2950	2109	13609	585	3736	0
OVCAR-5-7								0	0	0	0	957	21830	0	0	0
OVCAR-5-8								0	0	0	89	2553	7100	2593	0	0
MCF-7-6								0	0	0	0	3539	1821	0	190	0
ADR-465-8								0	0	0	0	672	3521	0	0	0
HeLa-8								0	0	0	1629	225	4769	1418	0	0
SW480-7								0	0	0	246	841	4942	0	1427	0
SW480-8								0	0	0	0	870	4328	0	1166	0
HT29-8								0	0	0	1465	4781	2495	208	49	0
C33A-7								0	0	0	0	2052	2718	1002	837	0
C33A-8								0	0	0	0	5683	451	865	0	0
U2OS-7								0	0	0	2235	4649	3018	877	1215	0
U2OS-8								0	0	0	31	4860	8016	0	0	0
He6-7								0	0	0	10767	346	3155	144	0	0
He6-8								0	0	0	1446	1163	3374	1882	0	0
WI 38-8								0	0	0	0	1470	0	3574	0	458
454 modulator RNA								0	0	0	3788	0	299	4182	0	0
CR11572_3/1/89								0	0	0	4415	543	27	578	0	0
Bea-4								84	38610	0	0	1007	3021	1552	0	336
HT375								0	32554	0	0	7887	21100	3573	29	0
HT375								0	27558	0	386	662	2980	318	0	0
HT308								0	76812	0	0	143701	8954	1359	0	0
Bea-3								173	38521	651	0	0	32309	1103	165	873
Bea-5								173	19950	36	0	0	1954	1010	78	178
Bea-9								177	39076	0	142	303	0	643	0	118
h. keratinocytes 2/25/92 #10								237	50327	0	0	3049	556	49	0	1796
Bea-10								0	45162	257	0	245	733	2244	400	105
HTB10								0	86289	0	0	1379	3583	0	0	0
h. fibroblasts 3/31/92 #12								0	44374	88	0	0	4810	70	0	261
prostate h								0	28035	7	0	0	5782	14	0	0
MMNK-OS poly A+								0	24878	236	1075	3562	3701	1721	1048	0
SA-OS (Mundy) poly A+								0	27087	0	0	10786	5681	874	0	0
MK poly A+								0	32124	0	261	12609	10417	478	1862	363
HCT-116-3								0	0	0	0	11	1768	4464	287	24
HCT-116-4								0	0	0	0	0	1318	7070	113	0
HCT-116-5								0	0	0	0	1783	1890	3247	0	0
HCT-116-6								0	0	0	0	588	2679	7818	267	248
AS49-6								0	0	0	0	2201	52	0	302	0
HT29-3								0	0	0	0	148	4624	7875	1143	513
EXV-6								0	0	0	0	0	1949	2376	0	435
HT29-4								0	0	0	0	1230	323	3234	181	0
HT29-5								0	0	0	0	1070	3846	3667	0	363
OVCAR-4-3								0	0	0	0	0	2090	5879	800	0
OVCAR-4-4								0	0	0	0	1263	1813	11856	870	1056
OVCAR-4-5								0	0	0	0	0	708	8721	0	589
OVCAR-4-6								0	0	0	0	899	3034	13755	1759	3849
SP339-3								0	0	0	0	813	10679	2575	2111	284
SP339-4								0	0	0	0	1268	4133	1872	158	148
SP339-5								0	0	0	0	0	1803	3256	0	199
SP339-6								0	0	0	0	946	1292	2380	414	0
OVCAR-5-3								0	0	0	0	589	5490	0	540	908
OVCAR-5-4								0	0	0	0	1547	6457	7120	0	111
OVCAR-5-5								0	0	0	0	0	3700	2419	28	400
ADR-465-6								0	0	0	0	236	388	1633	13	0
MCF-7-6								0	0	0	0	636	2829	2267	433	0
HeLa-6								0	0	0	0	0	1854	2859	84	718
H1299-6								0	0	0	0	1327	1884	4791	129	182
SW480-3								0	0	0	0	309	0	372	0	0
SW480-4								0	0	0	0	0	699	3590	283	2508
SW480-5								0	0	0	0	377	3939	522	1084	0
SW480-6								0	0	0	0	2315	1275	4248	390	14325
C33A-3								0	0	0	0	1702	1828	4535	50	1577
C33A-4								0	0	0	0	0	0	1983	0	298
C33A-5								0	0	0	0	72	775	451	0	608
C33A-6								0	0	0	0	0	5487	0	0	0
HeLa-6								0	0	0	0	0	10	21373	0	0
U2OS-3								0	0	0	0	378	41	8477	3651	284
U2OS-4								0	0	0	0	1430	11028	8671	10033	5133
U2OS-5								0	0	0	0	1199	6148	5864	1918	2063
U2OS-6								0	0	0	0	1755	8155	2588	0	3200
WI 38-6								0	0	0	0	606	17887	518	502	210
He6-3								0	0	0	0	1829	2316	2948	299	0
He6-4								0	0	0	0	2401	8407	7121	105	529
SP-208-3								0	0	0	0	2780	5162	20959	1817	0
SP-208-4								0	0	0	0	1194	5180	8451	0	0
SP-208-5								0	0	0	0	1417	7882	4751	1674	22
SP-208-6								0	0	0	0	1835	3820	3241	0	0
DuPang-13								0	0	0	0	1614	4399	84	402	0
MDAMB-20								0	0	0	0	5019	12553	12086	2259	8095
MDAMB-21								0	0	0	0	4071	10817	12459	2847	7190
MDAMB-22								0	0	0	0	2819	4667	7880	589	3267
OVCAR-5-5								0	0	0	0	3963	3314	2633	7314	651
MDAMB-10								0	0	0	0	4563	8871	4413	260	2940
MDAMB-11								0	0	0	0	3874	538	478	153	4323
MDAMB-12								0	0	0	0	2320	0	12	305	4593
MDAMB-13								0	0	0	0	1877	2702	1025	612	17009
MDAMB-14								0	0	0	0	1770	11411	1191	2922	2511
MDAMB-15								0	0	0						

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor-to	Tumor cells	Normal	Enzyme	p53	SEQ 44	TRSEQ 45	AA SEQ 47	AA SEQ 48	AA SEQ 49	AA SEQ 51	AA SEQ 52	AA SEQ 54	AA SEQ 55	AA SEQ 56
adrenal gland - h	1							10624	0	205	166	7815	2253	1792	20262	37891	
lymph node - h	2							2518	0	267	584	8574	2178	2178	7791	79790	
bone marrow - h	3							1948	0	237	0	5663	3816	1381	1112	45217	
mammary gland - h	4							441	0	0	0	2755	1143	280	0	3250	
brain - h	5							4661	0	189	230	6495	809	987	11958	31129	
pancreas - h	6							368	0	0	344	7076	3342	888	8722	44206	
coronary artery - h	7							658	0	70	0	7609	2936	3189	13785	85793	
pituitary gland - h	8							10870	0	80	231	8538	8192	827	32292	176020	
testis - h	9							52140	0	257	89	7743	5614	3007	25437	47438	
placenta - h	10							4424	0	51	87	8183	2360	2312	41080	35806	
fetal kidney - h	11							2337	0	223	0	8234	8423	1378	30344	73605	
prostate - h	12							2023	0	174	0	7873	3767	334	5551	21551	
fetal liver - h	13							2978	0	110	180	8958	1882	810	4385	47110	
salivary gland - h	14							6290	0	130	0	8905	3418	1128	5531	28923	
fetal lung - h	15							32869	0	319	348	10713	8378	1758	20642	64752	
skeletal muscle - h	16							8442	0	10	101	5123	472	1022	2810	14787	
heart - h	17							2750	0	16	144	7037	2965	443	4172	22280	
small intestine - h	18							0	0	181	225	8344	2662	781	7039	31845	
kidney - h	19							0	0	136	0	5679	2846	558	1254	14331	
apical cord - h	20							0	0	0	0	4814	0	833	0	15780	
liver - h	21							8349	0	0	0	0	0	0	0	0	
Spleen - h	22							2363	0	0	186	5447	3308	831	997	18460	
lung - h	23							20111	0	195	177	3986	2134	873	3438	24017	
stomach - h	24							2682	0	174	0	3808	812	781	1243	17607	
testis - h	25							20445	0	1180	200	5628	8251	11884	321778	49537	
Pancreas - h	26							1202	0	47	23	8191	4923	1638	11408	85005	
HPAEC	27							356	0	0	35	5356	0	0	0	9076	
thyroid gland - h	28							805	0	158	0	5206	1800	556	845	0	
RPTEC	29							188	0	19	98	4184	10744	54	0	8460	
kidney - h	30							3411	0	79	0	8162	4192	1597	9586	34959	
HPAEC	31							0	0	32	188	4406	144	19	393	9796	
Uterus - h	32							3981	0	82	307	7257	724	1368	7394	36540	
MCAEC	33							194	0	26	70	5751	6835	218	66	4988	
Pancreas - h	34							570	0	0	0	6288	0	0	0	21419	
lymph node - h	35							1518	0	118	0	5373	2084	118	9607	25025	
Skeletal muscle - h	36							399	0	14	0	3413	0	31	0	2433	
fetal liver - h	37							6035	0	0	0	6881	9072	134	0	23681	
Heart - h	38							888	0	17	33	4065	10804	4	0	2701	
Thymus - h	39							190	0	0	0	57	4633	8751	0	26436	
Duodenum - h	40							92	0	0	0	3050	0	0	0	2075	
Fetal brain - h	41							11823	0	0	0	5863	8204	145	0	18676	
Salivary gland - h	42							0	0	0	407	5511	1427	0	0	16286	
testis - h	43							1732	0	27	53	7444	19562	115	12733	22790	
HT218-normal								571	0	0	0	301	0	0	0	0	
HT213-normal								363	0	0	0	295	0	0	0	482	
HT151-normal								361	0	0	47	1307	387	21	0	8482	
Bea-13								5180	0	0	403	8650	2907	248	0	6825	
Bea-12								354	354	0	40	8406	346	316	330	2534	
coronary artery - h								344	0	0	71	0	1862	487	90	380	
brain - h								334	0	0	0	1829	1179	0	288	7542	
RPTEC								0	0	0	0	8040	117	0	0	6884	
lymph node - h								332	0	0	6	4034	0	531	0	27819	
in adult SAC 10/21/92 #17								330	0	0	0	326	4482	0	87	551	
Fetal brain - h								328	0	0	250	10	7086	29	603	4350	
HT385-normal								327	0	0	118	176	4837	0	42	409	
Thymus - h								326	0	0	0	250	5583	0	652	547	
HT148 - normal								321	0	0	0	3450	0	0	0	7102	
HEPM 3d untreated								318	0	0	0	6	3821	0	0	3657	
uterus - h								318	0	0	213	0	6339	8543	0	6884	
trachea - h								316	0	0	29	184	4057	2227	167	5551	
thyroid gland - h								314	0	0	229	175	2272	443	383	5888	
salivary gland - h								311	0	0	64	0	5050	810	27	0	
prostate - h								309	0	0	0	5458	708	0	0	17721	
pituitary gland - h								307	0	0	0	370	3428	0	66	205	
Pancreas - h								305	0	0	34	250	5133	2282	68	622	
mammary gland - h								303	0	0	362	33	5378	4075	0	37188	
muscle - h								302	0	0	370	104	1673	145	1017	7889	
testis - h								300	0	0	233	64	8509	12917	844	2097	
liver - h								297	0	0	8	414	4872	0	44	1583	
Spleen - h								296	0	0	114	0	3615	3035	0	462	
apical cord - h								294	0	0	84	0	5811	2045	304	64	
skeletal muscle - h								292	0	0	86	0	2932	657	176	134	
bone marrow - h								290	0	0	245	0	5290	831	58	824	
adrenal gland - h								277	0	0	88	338	8448	116	0	8531	
HPAEC								189	0	0	0	474	1192	6	1346	10122	
HT382-normal								275	275	0	41	181	3704	874	83	0	
HT382-normal								258	0	0	7	0	3563	242	349	0	
HT382-normal								256	0	0	82	118	3680	303	94	474	
Bea-11								239	239	0	182	0	7854	7092	0	52	
Bea-8								235	235	0	154	8	4088	580	0	4562	
Bea-7								234	233	0	0	0	6155	542	568	0	
Bea-6								233	233	0	47	0	4956	0	0	6731	
Bea-2								231	231	0	139	168	4139	2231	118	417	
Bea-1								229	229	0	80	169	3519	4889	152	0	
muscle - h								227	227	0	107	0	4155	717	0	4163	
heart - h								222	0	0	14	3	2450	0	53	0	
coronary artery - h								215	0	0	124	0	5047	0	0	6958	
fetal liver - h								214	0	0	41	143	8056	1680	0	1381	
placenta - h								213	0	0	90	78	3033	0	133	0	
MCAEC								212	0	0	77	5011	1564	155	771	19059	
HPAEC								211	211	0	0	0	0	0	0	0	
fetal brain - h								210	0	0	173	0	5900	4194	160	691	
HPAEC								209	0	0	11	0	2824	3235	36	596	
Duodenum - h								208	0	0	132	4247	0	0	0	3634	
Skeletal muscle - h								203	0	0	0	3633	0	110	0	278	
Pancreas - h								201	0	0	29	0	3178	166	0	4188	
testis - h								199	0	0	15	0	2838	0	20	0	
Salivary gland - h								197	0	0	15	0	2207	18730	52	4299	
HEPM 3d TGFβ1 antagonist-DNase								195	0	0	44	0	1367	174	62	27	
Thymus - h								193	0	0	23	0	3008	565	77	0	
WJ-28 T2b								179	0	0	0	1150	0	0	489	70	
lymph node - h								81	0	0	61	88	3420	855	0	8805	
lung - h								59	0	0	0	7062	1000	0	0	25022	
kidney - h								57	0	0	0	4677	2940	74	388	22336	

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Table 3 (cont'd)

Tissue	Tumor + ym	Normal + ym	Tumor + %	Tumor cells	Normal	C-myc	p53	SEQ 644	TRE0 45	AN SEQ 47	AN SEQ 48	AN SEQ 49	AN SEQ 51	KIA SEQ 52	AN SEQ 54	CQ SEQ 55	CL	
Colon				105				0	0	47	88	40121	0	154	256	6448		
T-47D				107				40177	0	0	912	7668	46	0	21583	20885		
Kem-3				171				0	0	70	212	4456	73	295	6531	7187		
CR1441 RNA 8/30				181				0	0	0	25	1845	278	6	0	291		
7811 untreated - D-Nase				183				0	0	0	562	1309	120	385	192	0		
K3 poly A+				184				0	0	31	0	667	0	11	212	410		
HOS poly A+				184				0	0	0	135	1653	24	52	211	7891		
ACHN				196				282	0	48	0	2417	0	64	84	3261		
UACC-42				198				0	0	0	0	2832	209	171	6142	1184		
MCF-7/ADR-RES				200				365	0	39	131	1296	0	0	1277	1373		
UTOS (Mundy) poly A+				202				0	0	39	0	1357	700	0	1430	1020		
WISH (Collagen) poly A+				204				0	0	0	171	22	0	0	0	3420		
458 medullar mDNA				206				0	0	0	0	742	843	44	42	1121		
CC-137 RNA 3/21/88				208				5841	0	0	0	7137	0	0	0	5852		
WIL37 2h 0.5%FBS, 24h 10% FBS				218				0	0	80	141	1194	3	100	0	827		
CR1441 + TPA (24h) 8/30				220				0	0	0	0	2129	0	77	0	892		
Kem-3				221				669	0	0	0	18	1572	0	0	0	1257	
Kem-2				223				0	0	0	0	2235	330	85	0	1861		
Kem-4				226				726	0	172	0	2128	0	0	0	1331		
HOP-92				241				128	0	0	3	1124	372	0	0	1758		
MDA-MB-231				242				1229	0	0	0	4186	1258	0	2452	5190		
MDA-MB-231				243				804	0	0	0	129	2740	139	217	3610	7440	
NCL-H226				244				0	0	0	0	3654	3072	514	1498	10317		
MDA-MB-231				245				237	0	10	183	3578	1813	221	3367	6535		
ASB-WATCC				246				0	0	88	413	2687	7118	182	0	738		
SR				248				0	0	86	0	2059	0	0	0	1084		
OVCAR-3				249				0	0	17	267	2188	1910	33	261	2209		
HCT-15				250				1042	0	0	62	4098	1567	230	640	13041		
OVCAR-4				251				347	0	0	53	15	552	0	7	890	847	
UO-31				252				0	0	0	66	55	0	0	0	1047		
OVCAR-5				253				0	0	89	722	6152	0	0	4788	6833		
SMC-2				254				811	0	0	0	3554	2301	0	10455	6556		
LOX IMVI				255				322	0	0	13	2581	872	0	2102	1742		
IGROV1				256				0	0	71	0	343	8201	4992	283	2950	8100	
SK-MEL-2				257				894	0	94	0	3889	571	0	2267	3931		
SK-OV-3				258				0	0	115	0	2345	401	338	1374	2004		
SK-MEL-3				259				0	0	0	0	1166	0	164	1499	1437		
SP-539				260				0	0	0	472	1328	199	0	199	1498		
SK-MEL-28				261				1273	0	188	456	6873	2291	0	7414	2658		
K-562				262				857	0	0	0	3750	861	0	2959	2053		
UACC-257				263				628	0	85	31	8148	4336	216	2537	1782		
M14				264				0	0	0	0	2801	0	11	421	1280		
MCF7				265				0	0	74	0	8771	151	181	0	1458		
MDA-MB-435				267				5620	0	0	26	8238	0	0	17404	29802		
HT279				269				1743	0	0	60	227	1924	0	744	1343		
MDA-N				270				0	0	0	1555	1810	0	0	141693	38706		
MDA-N				271				0	0	17	0	4127	2893	0	2694	2054		
Y79 poly A+				272				8005	0	137	0	7232	1809	43	856	18372		
KHOS poly A+				273				2709	0	18	269	3265	32	264	579	8284		
HTB36 24h TPA RNA 8/2				274				0	0	10	0	2952	648	171	96	6578		
HELA-EXP-G31899				300				0	0	19	49	2177	949	24	0	10940		
HTB36 2h RNA				313				0	0	0	0	199	4154	686	428	773	4214	
HT341				322				443	0	0	0	3448	3812	0	169	58352		
458 medullar RNA				323				2289	0	55	0	3454	0	11	761	1191		
NCL-H226				326				0	0	0	38	2966	0	100	0	1149		
KOR-63				327				0	0	0	257	3132	301	181	5222	2879		
MDA-MB-231				328				7560	0	0	0	8113	4555	0	8554	26931		
UT51				329				10046	0	66	0	11558	1810	202	141693	38706		
P2 cells poly A+				340				0	0	0	0	1986	0	0	2481	2005		
PC-3				341				0	0	0	227	3870	708	83	584	818		
HCC-2998				343				0	0	0	0	2180	0	139	0	1570		
SW-620				345				0	0	72	63	2072	0	106	0	0		
HT160				346				578	0	50	25	4300	509	0	3475	19731		
CRL-0-205				347				0	0	26	45	703	688	0	0	0		
HT218				348				4211	0	0	0	1703	0	0	0	10955		
KM-12				349				0	0	44	137	1724	842	163	0	1130		
HT151				350				0	0	30	202	3787	1563	299	0	8776		
Adren				351				7849	0	0	184	1848	0	200	0	0		
HT393				352				286	0	0	0	6021	0	0	0	18131		
RUF 393				353				0	0	114	0	2870	0	0	0	0		
TX-10				355				5344	0	0	0	7556	2225	0	3008	17069		
Hs-578T				356				2845	0	0	0	26180	15570	313	37531	7453		
MDA-MB-231				357				0	0	0	0	1858	0	0	896	1109		
HT213				50				0	0	162	0	18922	1272	37	0	4385		
HT268				52				196	0	197	0	5482	437	0	429	48948		
HT139				54				0	0	0	31	3241	0	0	0	2708		
HT155				56				0	0	114	0	2861	0	0	0	12179		
HT163				58				0	0	35	26	3238	588	0	0	348		
HT170				60				337	0	28	0	6032	0	0	0	12650		
HT172				62				0	0	5	0	4071	0	84	104	2202		
HT138				63				1382	0	0	0	3571	121	0	0	26749		
HT178				64				0	0	0	201	5024	0	0	0	2951		
HT154				65				66	0	0	0	8175	1963	0	0	1773		
HT180				66				1835	0	0	0	6948	0	0	0	2924		
HT189				67				0	0	72	0	824	24	45	243	1389		
HT143				68				0	0	26	5	4352	0	440	0	3840		
HT190				69				5	0	0	1176	3224	0	57	0	296		
HT145				70				2669	0	61	0	4240	876	150	634	4445		
HT227				71				3801	0	0	0	5818	0	0	0	3685		
HT202				72				0	0	30	114	4628	0	0	0	4727		
HT314				73				420	0	0	133	8415	97	32	419	6154		
HT317				74				429	0	0	0	4709	6214	0	0	5832		
MDA-MB-231 8/25 11/8				76				443	0	27	0	6318	578	220	287	2212		
HT323				77				295	0	33	328	3199	578	220	287	2212		
HT327				80				80	0	110	0	6528	2604	1971	0	5220		
HT335				82				0	0	128	0	3771	1776	60	14	2370		
HT146				83				0	0	11	0	4499	11023	0	422	17130		
HT348				85				432	0	120	0	11411	0	419	0	384		
HT311				87				0	0	0	0	5314	16456	0	304	21360		
HT386				185				369	0	26	0	3141	4953	255	0	5243		
HT140				187				0	0	166	0	3260	0	229	0	3166		
HT281				191				0	0	0	0	812	0	0	0	305		
HT372				193				0	0	244	0	2657	1134	0</				

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1e	Tumor cells	Normal	Endo	p33	SEQ 844	TRE6 45	ANSEQ 47	ANSEQ 48	ANSEQ 49	ANSEQ 51	KIASEQ 52	ANSEQ 54	COSEQ 55	CL
MA-57AT	155							4159	0	64	0	4775	0	670	1535	18295	
MCF-7/ADR-RES	153							0	0	188	3752	0	110	1947	4938		
MCF7	151							3033	0	161	8	7051	0	1602	0	27225	
M14	149							0	0	150	0	3887	1681	502	0	5625	
UACC-257	147							0	0	47	45	5235	596	0	913	14636	
UACC-62	145							0	0	0	0	3298	319	44	1253	4501	
SK-MEL-26	144							895	0	101	0	4298	199	22	96	6386	
UO-31	143							755	0	0	0	5134	1814	426	0	5096	
SK-MEL-5	142							506	0	14	0	4762	978	464	1913	6211	
KM-12	141							1090	0	0	29	2850	299	437	868	1786	
SK-MEL-2	140							0	0	4	0	3963	399	177	1587	18358	
HCT-15	139							0	0	0	0	6167	0	368	370	16881	
Maumc-3M	138							1856	0	0	0	4947	25	311	1067	6770	
COLO 205	137							2152	0	222	339	5549	0	0	0	5235	
LOX IMV1	136							6439	0	0	181	5835	695	93	0	11410	
SW-620	135							1038	0	37	0	3684	1187	384	859	2486	
TK-10	134							1865	0	0	10	3678	1663	344	395	11194	
HCT 116	133							518	0	107	104	3803	1054	193	0	4067	
T86-0	132							2701	0	7	110	3530	0	370	374	8085	
HCC-2998	131							1371	0	0	0	6532	787	261	770	2945	
ACHN	130							0	0	0	0	4596	527	102	990	8637	
PC-3	129							0	0	0	0	3699	619	250	746	5609	
RUF 303	128							3345	0	11	212	3257	0	368	962	19597	
DJ-145	127							455	0	0	83	2437	231	91	0	2441	
C6H-1	126							0	0	132	180	4922	0	265	467	7704	
SR	125							1045	0	2	0	3578	0	0	0	8279	
A498	124							2368	0	126	305	4461	0	732	4011	12101	
RPMB 8226	123							0	0	0	84	3952	1414	102	6477	5650	
SM12C	122							0	0	0	258	4348	1782	350	1146	10454	
H-60	121							0	0	0	144	3536	0	293	0	7486	
MOLT-4	120							591	0	24	0	3217	559	83	3283	4657	
OVCAR-5	119							575	0	56	30	4828	0	85	4365	7866	
K-562	118							0	0	0	0	1270	0	372	2107	2643	
OVCAR-4	117							1705	0	0	0	8408	2352	302	4332	12924	
CCR6-CEM	116							518	0	70	0	3041	160	1813	852	14584	
OVCAR-3	115							2335	0	58	0	3837	0	180	281	5529	
SP-539	114							841	0	0	0	3003	513	0	183	4097	
HOP-62	113							527	0	2	188	3830	204	25	911	14232	
SP-295	112							678	0	9	210	5431	2145	397	1058	10018	
A549ATCC	111							1174	0	0	183	8431	1777	654	1209	11839	
SP-263	110							863	0	0	112	2981	434	107	1893	3998	
NCL-H522	109							0	0	21	0	5351	1071	603	863	6165	
U251	108							1687	0	0	474	4887	640	331	1215	7924	
NCL-H460	107							294	0	221	41	4589	651	345	0	8432	
SNB-15	106							893	0	76	3	2967	633	308	0	1015	
NCL-H322M	105							0	0	0	28	2890	134	348	0	8665	
SNB-19	104							20	0	63	0	3171	1079	491	2038	4580	
NCL-H225	103							4486	0	18	0	7057	1891	244	1819	7194	
SK-OV-3	102							243	0	58	0	3732	2018	625	0	11044	
NCL-H21	101							200	0	142	0	3780	1389	492	1750	8447	
IGROV1	100							0	0	0	0	4196	1010	790	0	4586	
ECV1	99							783	0	14	187	3052	0	445	38	8847	
OVCAR-8	98							0	0	72	283	3056	79	48	135	2411	
HOP-82	97							0	0	108	3869	1247	54	446	4634		
n Soroblasta 3/31/92 #12	48							1168	0	123	0	3977	1635	89	1338	2648	
n adult SMC 10/21/92 #17	47							2238	0	112	0	4164	0	96	742	4832	
n keratinocytes 2/25/92 #10	46							1043	0	328	3112	724	0	278	0	2214	
TCGP	26							0	0	115	0	3262	7036	256	311570	3115	
A549 - 1							wt	407	48	37	0	0	0	0	0	0	
A549 - 3							wt	317	105	0	0	0	0	0	0	0	
A549 - 4							wt	26	153	0	0	0	0	0	0	0	
A549 - 5							wt	321	109	62	0	0	0	0	0	0	
A549 - 7							wt	0	238	48	0	0	0	0	0	0	
ECV1 - 1							mutant	5881	2138	285	0	0	0	0	0	0	
ECV1 - 4							mutant	2147	841	0	0	0	0	0	0	0	
ECV1 - 3							mutant	2865	0	480	0	0	0	0	0	0	
ECV1 - 5							mutant	1030	0	0	0	0	0	0	0	0	
ECV1 - 7							mutant	1623	0	0	0	0	0	0	0	0	
MCF-7 - 1							wt	0	0	0	0	0	0	0	0	0	
MCF-7 - 3							wt	403	0	48	0	0	0	0	0	0	
MCF-7 - 4							wt	150	0	115	0	0	0	0	0	0	
MCF-7 - 5							wt	3124	0	0	0	0	0	0	0	0	
MCF-7 - 7							wt	849	0	9	0	0	0	0	0	0	
ADR-RES - 1							mutant	0	1818	135	0	0	0	0	0	0	
ADR-RES - 3							mutant	30924	0	290	0	0	0	0	0	0	
ADR-RES - 4							mutant	4757	279	109	0	0	0	0	0	0	
ADR-RES - 5							mutant	835	573	64	0	0	0	0	0	0	
ADR-RES - 7							mutant	748	381	11	0	0	0	0	0	0	
WI 38 - 1							wt	2518	51	178	0	0	0	0	0	0	
WI 38 - 3							wt	1849	0	80	0	0	0	0	0	0	
WI 38 - 4							wt	0	0	0	0	0	0	0	0	0	
WI 38 - 5							wt	3090	0	37	0	0	0	0	0	0	
WI 38 - 7							wt	812	0	43	0	0	0	0	0	0	
HsLa - 1							wt	0	0	399	0	0	0	0	0	0	
HsLa - 3							wt	852	0	50	0	0	0	0	0	0	
HsLa - 4							wt	848	0	115	0	0	0	0	0	0	
HsLa - 5							wt	2647	766	172	0	0	0	0	0	0	
HsLa - 7							wt	428	550	7	0	0	0	0	0	0	
H1299 - 1							mutant	0	0	27	0	0	0	0	0	0	
H1299 - 3							mutant	1149	0	193	0	0	0	0	0	0	
H1299 - 4							mutant	1155	0	36	0	0	0	0	0	0	
H1299 - 5							mutant	819	63	106	0	0	0	0	0	0	
H1299 - 7							mutant	0	0	71	0	0	0	0	0	0	
A549 - 2							wt	751	381	0	0	0	0	0	0	0	
ECV1 - 2							mutant	21741	2630	206	0	0	0	0	0	0	
HCT-116 - 1							wt	649	0	206	0	0	0	0	0	0	
HCT-116 - 2							wt	9208	862	430	0	0	0	0	0	0	
HT29 - 2							wt	407	255	55	0	0	0	0	0	0	
SP-539 - 1							wt	1107	261	0	0	0	0	0	0	0	
SP-539 - 2							wt	523	202	71	0	0	0	0	0	0	
SP-268-1							mutant	9794	164	139	0	0	0	0	0	0	
SP-268-2							mutant	11614	4311	265	0	0	0	0	0	0	
OVCAR-4 - 1							wt	2660	701	0	0	0	0	0	0	0	
OVCAR-4 - 2							wt	0	0	0	0	0	0	0	0	0	
OVCAR-5 - 1							wt	705	0	0	0	0	0	0	0	0	
OVCAR-5 - 2																	

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor - 1a	Tumor code	Normal	Endos	p31	SEQ 36	ANSEQ 37	WSEQ 66	ANSEQ 63	NESEQ 66	CASEQ 68	HRSEQ 110	RSEQ 73	HRSEQ 78	AA	
Cabo-1				105				865	4875	157	1025	971	1529	1954	17283	26096		
T06-0				169				533	9526	227	979	272	6856	5204	82251	53570		
T-47D				189				5605	8510	0	1074	352	5891	2901	18722	30931		
Non-3				171				0	1953	0	234	13	1371	1787	139	37972		
CR1441 RNA 8/30				181				278	3108	0	24	0	0	0	0	13079		
781T untreated - QNase				183				197	1800	0	62	0	0	0	0	0		
K562 poly A+				194				0	5094	0	103	0	1499	1818	668	31810		
ACHN				196				297	3285	8277	0	0	529	2815	866	52776		
UACC-62				200				0	8503	0	212	0	1158	4907	14597	26142		
MCF-7/ADR-RES				202				1492	9993	0	0	0	474	2225	2825	11714		
UTOS (transf) poly A+				204				185	2229	755	0	11	381	1444	2562	14607		
WISH (Collagen) poly A+				206				0	7812	0	104	0	0	1028	617	9607		
458 muscle mRNA				208				150	0	0	94	189	893	579	725	14442		
COL137 RNA 3/1/85				218				0	18178	0	623	53	0	232	2913	60563		
W138 T2b 0.5% FBS, 24h 10% FBS				219				219	1868	0	206	0	261	1447	815	23844		
CR1441 + TPA (24h) 8/30				220				271	3187	1196	0	34	403	2293	0	41474		
Non-1				221				0	1583	0	6	0	0	0	0	0		
Non-2				222				2280	2513	0	31	693	0	1068	63	18180		
Non-4				223				705	2806	0	115	0	302	2129	41	41277		
HOP-62				224				521	4040	0	31	0	1303	2242	89	30345		
MDA-MB-4				242				0	2362	0	218	0	87	1773	13338	19084		
SVX				243				848	6364	792	481	2078	3182	30419	23972	16317		
HL-60				243				0	13083	0	328	73	3139	6482	109714	30232		
MDA-MB-2				244				0	14211	0	23	4311	2402	3689	19999	39367		
RPM 8226				245				950	13087	5752	2285	187	2423	5364	95198	48201		
ASMBATCC				246				0	1320	489	179	0	344	2272	18218	26569		
SR				247				69	3450	0	519	394	691	1991	2365	18971		
OVCA-3				248				0	1814	383	9	23	244	2897	10201	17287		
HCT-15				249				0	7207	0	214	120	1028	2424	17041	20678		
OVCA-4				250				0	10765	599	1458	0	3539	4642	105642	27562		
UC-3				251				223	314	1330	0	189	473	605	1481	7613		
OVCA-5				252				372	3044	0	0	8	143	547	1109	6300		
SN12C				253				2585	8438	1811	623	102	1739	3348	12208	24504		
OVCA-8				254				0	5112	504	178	108	3335	278	28007	16317		
LOX BM1				255				0	3508	664	732	0	1122	1359	35633	14140		
IGROV1				256				627	17299	405	608	61	5903	5283	30147	38548		
SK-MEL-2				257				1184	8152	756	178	86	2032	3644	29934	31704		
SK-ONE-3				258				0	5305	19	0	0	0	0	0	0		
SK-MEL-5				259				65	3527	0	210	0	1050	3782	8319	17004		
SP-539				260				135	3911	0	48	103	1340	1148	3811	12542		
SK-MEL-28				261				383	1229	0	664	150	7673	5550	62279	51506		
K-562				262				0	7037	0	384	0	1715	1384	541	34907		
UACC-257				263				887	6200	1949	1885	95	9059	4576	195694	61730		
MDA-MB-435				264				0	6775	0	408	0	1590	2368	3496	29095		
MDA-MB-435				265				0	2620	0	0	0	0	0	0	0		
MCF7				267				629	18843	920	968	214	804	918	1178	17725		
MDA-MB-435				269				144	6378	477	543	0	968	1857	1148	24187		
MDA-MB-435				270				14	4493	0	0	0	891	2525	281	41491		
MDA-MB-435				271				278	7063	0	354	0	1299	1838	5886	18906		
MDA-MB-435				272				0	6994	0	279	0	3785	6028	24564	77861		
MDA-MB-435				273				0	20758	17445	371	238	6785	4375	30568	76061		
MDA-MB-435				274				783	3981	0	1456	0	2296	2492	221	33171		
MDA-MB-435				275				534	1812	0	247	0	1590	2848	4161	39714		
MDA-MB-435				276				1461	24484	0	0	989	3512	9180	3044	81844		
MDA-MB-435				277				404	4566	0	0	0	2939	3484	15822	40401		
MDA-MB-435				278				1527	40573	0	34	748	990	4386	478	69808		
MDA-MB-435				279				672	6101	721	345	0	1515	2181	2208	37118		
MDA-MB-435				280				0	15368	0	906	78	2908	1717	36486	21036		
MDA-MB-435				281				1105	85815	1171	9728	1217	25352	13718	258035	103170		
MDA-MB-435				282				122	30374	1217	18296	382	78758	33890	2025349	111822		
MDA-MB-435				283				483	14402	0	467	0	1887	2925	45467	16266		
MDA-MB-435				284				177	13879	82	362	2330	5703	8884	40554	71885		
MDA-MB-435				285				82	8206	0	552	599	1782	2288	23473	21578		
MDA-MB-435				286				26	7776	0	621	200	1291	2048	10731	24715		
MDA-MB-435				287				1001	7290	408	182	0	1412	5254	65925	65925		
MDA-MB-435				288				162	8047	0	306	0	689	1304	8913	8913		
MDA-MB-435				289				348	4819	0	77	158	0	1385	391	36349		
MDA-MB-435				290				349	48	0	406	0	891	1115	34049	17488		
MDA-MB-435				291				138	6054	0	723	3737	0	0	0	0		
MDA-MB-435				292				351	20305	0	401	1564	1038	2626	4743	30375		
MDA-MB-435				293				797	15335	57	0	0	2602	4435	5637	60953		
MDA-MB-435				294				0	8073	0	114	73	348	2720	7239	24306		
MDA-MB-435				295				738	78666	684	1703	2320	12534	12970	7152	7152		
MDA-MB-435				296				2111	93276	13897	36286	2444	55479	34972	201421	150800		
MDA-MB-435				297				0	9184	0	58	82	2391	2875	6581	48992		
MDA-MB-435				298				52	6740	0	47	0	1887	2925	45467	16266		
MDA-MB-435				299				179	80671	0	0	2127	783	2541	754	84143		
MDA-MB-435				300				54	8243	0	41	635	0	1926	276	65037		
MDA-MB-435				301				0	6890	0	281	632	2394	2131	2121	61017		
MDA-MB-435				302				1082	1302	368	0	253	281	1998	540	81243		
MDA-MB-435				303				37	15671	0	252	0	1652	4224	1547	13039		
MDA-MB-435				304				62	3378	0	0	17	284	875	0	46245		
MDA-MB-435				305				0	2623	0	0	43	797	1070	4034	45891		
MDA-MB-435				306				31	3195	0	0	145	349	974	800	51853		
MDA-MB-435				307				65	1277	2364	0	44	159	1138	0	52119		
MDA-MB-435				308				66	276	2597	0	58	0	862	865	197	43129	
MDA-MB-435				309				87	427	4940	0	0	229	269	455	1239	26580	
MDA-MB-435				310				69	4080	286	122	0	346	1043	3366	78481		
MDA-MB-435				311				70	5719	854	58	0	161	828	202	38405		
MDA-MB-435				312				0	5719	854	58	0	161	828	202	38405		
MDA-MB-435				313				1053	33011	539	0	74	3282	1833	230	56887		
MDA-MB-435				314				71	5735	0	83	183	2496	1928	257	65548		
MDA-MB-435				315				0	18129	0	439	112	0	2601	605	84861		
MDA-MB-435				316				74	10043	138	0	41	279	1755	1196	51087		
MDA-MB-435				317				75	26782	0	2002	651	98	5151	5403	100931		
MDA-MB-435				318														

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Table 3 (cont'd)

Tissue	Tumor - dym	Normal - dym	Tumor - fb	Tumor cells	Normal	Endo	p53	ISEQ 36	AA ISEQ 37	W ISEQ 60	AA ISEQ 63	ME ISEQ 66	C ISEQ 68	H ISEQ 110	RE ISEQ 73	HM ISEQ 78	AA
MA-52T	155							0	11445	647	1081	3442	20751	2567	4395	55874	
MCF-7/ADR-RES	153							2256	18577	3302	2810	488	22338	1868	39921	54013	
MCF7	151							3960	38669	160	1560	2864	11886	3485	22510	81756	
M4	149							776	16702	0	704	437	6271	3690	4021	69488	
LIACC-327	156							156	14876	1834	7208	183	6997	2195	17973	61725	
LIACC-62	145							600	9415	0	2146	4	8453	1599	4231	41288	
SK-MEL-28	144							40	12812	4856	577	770	5176	1071	2890	56931	
UO-31	143							448	6659	1716	624	99	14005	2232	3934	105691	
SK-MEL-5	142							1182	27282	1994	1944	404	2909	13115	1215	9595	42911
KM-12	135							325	5737	5512	104	0	1681	1317	64	44689	
SK-MEL-2	140							1867	14486	3221	795	1827	7349	1575	7479	62671	
MCT-15	139							740	12275	771	657	666	4927	2667	7421	71198	
U87MG-3M	136							1725	25340	2543	2991	2553	10072	2036	7321	42597	
COLO 205	137							2484	9160	2765	439	1943	13401	1681	2407	98313	
LOX IMV1	136							303	37237	202	3101	4339	32433	892	8051	33734	
SW-620	135							638	8511	0	1807	1939	10151	1195	2768	38389	
TX-10	134							545	8427	1312	1506	1082	23968	1771	11381	42220	
MCT-116	133							1015	7308	0	148	413	11784	2013	1498	38595	
786-0	132							686	8319	827	1162	947	28069	1670	7153	41603	
MCC-2998	131							1700	9369	0	337	1115	8212	1884	3255	74996	
AGRN	130							610	8638	1426	1253	845	21377	1466	7925	49256	
PC-3	129							377	10302	0	33	809	14268	1450	3151	45670	
RXP-353	128							1067	12023	1508	4327	377	20886	1894	13035	43831	
UO-145	127							1200	8043	180	126	178	4962	2174	3956	46338	
C-6-1	126							981	12916	561	2689	334	4496	1933	15623	42979	
SR	125							0	8755	0	1096	174	2308	4010	44617		
AM8	124							8013	19049	351	295	0	14129	2475	10969	49887	
RPM8 8226	123							0	5461	0	1	112	580	3030	5708	65175	
SNIC	122							0	1233	0	2502	124	8784	2447	10671	72056	
H4-60	121							303	4211	641	116	240	1354	2017	2880	56854	
MOLT-4	120							226	4496	2178	116	551	5501	13131	7213	70156	
OVCAR-5	119							859	10544	6273	2442	877	12121	968	33289	40584	
W-562	118							1044	118	2	360	58	8278	1771	9526	58039	
OVCAR-4	117							2174	13967	4168	2461	16401	14316	14061	21244	44925	
CCRFLCEM	116							1569	31473	569	4934	891	4841	1450	7736	55652	
OVCAR-3	115							555	6652	2366	1091	179	3448	1421	25044	42501	
GF-639	114							1113	114	0	668	0	10012	12471	4952	410759	
HOP-62	113							0	6296	2082	5259	887	16786	899	2499	25347	
SF-295	112							209	7254	304	1051	8751	678	16984	47319		
AK59ATCC	111							1371	14735	0	3749	2445	18286	1303	66894	51844	
SF-598	110							1333	15029	0	2289	1054	18314	1098	8420	32595	
NCH-H522	109							335	10129	1948	3305	1263	17962	2094	15285	42349	
U251	108							1614	8600	2187	3741	1811	29319	2229	10968	53640	
NCH-H460	107							1091	11864	2328	5799	8701	15224	1506	32438	40200	
SNB-75	106							252	753	127	25	20030	1060	1680	40398		
NCH-H322M	105							3683	13987	3336	3512	473	11090	2166	20853	68294	
SNB-19	104							0	7540	1418	588	329	14893	2894	9129	52718	
NCH-H26	103							822	18491	1502	2987	272	7803	4474	12465	103492	
SK-OV-3	102							0	10057	871	245	482	756	620	1758	51718	
NCH-H23	101							122	12635	1788	5027	718	1791	3129	30387	54491	
HGRV1	100							672	10901	3057	295	665	3356	3272	7830	55670	
OVX	99							0	8455	898	3388	217	4095	2078	31182	42470	
OVCAR-8	98							347	7233	2432	897	574	1949	1947	482	49955	
HOP-62	97							474	12057	2367	2897	792	12382	2385	31301	56630	
In fibroblast 3/31/82 #12	48							1606	4900	0	3536	215	24750	1814	3365	92909	
In vitro SMC 10/21/82 #17	47							0	3414	0	477	60	28787	1464	10148	75029	
In sarcomas 2/29/82 #10	46							0	10627	0	2529	7044	10941	1178	5161	27815	
TCGP	26							589	12403	55	30915	701	5429	2429	9414	61038	
AS49-1							wt	0	2606	567	13218	0	1876	331	14888	18283	
AS49-3							wt	0	3582	0	2633	0	3171	314	3847	10191	
AS49-4							wt	0	2789	0	1897	0	522	157	11425	16682	
AS49-5							wt	0	4423	0	2173	0	486	242	15448	13282	
AS49-7							wt	0	3415	0	579	0	1883	281	12240	20201	
BRVX-1							mutant	0	7018	218	15498	0	2368	602	27454	14020	
BRVX-4							mutant	0	5808	0	4440	0	2883	1003	78154	19451	
BRVX-3							mutant	0	4185	0	6533	0	1342	397	7118	16420	
BRVX-5							mutant	0	2052	442	1504	0	2086	781	18082	27269	
BRVX-7							wt	0	3306	1404	0	1233	1385	5245	36618		
MCF-7-1							wt	0	2485	0	3065	0	306	267	11222	15611	
MCF-7-3							wt	0	4324	0	2219	0	177	321	16676	14247	
MCF-7-4							wt	0	28711	952	297	0	707	181	16894	15090	
MCF-7-5							wt	0	46481	0	312	0	501	2435	2435	4498	
MCF-7-7							wt	0	2815	0	341	0	389	118	9134	14350	
ADR-RES-1							mutant	0	13125	0	44651	0	1135	960	48482	43329	
ADR-RES-3							mutant	0	7895	206	16431	0	583	715	8378	15827	
ADR-RES-4							mutant	0	3513	814	79	0	1047	533	10666	22994	
ADR-RES-5							mutant	0	1614	0	5674	0	572	116	18216	11995	
ADR-RES-7							mutant	0	5037	0	1519	0	636	310	4944	17965	
WI-38-1							wt	0	11054	0	1743	0	490	816	23088	21030	
WI-38-3							wt	0	9568	317	2833	0	371	777	23794	13274	
WI-38-4							wt	0	6701	0	184	0	2290	795	25508	14200	
WI-38-5							wt	0	8553	0	1887	0	1877	750	6930	17103	
WI-38-7							wt	0	8181	461	897	0	866	1033	12862	13392	
HeLa-1							wt	0	2972	10415	125	783	381	5646	33	13265	
HeLa-3							HPV E6	0	8135	209	2589	0	204	308	19037	12311	
HeLa-4							HPV E6	0	1802	787	1330	0	263	819	11306	10796	
HeLa-5							HPV E6	0	8774	3481	2858	0	2129	634	36267	18512	
HeLa-7							HPV E6	0	9057	0	1004	0	1873	860	18576	19187	
HI299-1							mutant	0	5732	0	1628	0	498	789	13209	13620	
HI299-3							mutant	0	7969	0	3636	0	581	547	4846	12467	
HI299-4							mutant	0	11578	0	2803	0	1997	567	32306	15929	
HI299-5							mutant	0	3280	0	2066	0	1547	552	9675	17847	
HI299-7							mutant	0	6749	87	2847	0	585	224	13576	13714	
AS49-2							wt	0	1778	0	7023	0	369	479	7747	14837	
BRVX-2							wt	0	4310	0	1255	0					

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor - te	Tumor calls	Normal	Endoca	p53	SEQ 75	AASEQ 882	MEQ 82	MUSEQ 84	RIFSEQ 84	AASEQ 85	AAASEQ 86	MISEQ 87	TSISEQ 88	SAASEQ 89
adipose gland - h		3	33	18727	26467	189725	3677	1388	205	1373							
lymph node - h		2	0	180	25285	38356	133216	11022									
bone marrow - h		3	0	407	9924	25669	90889	5374	4477	0							
mammary gland - h		16	0	0	4132	3251	36633	30	34	100							
testis - h		5	0	0	11469	8976	136665	8131	3710	51							
pancreas - h		6	0	530	9084	17022	100224	2001	1052	2411							
coracoclavicular - h		0	0	336	18449	11689	94237	10826									
ovary gland - h		8	127	162	5620	82715	134453	56871	4441	29							
testis - h		14	0	354	10959	22841	102430	3443	513	52							
placenta - h		10	717	338	10004	74254	187967	6384	356	201							
total body - h		11	256	639	28118	24184	87526	5311	903	224							
prostate - h		12	511	0	11315	8647	222874	127	1870	74							
total liver - h		13	436	207	43029	8496	116434	18241	4202	266							
salivary gl. - h		0	532	13840	7790	102290	6537	637	2036	75							
total lung - h		15	0	669	27774	19719	158648	6148	1076	177							
skeletal muscle - h		16	191	1969	164018	11019	104752	1936	22913	56							
heart - h		17	268	1694	158583	85081	93867	2229	61	45							
small intestine - h		18	320	288	25312	14109	103640	3395	1228	46							
kidney - h		19	218	5	5142	18392	91581	3869	3991	0							
spinal cord - h		20	85	340	7756	11094	84387	7363	8771	41							
testis - h		21	372	354	4036	13651	155877	174									
spleen - h		22	78	266	5062	14889	95360	2294	343	333							
lung - h		23	178	942	16006	13332	69515	2203	337	183							
stomach - h		24	0	28	2542	12134	71122	1805	1327	21							
testis - h		25	0	373	21247	22843	103440	8924	2892	887							
thyroid - h		26	177	456	21278	10733	112750	3463	700	290							
HPAEC		28	0	128	5788	13178	104764	240	529	269							
thyroid gland - h		29	0	238	13848	8826	110349	7250	1434	104							
SPTEC		30	122	0	42	4221	115750	2791	1171	322							
trachea - h		31	0	338	15632	13708	86718	1477	3478	182							
HMEC		32	0	797	16746	6112	158944	1037	366	421							
ovary - h		33	105	1070	11725	94558	36293	1834	81	1039							

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Table 3 (cont'd)

Tissue	Tumor cgm	Normal cgm	Tumor - to	Tumor cda	Normal	Endose	tp33	SEQ 78	AA	SEQ 047	SEQ 82	MUSE 84	RHSSEQ 89	AA	SEQ 89	AA	SEQ 90	MUSE 93	TS180	seq	1360
Cell-1	168			168				270	236	18781	1322	0		7842						0	1360
Cell-2	168			168				132	209	26330	4542	3023	41031	139						0	3568
Cell-3	168			168				23	19539	3870	85	2554		414						0	1668
T-47D	169			169				49	0	0	1622	6713	0	81						0	2573
Ren-3	171			181				0	244	0	0	1791	0	1				132	0	264	
CRL1441 RNA 8/30	183			183				28	0	0	0	111	0	58					135	0	3703
T817 untreated + DMSO	184			184				114	4	541	2231	0	0	101					190	2424	
KB pcy A+	186			186				218	0	1363	3269	0	0	101					190	2424	
HOS pcy A+	190			190				0	122	10672	1171	949	147	159					63	1871	
ACHN	200			200				186	0	2977	403	2173	344	0	0				183	4027	
UACC-4	204			204				100	0	1497	403	2173	149	0	0				0	2877	
UCC-77AD-RS	204			204				113	0	0	330	0	78	252				124	498		
UTOS (Mundt) pcy A+	206			206				0	269	613	637	315	0	0				0	1576		
WISH (Collagen) pcy A+	208			208				1168	0	2134	2543	826	880	0				107	8071		
458 medullary RNA	218			218				0	0	184	3263	416	635	194				6	2126		
CCL137 RNA 3/21/88	219			219				0	0	101	3263	416	635	194				6	3255		
WL38 7h 9.5%FB5, 24h 10% FB5	220			220				0	154	0	177	0	81	5				71	1173		
CRL1441 + TPA (2h) 8/30	221			221				18	55	0	2177	0	0	41				0	2554		
Kem-1	222			222				95	0	45	1182	144	0	133				0	1276		
Kem-2	223			223				0	239	0	622	0	11	24				0	2554		
Kem-4	241			241				0	0	1768	1868	963	185	218				0	2554		
HOP-82	242			242				85	163	8463	1026	2825	153	160				40	5219		
MDA-T-4	243			243				0	0	22018	1504	956	911	200				0	5045		
EOVX	244			244				0	226	14060	2051	0	44	215				0	4234		
Hs-60	245			245				0	1087	77132	1403	0	700	226				51	5648		
MCF-H21	246			246				0	0	0	611	928	0	0				7	24		
BRM-8228	247			247				0	0	0	353	0	188	89				0	2544		
ASH9ATCC	248			248				0	163	10413	855	1682	589	17				0	1023		
SR	249			249				0	148	5905	1324	158	0	60				218	4524		
OVCA3	250			250				129	0	45256	1486	201	589	0				55	4053		
HCT-116	251			251				171	0	2361	94	0	158	0				167	1032		
OVCA4	251			251				202	0	307	480	0	38	0				151	1421		
UOJ-1	252			252				0	80	577	3409	0	1477	0				0	4319		
OVCA5	252			252				486	0	6506	173	0	61	323				183	1823		
SK-MES-1	253			253				181	56	17468	195	36	0	66				0	4155		
OVCA6	254			254				0	2638	82675	1953	3515	1363	0				154	5249		
LOX MVI	256			256				140	73	32074	1309	565	128	0				226	4424		
IGROV1	257			257				0	167	4492	224	1854	0	48				567	1286		
SK-MEL-2	258			258				0	103	4761	313	1949	581	0				71	1009		
SK-OV-3	259			259				0	101	3676	172	0	28	0				41	1817		
SK-MEL-5	260			260				159	0	73632	1693	2598	925	496				174	4371		
SF-539	261			261				187	0	14342	546	0	1578	0				74	40	2890	
SK-MEL-28	262			262				0	118	28933	925	0	433	0				0	14843		
KC-52	263			263				0	83	6659	1900	175	91	109				0	1237		
UACC-257	264			264				0	21	1255	873	3737	0	121				0	2708		
M14	267			267				128	298	23780	5268	7090	0	715				0	14043		
MCF7	268			268				38	29	9781	363	0	147	290				125	4095		
MDA-MB-435	270			270				0	28	29	1054	0	67	170				29	3972		
HT-279	271			271				0	0	14738	415	0	447	336				0	4126		
Y79 pcy A+	273			273				11	351	8694	4474	0	1328	0				345	1718		
Y79 pcy A+	269			269				25	36	15960	4474	1554	2113	1061				0	21610		
KHOS pcy A+	300			300				71	0	0	6208	0	0	0				153	756		
HTB38 24h TPA RNA 8/23	313			313				31	52	0	4774	0	0	153				97	3084		
HELA-EXP-031899	322			322				344	0	618	8652	18719	0	680				0	4427		
HTB38 on RNA	323			323				282	0	109	58	270	377	462				83	5452		
HT347	324			324				942	14	0	8157	6597	491	550				170	1553		
458 medullary RNA	326			326				262	21	114633	1217	1515	0	171				0	3071		
MDA-MB-231	330			330				833	1127	131898	2335	15586	30722	6560	1667			45	13815		
U251	336			336				486	1740	72467	8086	60552	28673	1574				0	19652		
PT cells pcy A+	340			340				0	112	8025	779	0	445	128				27	2060		
PC-3	341			341				513	215	25573	1044	18117	1417	1081				0	5852		
HCC-2998	343			343				69	3	1505	1212	708	179	529				0	3005		
SW-620	346			346				46	0	1588	9307	0	15	245				0	2487		
HT18	347			347				17	60	2655	945	634	0	481				0	5660		
CCL-205	347			347				0	0	512	5263	0	72	0				0	2261		
HT215	348			348				0	81	8668	3508	813	0	158				0	1180		
KM-12	350			350				32	202	352	7122	0	182	355				32	1660		
HT151	351			351				637	11	8120	3778	2235	0	388				0	2292		
Asu8	352			352				225	131	0	14919	186	0	183				0	3423		
HT353	353			353				0	0	9025	2120	2003	152	219				0	1907		
ROF 203	355			355				2370	1831	50606	4835	36193	4080	568				173	6203		
TR-10	357			357				1422	1373	182135	14530	51377	8649	9671				88	6356		
MDA-MB-3A	358			358				184	46	21180	1269	1167	10333	150				12	528		
Hs 3787	50			50				0	0	707	2103	0	660	336				0	14318		
HT213	52			52				146	0	647	3338	0	89	694				0	19286		
HT258	54			54				174	0	0	2229	0	59	3071				27	5304		
HT139	55			55				0	0	13	2663	0	0	80				0	15006		
HT155	58			58				0	0	118	1568	0	412	181				117	6426		
HT183	61			61				713	0	2417	1494	1868	0	79				0	6974		
HT170	62			62				111	0	95	2243	0	0	0				0	5639		
HT172	63			63				384	24	92	3379	0	0	0				0	5639		
HT138	63			63				0	78	147	3414	0	621	40				0	6823		
HT176	65			65				208	0	374	2620	0	0	0				0	1510		
HT154	66			66				43	122	437	3649	0	0	0				45	3531		
HT186	66			66				0	0	118	0	1861	0	0				340	182	2939	
HT169	67			67				43	636	28331	3650	0	664	33				78	6073		
HT189	69			69				327	0	0	2961	0	0	0				0	1153		
HT143	70			70				365	71	1386	4366	0	209	268				0	1551		
HT190	72			72				84	68	2084	477	0	0	230				0	878		
HT145	72			72				12	0	215	3473	0	1015	484				0	2504		
HT227																					

Tissue	Tumor-sym	Normal-sym	Tumor - to	Tumor calls	Normal	Ende	p33	SEP 78	AN	SEP 82	MSG 82	MUSE 84	RIPSEP 85	ANSEP 85	ANSEP 90	MSSEP 93	TSEI 94	AL
MA 57AT	155							225	156	132745	45751	28160	30721	3261	3381	3393		
MAF-TADP-RES	153							454	156	82567	3752	172587		402	224	71	4602	
MCF7	151							0	90	22491	3843	2192511		4021	453	56	5548	
M14	149							34	0	102633	57261	68626	724	4831	781	8105		
UACC-257	147							0	190	24404	44491	45556	1177	17	77	77		
UACC-62	145							0	331	105560	8515	47918	1123	348	0	8143		
SK-MEL-28	144							0	103	35141	6515	65339	575	133	24	1529		
UO-31	143							508	100	20643	9249	72274	520	1892	2751	4295		
SK-MEL-5	142							104	0	22587	5756	73271	10551	79	79	79		
SK-MEL-2	141							0	0	3454	3354	80653	109	127	182	3169		
HCT-15	140							171	0	22819	3245	134928	27	167	132	2782		
MCF-15	139							0	47	15009	3913	104302	4991	0	1031	7894		
MCF-34	138							140	190	22408	3765	137483	473	273	273	273		
COLO 205	137							0	213	21011	6643	114441	642	91	74	5493		
QIM-64	136							158	1464	58997	3350	112245	14701	0	0	3197		
SW-620	135							168	0	11595	3617	104047	7681	0	210	5273		
TK-10	134							0	13	20867	41446	75274	10869	130	1536	0		
HCT 118	133							1060	59	71653	2016	119274	702	63	263	7449		
Hs57	132							225	0	26315	3039	102477	3314	0	42	8256		
HCC-2908	131							0	190	17087	5568	127191	495	16	0	3603		
ACHN	130							138	138	33733	3255	97608	473	165	14	273		
PC-3	129							160	194	4733	7715	90475	1017	248	0	740		
K562	128							134	204	35400	3502	59543	377	2981	65	7544		
DU-145	127							0	79	6324	2431	17433	259	54	0	247		
Gals-1	126							0	14	6161	2645	64362	3136	0	0	3203		
GR	125							0	79	8483	2584	28829	1849	80	47	10019		
A488	124							0	153	26453	2600	91356	15	1182	0	6992		
RPMB 8226	123							24	0	80	2614	12694	102	472	168	57		
SN12C	122							0	134	35731	7382	36641	542	371	84	11656		
AS 40	121							613	109	923	6301	450	369	3123	21428	0		
MOLT-4	120	</																

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Table 3 (cont'd)

Tissue	Tumor-ym	Metast-ym	Tumor - 10	Tumor cells	Normal	Endoc	p53	SEG 79	AN	SEG 80	SEG 81	SEG 82	SEG 83	SEG 84	SEG 85	SEG 86	SEG 87	SEG 88	SEG 89	SEG 90	SEG 91	SEG 92	SEG 93	SEG 94	SEG 95
DaPang-2								0	1187	2287	94057	0	2282	0	238	1528									
DaPang-8								0	2756	837	72028	0	1513	0	48	623									
DaPang-9								0	2223	15	36553	0	14291	0	103	750									
DaPang-11								0	11	2578	73553	0	8794	0	0	1249									
DaPang-12								0	0	1663	47835	0	7699	0	0	0									
DaPang-15								0	34	0	33603	0	10771	0	0	1770									
DaPang-1								0	257	704	90021	0	2318	0	56	200									
DaPang-2								0	408	205	148948	0	1211	0	46	393									
DaPang-2								0	213	6567	106848	0	2713	0	0	484									
DaPang-2								0	52	561	66193	0	659	0	354	801									
DaPang-4								0	2053	0	45199	0	0	0	249	623									
DaPang-5								0	1846	0	54509	0	58	0	19	492									
DaPang-6								wt	0	28	4742	66151	0	2099	0	2323									
AS49 - 8							mutant	0	164	4671	74530	0	7725	0	72	1568									
BOVX - 8							wt	0	173	636	22564	0	1578	0	0	1781									
HCT-116 - 7							wt	0	205	779	29245	0	2302	0	0	1781									
HCT-116 - 8							mutant	0	167	1301	47637	0	276	0	315	552									
HT29 - 1							mutant	0	0	80	14674	0	342	0	0	458									
HT29 - 7							wt	0	451	621	38186	0	30	0	95	441									
HT29 - 8							mutant	0	254	114	260091	0	1532	0	124	823									
SF539 - 7							wt	0	1007	176	38166	0	4118	0	323	851									
SF539 - 8							mutant	0	0	2013	52411	0	2540	0	167	1486									
SF-205 - 7							wt	0	1383	1825	39162	0	4136	0	126	1371									
SF-205 - 8							mutant	0	109	0	24681	0	534	0	140	2424									
OVCA4-4 - 7							wt	0	0	2400	56208	0	6736	0	0	3745									
OVCA4-4 - 8							wt	0	1141	660	99690	0	2132	0	0	571									
OVCA4-4 - 1							mutant	0	79	1	12621	0	1	0	0	242									
OVCA4-5 - 8							wt	0	204	0	40587	0	258	0	8	342									
MCF-7 - 8							wt	0	108	0	23503	0	501	0	269	651									
ADR-RES - 8							mutant	0	1303	1036	21952	0	1176	0	88	1433									
HeLa - 8							wt	0	226	483	28435	0	1176	0	330	879									
SW480 - 7							mutant	0	1123	0	27332	0	1872	0	330	879									
SW480 - 8							wt	0	215	1268	20150	0	2991	0	0	650									
H1299 - 8							mutant	0	1096	204	11111	0	3386	0	215	1683									
C33A - 7							wt	0	7771	321	70434	0	3386	0	113	979									
C33A - 8							mutant	0	720	1497	63571	0	3482	0	38	856									
U2OS - 7							wt	0	1329	826	33247	0	112	0	0	853									
U2OS - 8							mutant	0	86	522	75366	0	9362	0	0	1105									
HeLa - 7							wt	0	0	530	49109	0	1024	0	0	950									
HeLa - 8							wt	0	54	0	62906	0	142	0	0	243									
WI 38 - 8							wt	56	318	18715	14760	157513	855	88	0	243									
456 medullar DNA								0	0	154	1318	826	83	21	0	224									
CRL1572 3/1/89								64	110	70	3768	618	605	254	0	12872									
Beas-2								0	33	0	4338	137	22	588	549	7852									
HT368								0	30	0	4042	10	0	0	133	19627									
HT316								692	115	251	5516	1408	1123	1190	0	6463									
HT355								200	185	874	5319	0	287	356	0	4067									
HT308								173	105	0	1494	249	0	8	0	2746									
Beas-3								175	45	115	220	154	44	0	103	3483									
Beas-5								177	0	0	1799	0	54	0	60	5086									
Beas-9									103	0	2152	2734	0	81	77	2460									
h keratinocytes 2/25/92 #10								237	87	59	4051	559	416	154	8	1021									
Beas-10									49	73	821	8012	740	165	181	1882									
HTB10									0	0	391	3370	0	818	0	474									
h keratinocytes 3/1/92 #12									0	0	4330	0	0	0	0	1266									
prostate, h									235	87	4366	4893	295	495	375	11	6785								
MNNG-Q5 poly A+									532	0	3011	1291	6062	49	769	249	6785								
SA-Q5 (Mundy) poly A+									630	0	7825	1653	8543	271	1030	147	4771								
h6 poly A+									0	0	817	28908	0	1747	0	0									
HCT-116 - 3								wt	0	211	234	30187	0	5246	0	52	307								
HCT-116 - 4								wt	0	7	37	34589	0	2413	0	0	1024								
HCT-116 - 5								wt	0	186	363	35688	0	1998	0	66	1306								
HCT-116 - 6								wt	0	6	0	21787	0	0	0	807									
AS49 - 6								mutant	0	302	1078	19879	0	193	0	159	889								
HT29 - 3								wt	0	0	41	24371	0	187	0	92	1103								
BOVX - 6								mutant	0	132	0	25059	0	464	0	0	2528								
HT29 - 4								wt	0	31	1353	76872	0	629	0	0	622								
HT29 - 5								wt	0	470	0	42341	0	152	0	0	1325								
HT29 - 6								wt	0	235	328	29521	0	5211	0	0	878								
OVCA4-4 - 3								wt	0	438	397	301615	0	2662	0	0	1008								
OVCA4-4 - 4								wt	0	100	934	38312	0	80601	0	85	940								
OVCA4-4 - 5								wt	0	508	458	18032	0	312	0	515	1063								
OVCA4-4 - 6								wt	0	112	4566	32960	0	196	0	36	1062								
SF539 - 3								wt	0	0	2465	27211	0	2209	0	0	0								
SF539 - 4								wt	0	30	176	22964	0	1587	0	236	1238								
SF539 - 5								wt	0	211	1013	59830	0	0	0	262	824								
SF539 - 6								mutant	0	181	622	27675	0	148	0	0	0								
OVCA4-5 - 3								wt	0	402	984	18952	0	1208	0	3621	617								
OVCA4-5 - 4								wt	0	183	418	9373	0	483	0	0	477								
OVCA4-5 - 5								wt	0	34	87	24265	0	998	0	54	961								
ADR-RES - 6								wt	0	182															

Table 3 (cont'd)

Tissue	Tumor - sym	Normal - sym	Tumor - to	Tumor cells	Normal	Endos	p53	SEQ 95	AA SEQ 96	AA SEQ 97	AA SEQ 98	AA SEQ 99	AA SEQ 100	AA SEQ 101	AA SEQ 102	AA SEQ 103	AA SEQ 104	AA SEQ 105	AA SEQ 106	AA SEQ 107	AA SEQ 108	AA SEQ 109	AA SEQ 110	AA SEQ 111	AA SEQ 112	AA SEQ 113	AA SEQ 114	AA SEQ 115
adrenal gland - h	1							0	520	9317	15583	5311	3705	92945	560	18327												
lymph node - h	2							145	1220	11829	24716	19927	5369	19401	962	19488												
bone marrow - h	3							0	633	3256	4004	6045	4161	16648	1113	4801												
mammary gland - h	4							121	306	549	423	452	1581	525	3951													
brain - h	5							480	947	2451	11045	2517	5005	85645	745	12790												
pancreas - h	6							543	905	1776	11768	4289	4397	15743	1117	11149												
ovary - h	7							342	1137	14444	44717	4532	3800	78914	1308	51344												
pituitary gland - h	8							615	531	4032	21432	8617	4163	2727	1158	19044												
testis - h	9							0	1302	3571	20240	4681	7201	56138	1589	26240												
placenta - h	10							863	818	7524	4384	8783	3481	51723	1725	28256												
fetal kidney - h	11							1069	1190	8450	16797	9568	4326	34771	2075	48589												
prostate - h	12							53	1511	786	7209	610	3972	14456	1414	30916												
fetal liver - h	13							246	1238	3569	4142	1439	4358	14560	907	11283												
salivary gl. - h	14							641	486	3524	7759	2508	5648	20072	1120	18166												
fetal lung - h	15							1164	609	3215	13136	8897	5222	18167	1638	97919												
skeletal muscle - h	16							349	605	508	3019	533	2560	11312	1787	13079												
heart - h	17							32	708	3722	3365	1198	1481	41333	1154	37253												
small intestine - h	18							0	524	2431	8421	3280	2070	10971	1713	19616												
kidney - h	19							691	366	6026	14631	4976	4012	35666	1331	12278												
spinal cord - h	20							1080	294	1535	4310	1765	946	16499	1055	6030												
liver - h	21							0	428	1611	8137	1685	3116	19447	1435	4737												
spleen - h	22							336	348	4682	6027	3412	1391	8699	1068	4256												
lung - h	23							0	182	5215	8947	4125	1031	13020	992	28619												
stomach - h	24							0	443	2243	1225	1851	2148	6009	1235	3363												
testis - h	25							15438	2514	35048	4251	28181	6520	67369	890	24003												
thyroid - h	26							790	414	5036	18572	11138	4767	11603	362	13111												
HPAEC	28							703	187	0	239	1152	3658	4272	991	0												
thyroid gland - h	29							581	686	1236	4764	3196	2290	21667	519	24405												
RPTEC	30							181	516	0	390	1052	3123	1920	723	0												
testis - h	31							586	740	4304	9891	10717	2096	13172	1555	56690												
HMEC	32							0	544	250	55	115	3044	1027	1192	2038												
uterus - h	33							0	618	2911	6059	3666	1347	20290	1100	67028												
HCAEC	34							0	299	0	454	0	3409	1110	805	0												
pancreas - h	35							0	451	0	312	222	1822	988	630	0												
lymph node - h	36							746	475	443	301	11	1061	653	948	1325												
skeletal muscle - h	37							0	374	168	0	1441	1996	729	0	0												
fetal liver - h	38							0	842	0	363	0	3211	13921	1054	901												
heart - h	39							0	338	1343	0	0	1194	3263	558	149												
thyroid - h	40							143	522	0	499	362	2019	54	1219	0												
Quadriceps - h	41							896	299	518	136	191	2336	1094	0	0												
fetal brain - h	42							629	493	0	573	464	1760	3771	2223	0												
salivary gl. - h	43							0	421	154	0	145	1660	1341	1265	0												
testis - h	44							1653	626	2190	425	3678	3717	976	1846	0												
WT18-normal								365	0	0	0	746	52	348	0	0												
WT13-normal								362	0	0	288	151	0	120	0	134	0											
WT157-normal								361	0	0	18	0	83	2404	165	0												
Bov-12								356	356	4165	5699	345	634	8772	296	3419	16347											
Bov-13								7265	3210	1259	369	4808	80	4808	182	1521	16366											
corneal endothelium - h								344	0	254	82	225	35	64	559	0												
brain - h								342	0	0	32	268	0	248	0	452	264											
RPTEC								334	334	0	346	0	0	746	0	1668	0											
lymph node - h								332	0	11	19	24	81	45	836	0												
h adult SMC 10/21/92 #17								330	0	80	91	0	87	71	0	687	0											
WT206-normal								328	1667	2695	0	1912	109	2629	456	1452	7256											
WT206-normal								327	0	391	0	0	118	411	429	0												
thyroid - h								326	309	4778	86	727	0	1869	92	1894	9621											
WT149 - normal								321	218	45	0	0	0	72	755	0												
HEPM 3d untreated								320	0	780	0	283	238	2579	21	3311	0											
uterus - h								318	2610	1182	774	2029	2189	4203	471	1067	2668											
nucleus - h								316	812	74	0	1132	1663	2543	0	701	1532											
thyroid gland - h								314	195	271	0	749	2547	2242	333	730	2522											
salivary gl. - h								311	0	0	153	47	56	251	1072	0												
prostate - h								309	58	551	477	135	242	187	452	0												
pituitary gland - h								307	306	610	156	464	96	1674	0	401	0											
pancreas - h								305	0	79	0	397	200	520	535	749	0											
mammary gland - h								303	0	1875	0	1864	675	1375	48	833	0											
testis - h								302	0	306	123	72	306	254	968	228												
liver - h								298	7748	6576	2195	2065	3729	4087	1220	1487	4479											
liver - h								297	2003	4962	0	2022	2522	2776	0	2119	1673											
spleen - h								296	0	260	0	807	515	359	881	931	0											
spinal cord - h								294	1237	1442	100	2031	111	75	1715	460												
small intestine - h								292	0	0	1415	285	810	0	548</													

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Table 3 (cont'd)

Tissue	Tumor - ym	Normal - ym	Tumor - 1e	Tumor cells	Normal	Endos	p33	SEQ 93	AN SEQ 96	AN SEQ 97	MO SEQ 100	AN SEQ 101	AN SEQ 110	AN SEQ 111	AN SEQ 112	AN SEQ 114	M
Cable-1				155				0	377	308	131	1114	713	62	302	0	
Cable-2				156				238	356	21	45	4121	1018	0	1025	0	
Cable-3				157				0	152	14	104	590	1078	0	708	0	
Cable-4				158				0	31	150	65	0	336	0	530	0	
Cable-5				159				0	0	0	0	0	0	0	0	0	
Cable-6				160				0	0	0	0	0	0	0	0	0	
Cable-7				161				0	0	0	0	0	0	0	0	0	
Cable-8				162				0	0	0	0	0	0	0	0	0	
Cable-9				163				0	0	0	0	0	0	0	0	0	
Cable-10				164				0	0	0	0	0	0	0	0	0	
Cable-11				165				0	0	0	0	0	0	0	0	0	
Cable-12				166				0	0	0	0	0	0	0	0	0	
Cable-13				167				0	0	0	0	0	0	0	0	0	
Cable-14				168				0	0	0	0	0	0	0	0	0	
Cable-15				169				0	0	0	0	0	0	0	0	0	
Cable-16				170				0	0	0	0	0	0	0	0	0	
Cable-17				171				0	0	0	0	0	0	0	0	0	
Cable-18				172				0	0	0	0	0	0	0	0	0	
Cable-19				173				0	0	0	0	0	0	0	0	0	
Cable-20				174				0	0	0	0	0	0	0	0	0	
Cable-21				175				0	0	0	0	0	0	0	0	0	
Cable-22				176				0	0	0	0	0	0	0	0	0	
Cable-23				177				0	0	0	0	0	0	0	0	0	
Cable-24				178				0	0	0	0	0	0	0	0	0	
Cable-25				179				0	0	0	0	0	0	0	0	0	
Cable-26				180				0	0	0	0	0	0	0	0	0	
Cable-27				181				0	0	0	0	0	0	0	0	0	
Cable-28				182				0	0	0	0	0	0	0	0	0	
Cable-29				183				0	0	0	0	0	0	0	0	0	
Cable-30				184				0	0	0	0	0	0	0	0	0	
Cable-31				185				0	0	0	0	0	0	0	0	0	
Cable-32				186				0	0	0	0	0	0	0	0	0	
Cable-33				187				0	0	0	0	0	0	0	0	0	
Cable-34				188				0	0	0	0	0	0	0	0	0	
Cable-35				189				0	0	0	0	0	0	0	0	0	
Cable-36				190				0	0	0	0	0	0	0	0	0	
Cable-37				191				0	0	0	0	0	0	0	0	0	
Cable-38				192				0	0	0	0	0	0	0	0	0	
Cable-39				193				0	0	0	0	0	0	0	0	0	
Cable-40				194				0	0	0	0	0	0	0	0	0	
Cable-41				195				0	0	0	0	0	0	0	0	0	
Cable-42				196				0	0	0	0	0	0	0	0	0	
Cable-43				197				0	0	0	0	0	0	0	0	0	
Cable-44				198				0	0	0	0	0	0	0	0	0	
Cable-45				199				0	0	0	0	0	0	0	0	0	
Cable-46				200				0	0	0	0	0	0	0	0	0	
Cable-47				201				0	0	0	0	0	0	0	0	0	
Cable-48				202				0	0	0	0	0	0	0	0	0	
Cable-49				203				0	0	0	0	0	0	0	0	0	
Cable-50				204				0	0	0	0	0	0	0	0	0	
Cable-51				205				0	0	0	0	0	0	0	0	0	
Cable-52				206				0	0	0	0	0	0	0	0	0	
Cable-53				207				0	0	0	0	0	0	0	0	0	
Cable-54				208				0	0	0	0	0	0	0	0	0	
Cable-55				209				0	0	0	0	0	0	0	0	0	
Cable-56				210				0	0	0	0	0	0	0	0	0	
Cable-57				211				0	0	0	0	0	0	0	0	0	
Cable-58				212				0	0	0	0	0	0	0	0	0	
Cable-59				213				0	0	0	0	0	0	0	0	0	
Cable-60				214				0	0	0	0	0	0	0	0	0	
Cable-61				215				0	0	0	0	0	0	0	0	0	
Cable-62				216				0	0	0	0	0	0	0	0	0	
Cable-63				217				0	0	0	0	0	0	0	0	0	
Cable-64				218				0	0	0	0	0	0	0	0	0	
Cable-65				219				0	0	0	0	0	0	0	0	0	
Cable-66				220				0	0	0	0	0	0	0	0	0	
Cable-67				221				0	0	0	0	0	0	0	0	0	
Cable-68				222				0	0	0	0	0	0	0	0	0	
Cable-69				223				0	0	0	0	0	0	0	0	0	
Cable-70				224				0	0	0	0	0	0	0	0	0	
Cable-71				225				0	0	0	0	0	0	0	0	0	
Cable-72				226				0	0	0	0	0	0	0	0	0	
Cable-73				227				0	0	0	0	0	0	0	0	0	
Cable-74				228				0	0	0	0	0	0	0	0	0	
Cable-75				229				0	0	0	0	0	0	0	0	0	
Cable-76				230				0	0	0	0	0	0	0	0	0	
Cable-77				231				0	0	0	0	0	0	0	0	0	
Cable-78				232				0	0	0	0	0	0	0	0	0	
Cable-79				233				0	0	0	0	0	0	0	0	0	
Cable-80				234				0	0	0	0	0	0	0	0	0	
Cable-81				235				0	0	0	0	0	0	0	0	0	
Cable-82				236				0	0	0	0	0	0	0	0	0	
Cable-83				237				0	0	0	0	0	0	0	0	0	
Cable-84				238				0	0	0	0	0	0	0	0	0	
Cable-85				239				0	0	0	0	0	0	0	0	0	
Cable-86				240				0	0	0	0	0	0	0	0	0	
Cable-87				241				0	0	0	0	0	0	0	0	0	
Cable-88				242				0	0	0	0	0	0	0	0	0	
Cable-89				243				0	0	0	0	0	0	0	0	0	
Cable-90				244				0	0	0	0	0	0	0	0	0	
Cable-91				245				0	0	0	0	0	0	0	0	0	
Cable-92				246				0	0	0	0	0	0	0	0	0	
Cable-93				247				0	0	0	0	0	0	0	0	0	
Cable-94				248				0	0	0	0	0	0	0	0	0	
Cable-95				249				0	0	0	0	0	0	0	0	0	
Cable-96				250				0	0	0	0	0	0	0	0	0	
Cable-97				251				0	0	0	0	0	0	0	0	0	
Cable-98				252				0	0	0	0	0	0	0	0	0	
Cable-99				253				0	0	0	0	0	0	0	0	0	
Cable-100				254				0	0	0	0	0	0	0	0	0	
Cable-101				255				0	0	0	0	0	0	0	0	0	
Cable-102				256				0	0	0	0	0	0	0	0	0	
Cable-103				257				0	0	0	0	0	0	0	0	0	
Cable-104				258				0	0	0	0	0	0	0	0	0	
Cable-105				259				0	0	0	0	0	0	0	0	0	
Cable-106				260				0	0	0	0	0	0	0	0	0	
Cable-107				261				0	0	0	0	0	0	0	0	0	
Cable-108				262				0	0	0	0	0	0	0	0	0	
Cable-109				263				0	0	0	0	0	0	0	0	0	
Cable-110				264				0	0	0	0	0	0	0	0	0	
Cable-111				265				0	0	0	0	0	0	0	0	0	
Cable-112				266				0	0	0	0	0	0	0	0	0	
Cable-113				267				0	0	0	0	0	0	0	0	0	
Cable-114				268				0	0	0	0	0	0	0	0	0	
Cable-115				269				0	0	0	0	0	0	0	0	0	
Cable-116				270				0									

Table 3 (cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - Yo	Tumor cells	Normal	Endoc	p33	SEQ 85	ALSEP 36	ALSEP 97	H3SE0	189	ALSEP 101	ALSEP 110	ALSEP 111	ALSEP 112	ALSEP 114
BLADDER								2521	943	0	1798	2068	12004	1043	6551	14282	
BLADDER-RES	153							491	517	1877	891	696	10679	6254	892	0	
MCF-7	151							5433	1235	160	6896	3069	25634	2094	1309	2238	
M14	149							3531	0	450	2401	1993	3476	1399	1035	0	
UACC-257	147							4023	288	1268	2276	2137	11033	6230	613	947	
UACC-82	145							2545	157	706	756	1215	1403	2439	585	429	
SK-MEL-28	144							5634	60	3906	1173	721	2090	1531	805	2945	
UO-31	143							5324	487	3107	504	442	3000	1020	1536	11997	
SK-MEL-5	142							1330	0	1009	2261	2826	16384	2804	681	3368	
SK-MEL-2	141							261	319	0	489	0	3403	379	443	0	
HCT-15	140							2614	185	1844	1741	478	19972	1717	918	3611	
MCF-19	139							4882	486	655	1930	389	9956	662	979	1820	
HepG2	138							1296	545	2261	1148	7970	2214	9413	2639	0	
COLO 205	137							3538	191	1993	1664	1417	11150	231	1214	1103	
LOX IMVI	136							3524	52	1973	1526	677	23802	2457	967	1995	
SW-620	135							4591	493	1395	1150	826	12216	571	850	1736	
TK-10	134							4846	318	1845	885	484	3644	2032	937	1147	
HCT-116	133							1224	394	579	1524	333	9640	355	768	0	
JMS-0	132							2284	162	1883	628	792	11840	2318	722	0	
HCC-2998	131							2604	290	0	1232	719	5639	858	904	0	
ACHN	130							3287	488	2068	936	36099	2818	652	652	0	
HCC-3	129							5812	370	0	719	646	13846	2599	543	0	
RUF-393	128							614	317	8314	911	540	2671	7592	524	105	
DLL145	127							1412	83	0	906	461	3331	1531	666	0	
Caco-1	126							2183	11	0	1328	635	8406	3126	52	1596	
SR	125							3471	320	0	841	330	19003	1183	345	84	
A498	124							5481	0	1125	1967	269	26934	10429	628	1032	
RPK4 E276	123							1951	46	44	229	354	1926	0	563	854	
SW-630	122							2060	104	802	178	1832	11740	11028	824	837	
4-50	121							930	0	0	545	2164	395	634	0	0	
MOLT-1	120							5683	0	1010	522	1507	4271	753	1205	0	
OVCAR-5	119							1580	119	1759	1966	2515	8653	1940	5625	5625	
SK-MEL-27	118							3767	0	0	850	252	8345	1008	1001	269	
OVCAR-4	117							1258	284	0	1029	2229	11490	3963	1253	657	
CCRF-CEM	116							5623	86	1509	2572	1628	25692	2316	981	1348	
OVCAR-3	115							2690	150	1853	934	1562	12158	1242	552	1532	
HIF-639	114							3527	457	10	717	367	18956	893	882	1468	
HOP-62	113							455	0	1559	673	285	19248	3406	282	1027	
SP-295	112							2817	539	75	1118	801	17954	1500	941	0	
AS49ATCC	111							1680	940	1723	2304	1071	30228	3271	1014	3711	
HIF-268	110							2250	208	1443	563	1814	11939	4509	643	1666	
NCLH522	109							1264	0	1176	1767	1721	7210	1466	976	1034	
U251	108							2200	209	729	977	730	8651	3518	526	2250	
NCLH460	107							2274	449	1277	926	1836	17628	1802	676	0	
NCLH-75	106							1148	228	0	405	289	4322	1304	722	0	
NCLH-H322M	105							3368	435	0	3525	1047	20442	308	559	327	
NBL-19	104							2006	316	0	1860	455	4358	2106	812	1908	
NCLH-226	103							6463	125	0	1140	759	4785	1532	1091	0	
SK-OV-3	102							6105	418	0	1065	615	13274	5271	587	3219	
NCLH-23	101							6602	311	0	1162	841	7912	446	380	0	
RGROV1	100							612	0	0	1863	969	10757	0	453	0	
EXVX	99							1811	77	0	1733	915	17090	1757	340	942	
OVCAR-8	98							3854	0	477	422	150	7006	376	782	0	
HOP-92	97							2307	158	0	686	928	12320	5619	887	481	
in fibroblasts 301/92 #12	46							334	84	6	260	21	1718	823	1424	0	
in fibroblasts 1021/92 #17	47							269	10	109	251	0	1286	802	1342	0	
in fibroblasts 275/92 #10	48							534	336	0	193	82	5234	5718	1436	7682	
TCGP	26							1066	737	4716	402	636	2721	1965	34	1742	
AS49-1							wt	0	0	0	5421	0	0	0	353	0	
AS49-3							wt	0	0	0	4212	30	0	0	402	0	
AS49-4							wt	0	0	0	5323	49	0	587	404	0	
AS49-5							wt	0	0	0	2872	210	0	50	635	0	
AS49-7							wt	0	0	0	462	118	0	530	563	0	
EXVX-1						mutant	wt	0	0	0	1343	0	0	428	617	0	
EXVX-4						mutant	wt	0	0	0	43690	11	0	557	705	0	
EXVX-3						mutant	wt	0	0	0	934	0	0	0	708	0	
EXVX-5						mutant	wt	0	0	0	0	0	0	283	158	0	
EXVX-7						mutant	wt	0	0	0	1576	72	0	126	602	0	
MCF-7-1						wt	wt	0	0	0	718	84	0	0	621	0	
MCF-7-3						wt	wt	0	0	0	5245	65	0	558	641	0	
MCF-7-4						wt	wt	0	0	0	1155	73	0	353	895	0	
MCF-7-5						wt	wt	0	0	0	1050	189	0	0	685	0	
MCF-7-7						wt	wt	0	0	0	1337	145	0	217	659	0	
ADR-RES-1						mutant	mutant	0	0	0	3885	0	0	26	234	0	
ADR-RES-2						mutant	mutant	0	0	0	524	99	0	199	966	0	
ADR-RES-4						mutant	wt	0	0	0	951	0	0	0	835	0	
ADR-RES-5						mutant	mutant	0	0	0	472	112	0	0	569	0	
ADR-RES-7						mutant	mutant	0	0	0	7562	0	0	329	670	0	
WI 38-1						wt	wt	0	0	0	0	0	0	2187	521	0	
WI 38-3						wt	wt	0	0	0	217	79	0	561	559	0	
WI 38-4						wt	wt	0	0	0	751	87	0	548	548	0	
WI 38-5						wt	wt	0	0	0	3124	114	0	1914	828	0	
WI 38-7						wt	wt	0	0	0	4617	0	0	0	1096	0	
HsLx-1						HPV E6	wt	0	0	0	12621	108	0	0	973	0	
HsLx-3						HPV E6	wt	0	0	0	643	263	0	74	894	0	
HsLx-4						HPV E6	wt	0	0	0	3311	170	0	505	871	0	
HsLx-5						HPV E6	wt	0	0	0	1166	818	0	1402	1155	0	
HsLx-7						HPV E6	wt	0	0	0	1048	450	0	0	803	0	
H1299-1						mutant	mutant	0	0	0	0	0	0	0	701	0	
H1299-3						mutant	wt	0	0	0	0	0	0	212	969	0	
H1299-4						mutant	wt	0	0	0	2070	530	0	147	1242	0	
H1299-5						mutant	wt	0	0	0	1606	193	0	958	578	0	
H1299-7						mutant	wt	0	0	0	0	0	0	0	719	0	
AS49-2						wt	wt	0	0	0	4270	141	0	409	565	0	
EXVX-2						mutant	wt	0	0	0	2003	86	0	0	373	0	
HCT-116-1						wt	wt	0	0	0	5597	143	0	1327	1078	0	
HCT-116-2						wt	wt	0	0	0	3756	44	0	2663	516	0	
HT29-2						mutant	wt	0	0	0	1380	188	0	1005	1048	0	
SF539-1						wt	wt	0	0	0	1849	196	0	220	659	0	
SF539-2						wt	wt	0	0	0	2474	10	0	387	719	0	
SF-768-1						mutant	wt	0	0	0	317	2004	0	1212	585	0	
SF-768-2						mutant	wt	0	0	0	451	550	0	823	631	0	
OVCAR-4-1						wt	wt	0									

Table 186
Table 3 (cont'd)

Tissue	Tumor type	Normal type	Tumor to	Tumor cells	Normal	Endos	P33	SEQ 25	AA	SEQ 06	AA	SEQ 07	HA	SEQ 100	AGE	101	AGE	110	AGE	111	AGE	112	AGE	114	AGE			
DuPanc-2							0	0	0	0	4153	258	0	11981	758	0	11981	758	0	11981	758	0	11981	758	0			
DuPanc-3							0	0	0	0	127	0	0	1132	264	0	1132	264	0	1132	264	0	1132	264	0			
DuPanc-4							0	0	0	0	251	17	0	24071	6031	0	24071	6031	0	24071	6031	0	24071	6031	0			
DuPanc-5							0	0	0	0	2910	477	0	1191	732	0	1191	732	0	1191	732	0	1191	732	0			
DuPanc-11							0	0	0	0	0	50	0	5703	358	0	5703	358	0	5703	358	0	5703	358	0			
DuPanc-12							0	0	0	0	11437	102	0	910	543	0	910	543	0	910	543	0	910	543	0			
DuPanc-10							0	0	0	0	80	0	0	170	438	0	170	438	0	170	438	0	170	438	0			
DuPanc-1							0	0	0	0	763	0	0	206	737	0	206	737	0	206	737	0	206	737	0			
DuPanc-2							0	0	0	0	5099	69	0	337	970	0	337	970	0	337	970	0	337	970	0			
DuPanc-3							0	0	0	0	3575	0	0	3304	76	0	3304	76	0	3304	76	0	3304	76	0			
DuPanc-4							0	0	0	0	217	71	0	1090	845	0	1090	845	0	1090	845	0	1090	845	0			
DuPanc-5							0	0	0	0	0	40	0	62	1967	0	62	1967	0	62	1967	0	62	1967	0			
DuPanc-6							wt	0	0	0	1853	79	0	59	622	0	59	622	0	59	622	0	59	622	0			
AS49 - 8							mutant	0	0	0	6488	207	0	224	57	0	224	57	0	224	57	0	224	57	0			
EXVX - 6							wt	0	0	0	0	209	0	54	373	0	54	373	0	54	373	0	54	373	0			
HCT-116 - 7							wt	0	0	0	845	122	0	176	675	0	176	675	0	176	675	0	176	675	0			
HCT-116 - 8							mutant	0	0	0	3501	0	0	855	844	0	855	844	0	855	844	0	855	844	0			
HT29 - 1							mutant	0	0	0	3147	201	0	214	233	0	214	233	0	214	233	0	214	233	0			
HT29 - 7							mutant	0	0	0	467	0	0	200	769	0	200	769	0	200	769	0	200	769	0			
HT29 - 8							wt	0	0	0	375	53	0	21	654	0	21	654	0	21	654	0	21	654	0			
SF539 - 7							wt	0	0	0	0	252	0	21	853	0	21	853	0	21	853	0	21	853	0			
SF539 - 8							mutant	0	0	0	446	164	0	706	329	0	706	329	0	706	329	0	706	329	0			
SF-268-7							mutant	0	0	0	0	183	0	203	848	0	203	848	0	203	848	0	203	848	0			
SF-268-4							wt	0	0	0	1305	423	0	0	935	0	0	935	0	0	935	0	0	935	0			
OVCAR-4 - 7							wt	0	0	0	527	329	0	2772	802	0	2772	802	0	2772	802	0	2772	802	0			
OVCAR-4 - 8							mutant	0	0	0	328	91	0	603	2164	0	603	2164	0	603	2164	0	603	2164	0			
OVCAR-5 - 7							mutant	0	0	0	0	315	0	511	558	0	511	558	0	511	558	0	511	558	0			
OVCAR-5 - 8							wt	0	0	0	240	194	0	510	800	0	510	800	0	510	800	0	510	800	0			
MCF-7 - 6							mutant	0	0	0	3012	0	0	295	1032	0	295	1032	0	295	1032	0	295	1032	0			
ADR-RES - 8							HPV E6	0	0	0	2243	117	0	139	875	0	139	875	0	139	875	0	139	875	0			
HEL - 6							mutant	0	0	0	1081	452	0	0	1025	0	0	1025	0	0	1025	0	0	1025	0			
SW480 - 7							mutant	0	0	0	7238	417	0	302	712	0	302	712	0	302	712	0	302	712	0			
SW480 - 8							mutant	0	0	0	2263	0	0	0	737	0	0	737	0	0	737	0	0	737	0			
HT29 - 8							mutant	0	0	0	3128	0	0	183	760	0	183	760	0	183	760	0	183	760	0			
C33A - 7							mutant	0	0	0	1813	0	0	538	1063	0	538	1063	0	538	1063	0	538	1063	0			
C33A - 8							wt	0	0	0	2184	0	0	13	851	0	13	851	0	13	851	0	13	851	0			
UZOS - 7							mutant	0	0	0	0	167	0	656	808	0	656	808	0	656	808	0	656	808	0			
UZOS - 8							wt	0	0	0	4024	909	0	171	615	0	171	615	0	171	615	0	171	615	0			
HEL - 7							wt	0	0	0	4497	0	0	301	519	0	301	519	0	301	519	0	301	519	0			
HEL - 8							wt	0	0	0	573	8	0	304	972	0	304	972	0	304	972	0	304	972	0			
WI38 - 8							wt	0	0	0	266	38	304	1464	1336	1471	1814	0	1471	1814	0	1471	1814	0				
458 amduko RNA							0	104	154	32	0	42	445	338	1013	0	445	338	1013	0	445	338	1013	0				
CR11572 3/17/89							0	274	494	0	25	653	672	2312	1229	2098	0	2312	1229	2098	0	2312	1229	2098	0			
Dem1							1226	1327	0	217	70	5103	0	0	939	0	0	939	0	0	939	0	0	939	0			
HT368							0	30	184	0	163	55	723	0	921	0	0	921	0	0	921	0	0	921	0			
HT378							278	2801	0	670	60	4081	375	1937	3835	0	375	1937	3835	0	375	1937	3835	0				
HT385							0	234	0	449	0	494	95	2033	8204	0	494	95	2033	8204	0	494	95	2033	8204	0		
HT308							173	0	2	188	34	115	0	0	0	0	0	0	0	0	0	0	0	0	0			
Ben-3							175	0	336	790	0	0	18	101	345	0	18	101	345	0	18	101	345	0				
Ben-5							177	576	386	241	104	0	483	119	621	0	483	119	621	0	483	119	621	0				
Ben-9							0	1129	385	0	0	0	706	166	819	0	706	166	819	0	706	166	819	0				
h. lat. microcytes 3/25/92 #10							237	0	0	10	0	16	0	15161	899	0	15161	899	0	15161	899	0	15161	899	0			
Ben-10							0	0	189	242	0	463	466	1308	0	0	466	1308	0	0	466	1308	0	0	466	1308	0	
HTB10							0	382	205	91	46	0	94	10571	0	0	94	10571	0	0	94	10571	0	0	94	10571	0	
h. fibroblasts 3/31/92 #12							0	182	69	187	69	196	0	1032	0	0	1032	0	0	1032	0	0	1032	0	0	1032	0	
prostate							wt	52	0	0	490	848	1533	0	632	0	0	632	0	0	632	0	0	632	0	0		
HPV16-CIS poly A+							0	1046	78	0	572	830	2118	211	606	690	0	211	606	690	0	211	606	690	0			
SA-OS (bumpy) poly A+							0	1104	1914	0	778	1366	2288	280	1231	186	0	280	1231	186	0	280	1231	186	0			
Mt. poly A+							wt	0	0	0	2054	180	0	262	815	180	0	262	815	180	0	262	815	180	0			
HCT-116 - 3							wt	0	0	0	0	56	0	1404	0	0	1404	0	0	1404	0	0	1404	0	0	1404	0	
HCT-116 - 4							wt	0	0	0	3177	14	0	754	414	0	754	414	0	754	414	0	754	414	0	754	414	0
HCT-116 - 5							wt	0	0	0	249	0	0	1034	589	0	1034	589	0	1034	589	0	1034	589	0	1034	589	0
HCT-116 - 6							wt	0	0	0	4346	0	0	245	915	0	245	915	0	245	915	0	245	915	0	245	915	0
LSH - 8							wt	0	0	0	3771	100	0	378	903	0	378	903	0	378	903	0	378	903	0	378	903	0
HT29 - 3							mutant	0	0	0	0	0	0	175	368	0	175	368	0	175	368	0	175	368	0	175	368	0
HT29 - 4							mutant	0	0	0	0	0	0	913	644	0	913	644	0	913	644	0	913	644	0	913	644	0
HT29 - 5							mutant	0	0	0	1269	256	0	238	910	0	238	910	0	238	910	0	238	910	0	238	910	0
HT29 - 6							wt	0	0	0	154	0	0	154	0	0	154	0	0	154	0	0	154	0	0	154	0	0
OVCAR-4 - 3							mutant	0	0	0	1208	42	0	650	558	0	650	558	0	650	5							

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor - to	Tumor cells	Normal	Endos	p33	SEQ 116	S
adrenal gland - h		1						84	
lymph node - h		2						854	
bone marrow - h		3						923	
mammary gland - h		4						0	
brain - h		5						2601	
pancreas - h		6						235	
cerebellum - h		7						666	
pituitary gland - h		8						2327	
fetal brain - h		9						2719	
placenta - h		10						1303	
fetal kidney - h		11						717	
prostate - h		12						762	
fetal liver - h		13						537	
salivary gl. - h		14						548	
fetal lung - h		15						410	
skletal muscle - h		16						0	
heart - h		17						154	
small intestine - h		18						514	
kidney - h		19						252	
spinal cord - h		20						250	
liver - h		21						51	
spleen - h		22						167	
lung - h		23						456	
stomach - h		24						694	
testis - h		25						69	
thymus - h		27						141	
HPAEC		28				28		332	
thyroid gland - h		29						0	
RPTEC		30				30		166	
trachea - h		31						3128	
HMEC		32						91	
uterus - h		33						190	
HCAEC		34						180	
Pancreas - h		35						0	
lymph node - h		36						178	
Skletal muscle - h		37						71	
fetal liver - h		38						1036	
Heart - h		39						162	
thymus - h		40						145	
Quodenum - h		41						123	
Fetal brain - h		42						537	
Salivary gl. - h		43						140	
testis - h		44						0	
HT218-normal					365			0	
HT213-normal					363			0	
HT157-normal					361			0	
Bev-13					356	356		1252	
Bev-12					354	354		1237	
cerebellum - h					344			85	
brain - h					342			0	
RPTEC					334	334		0	
lymph node - h					332			139	
h adult SMC 10/21/92 #17					330			141	
Fetal brain - h					328			70	
HT208-normal					327			89	
thymus - h					326			300	
HT149 - normal					321			0	
HEPM 3d untreated					320			0	
uterus - h					318			149	
trachea - h					316			203	
thyroid gland - h					314			173	
salivary gl. - h					311			0	
prostate - h					309			66	
pituitary gland - h					307			180	
pancreas - h					305			0	
mammary gland - h					302			0	
intestine - h					302			307	
testis - h					298			16	
liver - h					297			60	
Spleen - h					296			11	
spinal cord - h					294			111	
small intestine - h					292			0	
skletal muscle - h					290			0	
bone marrow - h					279			267	
adrenal gland - h					277			136	
HPAEC					275	275		0	
HT392-normal					266			0	
HT382-normal					266			69	
Bev-11					239	239		331	
Bev-6					233	235		222	
HT372-normal					234			0	
Bev-7					233	233		356	
Bev-6					231	231		467	
Bev-2					229	229		82	
Bev-1					227	227		442	
bladder - h					222			80	
Heart - h					215			0	
stomach - h					214			1006	
fetal liver - h					213			0	
placenta - h					212			122	
HCAEC					211	211		0	
fetal brain - h					210			0	
HMEC					209			0	
Quodenum - h					205			267	
Skletal muscle - h					203			0	
Pancreas - h					201			0	
testis - h					199			0	
Salivary gl. - h					197			0	
HEPM 3d TGF-β1 antagonist-DNase					195			46	
thymus - h					193			0	
WI-36 72h					179			0	
lymph node - h					61			0	
lung - h					59			0	
kidney - h					57			0	
heart - h					55			0	
fetal lung - h					53			0	
fetal liver - h					51			20	
fetal kidney - h					49			0	
HELA-2h-031899					79			0	
HELA-4h-031899					81			524	
HELA-6h-031899					83			71	
HELA-8h-031899					86			674	
HELA-6h-031899					88			37	
HELA-8h-031899					90			151	
HELA-10h-031899					92			0	
HELA-11h-031899					94			91	
HELA-12h-031899					96			120	
NCI-H322M					148			9	
NCI-H460					148			9	
NCI-H522					150			96	
SNB-19					152			294	
SNB-75					154			0	
SF-295					156			137	
SP-295					158			0	
CCRF-CEM					160			165	
OU-145					163			0	
HCT 116					164			0	

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Table 3 (cont'd)

Tissue	Tumor-eym	Normal-eym	Tumor - 1c	Tumor cells	Normal	Endos	p53	SEQ 118 3
CaL1				164				4
F88-0				168				0
T-47D				163				72
Kem-3				181				0
CRL 1441 RNA 8/20				183				188
781T untreated + DNase				184				87
K562 poly A+				198				0
HOS poly A+				198				52
ACHN				200				0
UACC-42				201				56
MCF-7/ADR-RES				204				0
UTOS (Mammary) poly A+				204				34
WISH (Colo rect) poly A+				203				208
458 melanoma mRNA				218				0
CCL137 RNA 3/21/88				219				0
W138 72h 0.5% FBS, 24h 10% FBS				220				242
CRL 1441 + TPA (24h) 8/28				221				96
Kem-1				222				79
Kem-2				222				0
Kem-4				241				0
MOP-82				242				0
MOLT-4				243				0
EXV4				244				0
HE-40				245				0
NCI-H23				246				60
RPM8 8228				247				21
ASB/ATCC				248				0
SR				249				85
OVCAR-3				250				0
HCT-15				251				0
OVCAR-4				252				0
UO-31				253				249
OVCAR-5				254				0
SN12C				255				0
OVCAR-8				256				0
LOX RW1				257				0
IGROV1				258				153
SK-MEL-2				259				0
SK-OV-3				260				0
SK-MEL-3				261				0
LS-532				262				0
SK-MEL-28				263				22
K-562				264				33
UACC-257				265				0
M16				267				49
MCF7				268				188
MDA-MB-435				270				0
HT-279				271				0
NDA-41				273				0
Y79 poly A+				289				26
KHOS poly A+				300				147
HTB36 24h TPA RNA 8/73				313				83
MDA-MB-435 02/18/90				322				0
HTB36 0h RNA				323				0
HT347				324				125
458 melanoma RNA				336				0
NCI-H225				337				0
MOP-42				338				61
MDA-MB-231				339				8
UCS1				340				0
PT cells poly A+				341				0
PC-3				343				0
HCC-2998				345				0
SW-620				346				148
HT192				347				0
COL O 205				348				0
HT218				349				0
MDA-12				350				20
HT151				351				0
A498				352				460
HT393				353				0
EXF 293				355				263
TK-10				357				241
Melma-3M				358				0
Me 578T			50					312
HT113			52					0
HT288			54					0
HT139			56					0
HT155			58					185
HT183			60					61
HT170			62					137
HT172			63					0
HT138			64					32
HT178			65					19
HT154			66					40
HT180			67					140
HT169			68					0
HT180			69					0
HT143			70					50
HT190			71					130
HT145			72					151
HT227			73					0
HT302			74					0
HT314			76					0
HT317			77					0
Melanoblastoma 8425 11/8			78					21
HT323			80					137
HT327			82					0
HT335			85					98
HT148			87					29
HT348			170					18
HT311			185					0
HT296			187					0
HT140			189					205
HT281			191					75
HT372			207					40
TCGP			218					48
HT180			217					62
HT307			224					254
HT368			226					0
HT376			228					114
HT371			230					125
HT377			236					112
HT382			281					468
nanoblastoma RNA			299					231
HT334			301					0
HT338			315					63
HT392			317					0
HT394			319					0
HT312			325					0
HT162			358					46
HT395			360					13
HT197								80
T-47D	183							0
MDA-MB-435	161							0
MDA-MB-435	159							0
MDA-MB-231	157							36

Table 3¹⁸⁹
(cont'd)

Tissue	Tumor-sym	Normal-sym	Tumor - 1a	Tumor cells	Normal	Endos	p53	SEQ 118	S
HA-STR	155							0	0
MCF-7/ADR-RES	153							0	0
MCF7	151							0	0
M14	149							7	7
UACC-257	147							22	22
UACC-42	145							0	0
SK-MEL-28	144							33	33
UO-31	143							0	0
SK-MEL-5	142							91	91
HA-M12	141							4	4
SK-MEL-2	140							263	263
HCT-15	139							329	329
Mamma-3M	138							181	181
COLD 205	137							250	250
LOX MV1	136							0	0
SW-620	135							0	0
TK-10	134							0	0
HCT-116	133							0	0
T84-6	132							82	82
HCC-2098	131							76	76
ACHN	130							276	276
PC-3	129							0	0
HXP 193	128							336	336
DU-145	127							90	90
Caki-1	126							276	276
SR	125							0	0
A498	124							137	137
RPM 8226	123							0	0
SN12C	122							126	126
HL-60	121							0	0
MCA-1-4	120							118	118
QVCAR-5	119							0	0
K-562	118							36	36
OVCAR-4	117							643	643
COBF-CEM	116							806	806
QVCAR-3	115							181	181
SP-639	114							87	87
HOP-62	113							0	0
SP-299	112							181	181
AS4WATCC	111							110	110
SP-268	110							133	133
NCH-522	109							0	0
U251	108							204	204
NCLH460	107							0	0
SMB-75	106							26	26
NCLH622M	105							430	430
SMB-19	104							78	78
NCLH426	103							62	62
SK-OV-3	102							6	6
NCLH423	101							777	777
IGROV1	100							0	0
EKX2	99							54	54
QVCAR-8	98							3	3
HOP-82	97							43	43
h. fibroblasts 3Q1/92 #12	48							148	148
h. adult SMC 10/21/92 #17	47							210	210
h. keratinocytes 2/25/92 #10	46							135	135
TCOP	26							0	0
AS49 - 1							wt	5	5
AS49 - 3							wt	379	379
AS49 - 4							wt	458	458
AS49 - 5							wt	347	347
AS49 - 7							wt	73	73
EKX2 - 1							mutant	94	94
EKX2 - 4							mutant	290	290
EKX2 - 3							mutant	0	0
EKX2 - 5							mutant	483	483
EKX2 - 7							mutant	877	877
MCF-7 - 1							wt	0	0
MCF-7 - 3							wt	565	565
MCF-7 - 4							wt	315	315
MCF-7 - 5							wt	0	0
MCF-7 - 7							wt	0	0
ADR-RES - 1							mutant	3049	3049
ADR-RES - 2							mutant	159	159
ADR-RES - 4							mutant	79	79
ADR-RES - 5							mutant	18	18
ADR-RES - 7							mutant	95	95
WI38 - 1							wt	0	0
WI38 - 3							wt	283	283
WI38 - 4							wt	569	569
WI38 - 5							wt	589	589
WI38 - 7							wt	0	0
HaLa - 1							HPV ES	0	0
HaLa - 3							HPV ES	54	54
HaLa - 4							HPV ES	185	185
HaLa - 5							HPV ES	308	308
HaLa - 7							HPV ES	105	105
H1299 - 1							mutant	0	0
H1299 - 3							mutant	0	0
H1299 - 4							mutant	0	0
H1299 - 5							mutant	0	0
H1299 - 7							mutant	1	1
AS49 - 2							wt	192	192
EKX2 - 2							mutant	0	0
HCT-116 - 1							wt	0	0
HCT-116 - 2							wt	820	820
HT29 - 2							mutant	68	68
SP639 - 1							wt	0	0
SP639 - 2							wt	3	3
SP-704-1							mutant	209	209
SP-268-2							mutant	831	831
OVCAR-4 - 1							wt	0	0
OVCAR-4 - 2							wt	0	0
OVCAR-5 - 1							mutant	523	523
OVCAR-5 - 2							mutant	208	208
MCF-7 - 2							wt	85	85
ADR-RES - 2							mutant	221	221
HaLa - 2							HPV ES	173	173
SW480 - 1							mutant	0	0
SW480 - 2							mutant	191	191
H1299 - 2							mutant	1083	1083
G33A - 1							mutant	0	0
G33A - 2							mutant	0	0
U2OS - 1							mutant	271	271
U2OS - 2							mutant	557	557
Ha68 - 1							wt	0	0
Ha68 - 2							wt	24	24
WI38 - 2							wt	299	299
MaMa1 - 1								0	0
MaMa1 - 2								0	0
MaMa1 - 3								0	0
MaMa1 - 4								14520	14520
MaMa1 - 5								552	552
MaMa1 - 6								0	0
MaMa1 - 8								0	0
MaMa1 - 9								0	0

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Table 3 (cont'd)

Tissue	Tumor-ym	Normal-ym	Tumor-to	Tumor cells	Normal	Endo	433	SEQ 116 5
DuPang-7								1562
DuPang-8								2591
DuPang-9								603
DuPang-11								2563
DuPang-12								518
DuPang-10								368
DuPang-1								474
DuPang-2								0
DuPang-3								222
DuPang-4								0
DuPang-5								0
DuPang-6								0
A549-8							wt	0
EKX-8							mutant	56
HCT-116-7							wt	0
HCT-116-8							wt	0
HT29-1							mutant	310
HT29-7							mutant	69
HT29-8							mutant	0
SF539-7							wt	155
SF539-6							mutant	259
SF-268-7							mutant	218
SF-268-4							mutant	503
OVCAR-4-7							wt	405
OVCAR-4-6							wt	0
OVCAR-5-7							mutant	831
OVCAR-5-8							mutant	107
MCF-7-8							wt	35
ADR-RES-6							mutant	857
HeLa-8							HPV E6	0
SW480-7							mutant	0
SW480-6							mutant	0
HI299-8							mutant	0
C3A-7							mutant	0
C3A-8							mutant	129
U2OS-7							wt	37
U2OS-8							wt	0
HeLa-7							wt	0
HeLa-6							wt	0
WI38-8							wt	0
+58 modulator RNA								71
CR1872-31789						84		221
Bea-4								80
HT365								151
HT378								89
HT365								0
HT365						173		467
Bea-3						175		117
Bea-5						177		481
Bea-8								0
n. heterozygous 3725/92 #10						237		0
Bea-10								0
HTB10								0
n. homozygous 3/21/92 #12								0
primate 1								32
SAVING-OS poly A+								0
SA-OS (Runchi) poly A+								0
hct poly A+							wt	364
HCT-116-3							wt	0
HCT-116-4							wt	0
HCT-116-5							wt	0
HCT-116-6							wt	0
A549-6							mutant	974
HT29-3							mutant	121
EKX-6							mutant	940
HT29-4							mutant	0
HT29-5							mutant	177
HT29-6							wt	339
OVCAR-4-3							wt	0
OVCAR-4-4							wt	16
OVCAR-4-5							wt	0
OVCAR-4-6							wt	726
SF539-3							wt	83
SF539-4							wt	0
SF539-5							wt	0
SF539-6							mutant	2219
OVCAR-5-3							mutant	296
OVCAR-5-4							mutant	0
OVCAR-5-6							mutant	0
ADR-RES-6							wt	279
MCF-7-6							HPV E6	371
HeLa-6							mutant	0
HI299-6							mutant	61
SW480-3							mutant	0
SW480-4							mutant	293
SW480-5							mutant	225
SW480-6							mutant	173
C3A-3							mutant	182
C3A-4							mutant	0
C3A-5							mutant	55
C3A-6							wt	0
HeLa-6							mutant	620
U2OS-3							mutant	561
U2OS-4							mutant	844
U2OS-5							mutant	0
U2OS-6							wt	0
WI38-8							wt	298
HeLa-3							wt	821
HeLa-4							mutant	277
SF-268-3							mutant	0
SF-268-4							mutant	125
SF-268-5							mutant	33
SF-268-6							mutant	21
DuPang-13								368
Mbshul-20								0
Mbshul-21								0
Mbshul-22							mutant	611
OVCAR-6-5								96
Mbshul-10								260
Mbshul-11								694
Mbshul-12								309
Mbshul-13								150
Mbshul-14								332
Mbshul-15								0
Mbshul-16								129
Mbshul-17								0
Mbshul-18								174
Mbshul-19								0

Table 4

Gene Name	SP ID#	na ID#	aa	Family	Group	Length	AA	Extra-Catalytic Domains (Amino acid positions)
X69117_h beta_adrenergic	H	1	122	AGC	GRK	688		Regulator of G protein signaling domain 54-175; PH domain 559-652
AA144574_m	M	2	123	AGC	GRK	378		PH domain 249-337
AA210825_h	H	9	130	AGC	PKC	978		Phorbol esters/diacylglycerol binding domain (C1 domain) 238-287; PH domain 497-577
AA316804_h	H	11	132	AGC	PKC	890		Phorbol esters/diacylglycerol binding domain (C1 domain) 155-204 and 272-321; PH domain 417-532
AA887783_h	H	21	142	AGC	SGK	446		PX domain 13-120
AA021445_h 3	H	32	152	CAMK	EMK	1311		Vitamin K-dependent carboxylation/gamma-carboxyglutamic (GLA) domain 1072-1113
R31237_1_h AAC3348	H	34	154	CAMK	EMK	729		UBA domain 327-365
408786_5_h	H	36	156	CAMK	EMK	1330		PAS domain 133-186, 247-280, 354-386
Z36720_h	H	41	181	CAMK	MLCK	874		WD domain, G-beta repeat 674-711
SGK088_h	H	42	182	CAMK	Trio	2287		Immunoglobulin domain 1-62, 97-153, 221-277, 518-578, 1617-1678; Fibronectin type III domain 301-390, 1697-1779
R19772_h	H	44	184	CAMK	Trio	1287		RhoGEF domain 235-405; Fibronectin type III domain 870-955; Immunoglobulin domain 786-851; PH domain 419-528
17000139801197_h IRAH	H	76	195	Other	IRAK	596		Death domain 26-106
AA088547_h	H	78	197	Other	IRE	922		PQQ enzyme repeat 39-76
AA232253_h	H	82	201	Other	MLK	800		SAM domain (Sterile alpha motif) 337-408
AA599286_h	H	89	208	Other	SLOB	649		PX domain 16-122
AA836348_h	H	113	232	STE	NEK	836		Regulator of chromosome condensation (RCC1) 387-427, 427-480, 483-532, 598-650
PAK6_h	H	115	234	STE	STE20-02	719		P21-Rho-binding domain 11-69

FIGURE 1A

1
ID NO: 122_X69117_H BARK2_H
EAVLADVSYLMAMEKSKATPAARASKRIVLPEPSIRSVMQKYLAERNEITFDKIFN
FLLFKDFCLNEINEAVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSC
PFSKQAVEHVQSHLSKKQVTSTLFQPYIEEICESLRGDI FQKFMESDKFTRFCQWKNV
ELNIHLTMNEFSVHRIIGRGGFGEVYGCRKADTGKMYAMKCLDKKRIKMKQGETLALNER
IMLSLVSTGDCPFIVCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSEKEMRFYATE
IILGLEHVHNRFFVYRDLKPANILLDEHGHRISDLGLACDFS KKKPHASVGTHGYMAPE
VLQKGTAYDSSADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTVNVELPDTF SPE
LKSLLLEGLLQRDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVVYLQKYPPLIPPRGEVNAA
DAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERWQQEVETETVYEAVNADTDKIEARK
RAKNKQLGHEEDYALGKDCIMHGMYMLKLGNPFLTQWQRRYFYLPNRLEWRGEGESRQNL
LTMEQILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKELNETFKEAQRLLRR
APKFLNKPRSGTVELPKPSLCHRNSNGL

SEQ ID NO: 123_AA144574_M BARK2_M
CFVVYRDLKPANILLDEYGHVRIIDLGLACDFS KKKPHASVGTHGYMAPEVLQKGT CYDS
SADWFSLGCMFLKLLRGHSPFRQHKTDKHEIDRMTLTVNVQLPDAFSPELRSLLLEGLLO
RDVSQRLGCGGGGARELKEHIFFKGIDWQHVVYLKYPPLIPPRGEVNAA DAFDIGSFDE
EDTKGIKLLDCDQDLYKNFPLVISERWQQEVVETIYDAVNADTDKIEARKKAKNKQLGQE
EDYAMGKDCIMHGMYMLKLGNPFLTQWQRRYFYLPNRLEWRGEGESRQSLLTMEQIMSVE
ETQIKDRKCILLRIKGGKQFVLQCESDPEFAQWLKELTCTFNEAQRLLRRAPKFLNKPRA
AILEFSKPPLCHRNSNGL

SEQ ID NO: 124_AA826850_H
MGSSMSAATARRPVFDDKEDVNFDFHFIQILRAIGKGSFGKVCIVQKRDTEKMYAMKYMKNQ
QCIERDEVNRNVFRELEILQEIEHVFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVO
FSEDTVRLYICEMALALDYLRGQHIHRDVKPDNILLDERGHAHLTDFNIATIIKDGGERA
TALAGTKPYMAPEIFXS FVNGGTGYSFEVDWWSVGMAYELLRGWRPYDIHSSNAVESLV
QLFSTVSVQYVPTWSKEMVALLRKLLTVNPEHRLSSLQDVQAAPALAGVLWDHLSEKRVE
PGFVPNKGRLLHCDPTFELEEMILESRLPHKKKKRLAKNKS RDNSRDSSQSENDYLQDCLD
AIQQDFVIFNREKLRSQDLPREPLPAPESRDAAEPVEDEAERSALPMCGPICPSAGSG

SEQ ID NO: 125_AA960957_H
MGGNHSHKPPVFDENEEVNFDFHFIQILRAIGKGSFGKVCIVQKRDTKMYAMKYMKNQKCI
ERDEVNRNVFRELQIMQGLEHPFLVNLWYSFQDEEDMFMVVDLLLGGDLRYHLQQNVHFTE
GTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHHITDFNIATVVKGAERASSM
AGTKPYMAPEVFQVYMDRGPYSGYSPVDWWSLGITAYELLRGWRPYEIH SVTPIDEILNMF
KVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDVAFKKALMPGF
VPNKGRLLNCDPTFELEEMILESRLPHKKKKRLAKNKS RDGTDSCPLNGHLQHCLTVRE
EFIIIFNREKLRRQGGQGSQLLDTSRGGGQAQSKLQDGCNNLLTHTCTRGCSS

SEQ ID NO: 126_TBK1_H
MQSTSNHLWLLSDILGQGATANVFRGRHKKTGDLFAIKVFNNISFLRPVDVQMREFEVLK
KLNHNKIVKLFAIEEETTTRHKVLIMEFCPCGSLYTVLEEPSNAYGLPESEFLIVLRD VV
GGMNHLRENGIVHRDIKPGNIMRVIGEDGQSVYKLTDFGAARELEDDEQFVSLYGTEEYL
HPDMYERAVLRKDHQKKYGATVDLWSIGVTFYHAATGSLPFRPFEGPRRNKEVMYKIITG
KPSGAISGVQKAENGPIDWSGDMPVSCSLSRGLQVLLTPVLANILEADQEKCWGFDQFFA
ETSDILHRMVIHVFSLQQMTAHKIYIHSYNTATIFHEL VYKQTKIISNQELIYEGRRLV
LEPGRLAQHF PKTTEENPIFVVSREPLNTIGLIYEKISLPKVHPRYDLGDASMAKAITG
VVCYACRIASTLLLYQELMRKGIRWLIELIKDDYNETVHKKTEVVITLDFCIRNIEKTVK

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FIGURE 1B

VYEKLMKINLEAAELGEISDIHTKLLRLSSSQGTIETSLQDIDSRLSPGGSL-
GTHPKDRNVEKLQVLLNCMTEIYYQFKKDKAERRLAYNEEQIHKFDKQKLYYH-
FTDECVKKYEAFLNKSEEWIRKMLHLRKQLLSLTNQCFDIEEEVSKYQEYTNEL-
KMFTASSGIKHTMTPIYPSSNTLVEMTLGMKKLKEEMEGVVKELAENNHILERF-
GGLRNVDCI

SEQ ID NO: 127_AA305176_H
MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKI
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIIGDV
LLHIYGYFDEEMAVKYISEVALALDYLHRHGI IHRDLKPDNMLI SNEGHIKLTDGFLS
TLNRDINMMDILTTPSMAKPRQDYSRTPGQVLSLISSLGFNTPIAEKNQDPANILSAC
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLA
SASSQSHTFISSVESECHSSPKWEKDCQV

SEQ ID NO: 128_AA116841_M
TRPIPWPEGEEKLSDNAQSAMDMLLTIDDSKRAGMRELKQHPLFSEVDWENLQHQTMP
PQPDDTDTSYFEARNNAQHLLTVSGFSL

SEQ ID NO: 129_AA256100_H
MAMTAGTTTTFPMNSNHTRERVTVAKLTLENFYSNLILQHEERETRQKKLEVAMEEEGLAD
EEKKLRRSQHARKETEFRLRLKRTLGLDDFESLKVIGRGAFGEVRLVQKKDTGHIYAMKI
LRKSDMLEKEQVAHIRAERDILVEADGAWVKMFYSFQDKRNLYLIMEFLPGGDMMTLLM
KKDTLTEEETQFYISETVLDAIDAIHQLGFIHRDIKPDNLLLDAGHVKLSDFGLCTGLKK
AHRTEFYRNLTNPPSDFSFQNMNSKRKAETWKKNNRQLAYSTVGTDPDIAPEVFMQTGY
NKLCDWWSLGVIMYEMLIYPPFCSETPQETYRKVMNWKETLVFPPEVPISEKAKDLILR
FCIDSENIRIGNSGVEEIKGHPFFEGVDWEHIRERPAAPIEIKSIDDTSNFDDFPESDIL
QPVPNTTEPDYKSKDWVFLNYTYKRFEGLTQRGSIPTYMKAGKL

SEQ ID NO: 130_AA210825_H
DSLLPTPALGTPLPIPWVGSRLRTPLSLESTRSPTQRLLPSTPKDPAILRSPPPARSFLG
SPLSHLLTRSRGSRTQGPPGPPGGSRVGSRRVAVGLPPWPPPPHYAGLPGPSGPGSP
PPGGLELQSPPLLPQIPAPGSGVSFHIQIGLTREFVLLPAASELAHVQQLACSIVDQKF
PECGFYGLYDKILLFKHDPTSANLLQLVRSSGDIQEGDLVEVVLASATFEDFQIRPHAL
TVHSYRAPAFCDHCGEMLFGLVRQGLKCDGCLNYHKRCAFSIPNNCSGARKRRLSSTSL
ASGHSVRLGTSESLEPCTAEELSRSTTELLPRRPPSSSSSSASSYTGRPIELDKMLLSKV
KVPHTFLIHSYTRPTVCQACKLLKGLFRQGLQCKDKFNCHKRCATRVNDCLGEALIN
GDVPMEEATDFSEADKSALMDESEDGVI PGSHSENALHASEEEEEEGEGGKAQSSLGYIPL
MRVVQSVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQNNNTNRYYKEI
PLSEILTVEAQNFSLVPPGTNPHCFEIVTANATYFVGEMPGGTPGGPSGQGAEAARGLX
ETAIRQALMPVILQDAPSAPGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDEVVLGSG
QFGVVYGGKHKRKTGRDVAVKVIDKLRFPKQESQLRNEVAILQSLRHPGIVNLECMFETP
EKVFVMEKLLHGDMLEMILSSEKGRLLPERLTFLITQILVALRHLHFKNIVHCDLKPEN
LLASADPPFPQVKLCDFGFARIIGEKSFRRSVVGTAYLAPEVLLNQGYNRS LDMWSVGVI
MYVSLSGTFPFNEDEDINDQIQNAAFMYPASPSHISAGAIIDLINNLLQVKMRKRYSDVK
SLSHPWLOEYQTWLDLRELEGKMGERYITHESDDARWEQFAAEHPLPGSGLPTDRDLGGA
CPPQDHDMQGLAERISVL

SEQ ID NO: 131_AA127299_H
IQFIIIVGAKDLLAMDSNGLSDPYIKITNLSQKTKVIKTLTPTWNETFFVHFPEKTTLEL
ECWDHDTFSDDFIGKASISLAEIPALAEVDMWIDMKTKKGEFAGK

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FIGURE 1C

SEQ ID NO: 132_AA316804_H

MSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSARLSNGSFSAPSLTNSRGSVHTV
SFLQLIGLTRESVTIEAQELSLSAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSEN
ILQLITSADEIHEGDLVEVVL SALATVEDFQIRPHTLYVHSYKAPTFCDYCGEMLWGLVR
QGLKCEGCGLNYHKRCAPKIPNNCSGVRKRRLSNVSLPGPGLSVPRPLOPEYVALPSEES
HVHQEPSKRIPSWSGRPIWMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGM
QCKDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDNNDINSRSSRGLDDT
EESPSPEDKMFFLDPSDLDERDEEAVKTISPSTSNNIPLMRVVQSIKHTKRKSSSTMVKE
GWMVHYTSRDNLKRHYWRLLSKCLTLFQNESGSKYYKEIPLSEILRISSPRDFTNISQ
SNPHCFEIIITDTMVYFVGENNGDSSHPVLAATGVGLDVAQSWEKAIRQALMPVTPQASV
CTSPGQGDHKLSTSI SVSNCCI QENVDISTVYQIFADEVLGSGQFGIVYGGKHKRKTGR
DVAIKVIDKMRFP TKQESQLRNEVAI LQNLHHPGIVNLECMFETPERVFVMEKLHGDM
EMILSSEKSR LPERITKFMVTQILVALRNLHFKNIVHCDLKPENVLLASAEPFPQVKLCD
FGFARIIGEKSFRRSVVGTPAYLAPEVLRSKGYNRS LDMWSVGVI IYVSLSGTFPFNEDE
DINDQIQNAAFMYPNPWREISGEAIDLINLLQVKMRKYSVDKSLSHPWLDQYQTWLD
LREFETRIGERYITHESDDARWEIHAYTHNLVYPKHFIMAPNPDDMEEDP

SEQ ID NO: 133_PKNBETA_H

MEEGAPRQPGPSQWPPPEDEKEVIRRAIQKELKIKEGVENLRRVATDRRH LGHVQQLLRSS
NRRLEQLHGELRELHARILLPGPGPGAEPVASGPRPWAEQLRARHLEALRRQLHVELKV
KQGAENMTHTCASGTPKERKLLAAQAQMLRDSQLKVALLRMKISSLEASGSPEPGPELLA
EELQHRHLHVEAAVAEGAKNVVLLSSRRTQDRKALAEAAQALQESSQKLDLLRLALEQLL
EQLPPAHPLRSRVTR ELRAAVPGYPQPSGTPVKPTALTGT LQVRL LGCEQLLTAVPGRSP
AAALASSPSEGWLRTKAKHQGRGELASEVLAVLKVDNRVVGQTGWGQVAEQSWDQTFVI
PLERARELEIGVHWRDWRQLCGVAFLRLLEDFLDNACHQLSLSLVPQGLLFAQVTFCDPVI
ERRPRLQRQERIFSKRRGQDFLRRSQMNLGMAAWGRLVMNLLPPCSSPSTISPPKGCPR
PTTLREASDPATPSNFLPKKTP LG EEMTPPPKPPRLYL PQEPTSEETPRTKRPHMEPRTR
RGPSPASPTRKPPRLQDFRCLAVLGRGHFGKVLLVQFKGTGKYAIAKALKKQEVLSRDE
IESLYCEKRILEAVGCTGHPFLLSLLVCFQTSSHARFVTEFVPGGLMMQIHEDVFPEPQ
ARFYVACVVLGLQFLHEKKI IYRDLKLDNLLLD A QGFLKIADFG LCKEGIGFGDRTSTFC
GTPEFLAPEVLTQEAYTQAVDWWALGVLLYEMLVGECPPFGDTEEEVFDCI VNM DAPY PG
FLSVQGLEFIQKLLQKCPEKRLGAGEQDAEEIKVQPPFRRTTNWQALLARTIQPPFVPTLC
GPADLRYFEGEFTGLPPALTPPAPHSLLTARQQA AFRDFDFVSERFLEP

SEQ ID NO: 134_AI021023_M_PKNBETA_M

LKWDNLLLD A QGFLKIADFG LCKEGIGFGDRTSTFCGTPEFLAPEVLTQEAYTRAVDWWG
LGVLLYEMLVGECPPFGDTEEEVFDCI VNM DAPY PGFLSVQGLEFIQKLLQKCPEKRLGA
GEQDAEEIKVQPPFRRTTNWQALLARTIQPPFVPTLCGPADLRYFEGEFTGLPPALTPPAP
HSLLTARQQA AFRDFDFVSERFLEP

SEQ ID NO: 135_H19102_H

GGNIRGPWARGWKS LWTGLGTIRSDLEELWELRGHHY LHQESLKPA PVLVEKPLPEWPVP
QFINLFLPEFP IIRPIRGQQQLKILGLVAKGSFGTVLKVLDCTQKAVFAVKVVPKVVLQR
DTRVQCKEEVSIQRQINHPFVHSLGDSWQGRHLFIMCSYCSTDLYSLWSAVGCFPEASI
RLFAAELVLVLCYLDL GIMHRDV K MENILLDERGH LKLTDFGLSRHVPQGAQAYTICGT
LQYMAPEVLSGGPYNHAADWWSLGVLLFSLATGKFPVAAERD HVAMLASVTHSDSEIPAS
LNQGLSLLLHELLCQNPLHRLRYLHHFQVHPFFRGVAFDPELLQKQPVNFVTETQATQPS
SAETMPFDDFDCDLESFLLYPIPA

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FIGURE 1D

SEQ ID NO: 136_AA476563_H

MEFFRIDSKDSASELLGLDFGEKLYSLKSEPLKPFFTL PDGDSASRSFNTSESKVEFKAQ
DTISRGSDDSVPVISFKDAAFDDVSGTDEGRPDLLVNLPGELESTREAAAMGPTKFTQTN
IGIIENKLLLEAPDVLCLRLSTEQCQAHEEKGIEELSDPSGPKSYSITEKHYAQEDPRMLF
VAVDHHSSSGDMSLLPSSDPKFQGLGVVESAVTANNTEESLFRICSPLSGANEYIASTDT
LKTEEVLLFTDQTDLLAKEEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALAS
RFYIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHIQLTYFSRWSEVEDS
CSDAIERMYCAPEVGAITEETEACDWWSLGAVLFELLTGKTLVECHPAGINTHTTLNMP
ECVSEEARSLIQQLLQFNPLERLGAGVAGVEDIKSHPPFFTPVDWAEELMR

SEQ ID NO: 137_AA626690_H

MLPFAPQDEPWDREMEVFSGGGASSGEVNGLMVDEPMEEGEADSCHDEGVVKEIPITHH
VKEGYEKADPAQFELLKVLGQGSFGKVFLVRKKTGPDAGQLYAMKVLKKASLKVRDRVRT
KMERDILVEVNHPFIVKLHYAFQTEGKLYLILDFLRGGDVFTRLSKEVLFTTEEDVKFYLA
ELALALDHLHQLGIVYRDLKPENILLDEIGHIKLTDGFLSKESVDQEKKAYSFCGTVEYM
APEVVNRRGHSQSADWWSYGVLMFEMLTGTLFPQGKDRNETMNMILKAKLGMPQFLSAEA
QSLRLMLFKRNPANRLGSEGVEEIKRHLFFANIDWDKLYKREVQPPFKPASGKPDFTFCF
DPEFTAKTPKDSPLPASANAHQLFKGFSFVATSIAEEYKITPITSANVLPVQINGNAA
QFGEVYELKEDIGVGSYSVCKRCIHATTNMEFAVKIIDKSKRDPSEEIEILMRYGQHPNI
ITLKDVFDDGRYVYLVTDLMKG GELLDRILKQKCF SEREASDILYVISKTVDYLHCQGVV
HRDLKPSNILYMDESASADSIRICDFGFAKQLRGENGLLLTPCYTANFVAPEVLMQQGYD
AACDIWSLGVLFYTMLAGYTPFANGPNDTPEEILLRIGNGKFSLSGGNWDNISDGAKDLL
SHMLHMDPHQRYTAEQILKHSWITHRDQLPNDQPKRNDVSHVVKGAMVATYSALTHKTFQ
PVLEPVAASSLAQRSMKKRTSTGL

SEQ ID NO: 138_AA215680_H

MSLVACECLPSPGLEPEPCSRARSQAHVYLEQIRNRVALGVPMTKRDYLVDAATQIRLA
LERDVSEDEYAAFNHYQNGVDVLLRGIVDPNKERREAVKLKITKYLRAEEIFNCHLQR
PLSSGASPSAGFSSLRLRPITRLSSAVEQLRGCRVVGVIKVLVQDPATGGTFVVKSLP
RCHMVSRRERTIIPHGVPMYTKLLRYFVSEDSIFLHLEHVQGGTLWSHLLSQAHSRHSGL
SSGSTQERMKAQLNPHLNLTPARLP SGHAPGQDRIALEPRTSPNLLLAGAPSTRPQR
EAEGEPTARTSTSGSSDL PKAPGGHLHLQARRAGQNSDAGPPRGLTWVPEGAGPVLGGCG
RGMDQSCLSADGAGRGCGRATWSVREEQVKQWAAEMLVALEALHEQGVLCRDLHPGNLLL
DQAGHIRLTYFGQWSEVEPQCCGEAVDNLYSAPEVGGISELTEACDWWSFGSLLYELLTG
MALSQSHPSGIQAHTQLQLPEWLSRPAASLLTELLQFEPTRRLLGMGEGGVSKLKSHPFFS
TIQWSKLVG

SEQ ID NO: 139_SGK_H

MTVKTEAAKGTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIANN SYACKHPEVQSILKI
SQPQEPPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA
EVFYAVKVLQKKAILKKKEEKHIMSERNVLLKNV KHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQRERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
FGLCKENIEHNSTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSR
NTAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHVFFSLINW
DDLINKKITPPFNPVSGPNELRHFDPEFTEEPVPNSIGKSPDSVLVTASVKEAAEAFLG
FSYAPPTDSFL

SEQ ID NO: 140_AA107515_M

MTVKAEAAARSTLTYSRMRGMVAILIAFMKQRRMGLNDFIQKIASNTYACKHAEVQSILKM
SHPQEPPELMNANPSPPPSPSQQINLGPSSNPHAKPSDFHFLKVIGKGSFGKVLLARHKA

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FIGURE 1E

EVFYAVKVLQKKAILKKKEEKHIMSENVLLKNVKNHPFLVGLHFSFQTADKLYFVLDYIN
GGELFYHLQORERCFLEPRARFYAAEIASALGYLHSLNIVYRDLKPENILLDSQGHIVLTD
XFQLRRIEHNGTTSTFCGTPEYLAPEVLHKQPYDRTVDWWCLGAVLYEMLYGLPPFYSRN
TAEMYDNILNKPLQLKPNITNSARHLLLEGLLQKDRTKRLGAKDDFMEIKSHIFFSLINWD
DLINKKITPPFNPVSGPSDLRHFDPFTEEPVPSSIGRSPDSILVTASVKEAAEAFLGF
SYAPPVDSFL

SEQ ID NO: 141_AA109508_M
HLQRRERFLEPRARFYAAEIVASAIGYLHSLNIIYRDLKPENILLDCQGHVVLTDFGLCKE
GVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSDVSQMY
ENILHQPLQIPGGRTVAACDLLQSLHKKDQQRQLGSKADFLEIKNHVFFSPINWDDLYHK
RLTPPFNPVNTGPADLKHFDPEFTQEAVSKSIGCTPDTVASSSGASSAFLGFSYAPEDDD
ILDC

SEQ ID NO: 142_AA887783_H
MQRDHTMDYKESCPVXIPSSDEHREKKRFTVYKVLVSVGRSEWVFRRYAEFDKLYNT
LKKQFPAXALKIPAKRIFGDNFDPDFIKQRRAGLNEFIQNLVRYPELYNHPDVRAFLQMD
SPKHQSDPSEDEDERSSQKLHSTSONINLGPSGNPHAKPTDFDFLKVIGKGSFGKVLLAK
RKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKNHPFLVGLHYSFQTTEKLYFVL
DFVNGGEGHVLTDFGLCKEGIAISDTTTFCTGTPEYLAPEVIRKQPYDNTVDWWCLGAV
LYEMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSI LELLEKDRQNRLGAKEDF
LEIQNHPPFESLSWADLVQKKIPPPFNPVAGPDDIRNFDTAFTTEETVPYSVCVSSDYSI
VNASVLEADDAFVGFSYAPPSSEDLFL

SEQ ID NO: 143_R47805_H
MAHQGTGIHATEELKEFFAKARAGSVRLIKVVI EDEQLVLGASQEPVGRWDQDYDRAVLPL
LDAQQPCYLLYRLDSQNAQGFEWLFLAWSPDNSPVRLKMLYAATRATVKKEFGGGHIKDE
LFGTVKDDL SFAGYQKHLSSCAAPAPLTS AERELQQIRINEVKTEISVESKHQTLQGLAF
PLQPEAQRALQQLKQKMVNYIQMKLDLERETIELVHTEPTDVAQLPSRVPRDAARYHFFL
YKHTHEGDPLESVVFIYSMPGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIAKKIEIGDG
AELTAEFLYDEVHPKQAHAFKQAFAPKPGPGGKRGHKRLIRGPGENGDD

SEQ ID NO: 144_H60215_H
MSKLRMKRRASDRGAGETSARAKALGSGISGNNAKRAGPFILGPRLGNSPVPSIVQCLAR
KDGTDDFYQLKILTLEERGDQGISQEERQGMILLHTEYSLLSLHTQDGVVHHHGLFQD
RTCEIVEDTESSRMVKMKKRICLVLDCLCAHDFSDKTADLINLQHYVIKEKRLSERETV
VIFYDVVRVVEALHQKNIVHRDLKLGNMVLNKRTHRITITNFC LGKHLVSEGDLLKDQRG
SPAYISPDLVLSGRPYRGKPSDMWALGVVLF TMLYGQFPFYDSIPQELFRKIKAAEYTIPE
DGRVSENTVCLIRKLLVLDPPQRLAAADVLEALS AIASWQSLSSLSGPLQVVPDIDDQM
SNADSSQEAKVTEEC SQYEFENYMRQQLLLAEKSSIHDTRSWVPKRQFGSAPPVRRLGH
DAQPMTSLDTAILAQRYLRK

SEQ ID NO: 145_SGK324_H
MASTRSIELEHFEERDKRPRPGSRRGAPSSSGGSSSSGPKGNGLIPSPAHSACHSFYRTR
TLQALSSEKKAKKARFYRNGDRYFKGLVFAISSDRFRSFDALLIELTRSLSDNVNLPQGV
RTIYTIDGSRKVTSLDELLEGESYVCASNEPFRKVDYTKNINPNWSVNIKGGTSRALAAA
SSVKSEVKESKDFIKPKLVTVIRSGVKPRKAVRILLNKKTAHSFEQVLT DITEAIKXASC
VVKRLCTLDGKQVRVTCVHLPDFFGDDDVFIACGPEKFRYAQDDFVLDHSECRVLKSSYS
RSSAVKYSGSKSPGPSRRSQISAHGRSSSNVNGGPELDRCSPEGVNGNRCSESSTLLEK
YKIGKVI GDGNFAVVEKCIDRSTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNII

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FIGURE 1F

MLVEEMETATELFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHGLSIVH
RDIKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPXIIAETGYGLKVD
IWAAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSAKELISQMLQ
VNVEARCTAGQILSHPWVSDDASQENNMQAEVTGKLKQHFNNALPKQNSTTTGVSVMVS
GRRQVWPDCGAGLEVFELGSRELPSHGSWCLP.

SEQ ID NO: 146_W30246_M SGK324_M

TKSSSSSPTSPGSFRGLKISAQGRSSSNVNGGPELDRCLSPPEGVNGNRCSESFPLLEKYR
IGKVIKVDGNFAVVKECVDRTGKEFALKIIDKAKCCGKEHLIENEVSILRRVKHPNIIML
VEEMETATDLFLVMELVKGGDLFDAITSSTKYTERDGSAMVYNLANALRYLHLSLSIVHRD
IKPENLLVCEYPDGTSLKLGDFGLATVVEGPLYTVCGTPTYVAPEIIAETGYGLKVDVW
AAGVITYILLCGFPFRSENNLQEDLFDQILAGKLEFPAPYWDNITDSPCVCFRKCL

SEQ ID NO: 147_AA383293_H

PAAKRVVVYRNGDPFFPGSQLVVTQRRFPTMEAFLEVTSAVQAPLAVRALYTPCHGHPV
TNLADLKNRGQYVAAGFERFHKLPYQAFCLSVFRNGDLVSPFSLKLSQAASQDWETVL
KLLTEKVKLQSGAVRLCTLEGLPLSAGKELVTGHYYVAVGEDEFKDLPPALSTRGLLAA
GNEAHLRSGVGTVAGSPKPLGRKAKKETCLIVTLTKYQQSETSRDGQSFPSPGVIGVYGA
PHRRKETAGALEVADDEDQTTEEPLDQRAAQIVEQVTCLODFGDDDVFIACGPEKFRYA
QDDFVLDSRRRLREHQAGFEKLRRTRGEEKEAEKEKKPCMSGGRRMTLRDDQPAKLEK
EPKTRPEENKPERPSGRKPRPMGIIAANVEKHYETGRVIGDGNFAVVKECRHRETRQAYA
MKIIDKSRLKGKEDMVDSEILIIQSLSHPNIVKLHEVYETDMEIYLILEYVQGGDLFDAI
IESVKFPEPDAAALMIMDLCKALVHMHDKSIVHRDLKPENLLVQRNEDKSTTLKLADFLA
KHVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPXXGDQDE
LFNIIQLGHFEFLPPYWDNISDAAKDLVSRLLVDPKKRYTAHQVLQHPWIETAGKTNTV
KRQKQVSPSSDGHFRSQHKRVVEQVS

SEQ ID NO: 148_AA197883_M

MPTAPVLRPPPPATPAPPAPSRPAPPIPGHRGPCDHSLKCLSSKISERKLPGPWLPAGR
GPLEKPVLGPRGAVMPLFSPQSSLHSVRAEHSPLKPRVTVVKLGQQLRKATLLNRRS
VQTFEQLLSDISEALGFPRWKNDRVRKLFITLKGREVKSVSDFFREGDAFIAMGKEPLTLK
SIQLAMEELYPKNRALALAPHSRVSPRLRSRLPSKLLKGSHRCEAGSYSAEMESKAVS
RHQGTSTVLAPEDKARAQKWVRGKQSEEPGGPPSPGAATQEETHASGEKHLGVEIEKTS
GEIVRCEKCKRERELQLGLQREPCPLGTSELDLGRAQKRDSEKLVRTKSCRPSKAKFTD
GEEGWKGDSHRGSPRDPPOEMRRPNSNSDKKEIRGSESQDSYPQGAQKDFVEGPPAV
EEGPIDMRREDRHTCRSKHAAWLRREQQAEPPLPRTRGEEKQAEHEKKPGGLGERRAPE
KESKRKLEEKRPERPSGRKPRPKGIIISADVEKHYDIGGVIGDGNFATVKECRHRETRQAY
AMKMIDKSQKKGKEDIVDSEILIIQSLSHPNIVKLHEVYETEAEIYLIMEYVQGGDLFDA
IVENVKFPEPEAAVMITDLCKAFVHMHDKNIVHRDVKPENLLVQRNEDKSITLKLADFLA
AKYVVRPIFTVCGTPTYVAPEILSEKGYGLEVDMWAAGVILYILLCGFPFRSPERDQDE
LFNIIQVGQFEFLSPYWDNISDAAKDLVRNLLEVDPPKKRYTAEQVLQHPWIEMVGHTNTG
NSQKEESPNSLGHFQSQHKKVAEQMP

SEQ ID NO: 149_DRAK2_H

MSRRRFDCRSISGLLTTPQIPKIMENFNNFYILTSKELGRGKFAVVRQCISKSTGQEYA
AKFLKKRRRGQDCRAEILHEIAVLELAKSCPRVINLHEVYENTSEIILILEYAAGGEIFS
LCLPELAEMVSENDVIRLIKQILEGVYYLHQNNIHVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGHACELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYNLISQVNVYSEETFSSVSQLATDFIQSLLVKNPEKRPTAEICLSHSLWLQQWDFEN

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FIGURE 1G

LFHPEETSSSSQTQDHSVRSSDKTSKSSCNGTCGDREDKENI PEDSSMVSKRFRFDDSL
PNPHELVSDDL

SEQ ID NO: 150_W44160_M_DRAK2_M
MSRRRFDCRSVSGLLTTTPQTPIKTENFNNFYTLTPKELGRGKFAVVRQCISKSTGQEYA
AKSLKKRRRGQDCRAEILHEIAVLELARSCPHVINLHEVYENATEIILVLEYAAGGEIFN
LCLPELAEMVSENDVIRLIKQILEGVHYLHQNINIVHLDLKPQNILLSSIIYPLGDIKIVDF
GMSRKIGNASELREIMGTPEYLAPEILNYDPITTATDMWNIGIIAYMLLTHTSPFVGEDN
QETYLNISQVNVYSEEMFSSVSQLATDFIQSLLVKNPEKRPTAESCLSHSWLQQWDFGS
LFHPEETSGSSQIQDLTLRSSEKTSKSSCNGSCGAREDKENI PEDGSLVSKRFRFDDSL
PSPHELVPDLFC

SEQ ID NO: 151_H01248_H, DRAK1_H
MIPLEKPGSGGSSPGATSGSGRAGRGLSGPCRPPPPQARGLLTEIRAVVRTEPFQDGYS
LCPGRELGRGKFAVVRKCIKKDSGKEFAAKFMRKRRKGQDCRMEIIEIAVLELAQDNPW
VINLHEVYETASEMILVLEYAAGGEIFDQCVADREEAFKEKDVQRLMRQILEGVHFLHTR
DVVHLDLKPQNILLTSESPLGDIKIVDFGLSRILKNSEELREIMGTPEYVAPEILSYDPI
SMATDMWSIGVLTYVMLTGISPFLGNDKQETFLNISQMNLSYSEEEFDVLSESAVDFT
LLVKKPEDRATAEECLKHPWLTQSSIQEPSFRMEKALEEANALQEGHSVPEINSDTDKSE
TEESIVTEELIVVTSYTLGQCRQSEKEKMEQKAI SKRFKFEEPLLQEIPGEFIY

SEQ ID NO: 152_AA021445_H
MPARIGYYEIDRTIGKGNFAVVRKATHLVTKAKVAIKIIDKTQLDEENLKKIFREVQIMK
MLCHPHIIRLYQVMETERMIYLVTEYASGGEIFDHLVAHGRMAEKEARRKFKQIVTAVYF
CHCRNIVHRDLKAENLLLDANLNKIAADFGFSNLTFTPGQLLKTWCGSPPYAAPELFEGKE
YDGPVKVDIWSLGVVLYVLVCGALPFDGSTLQNLRLARVLSGKFRI PFFMSTECEHLIRHML
VLDPNKRLSMEQICKHKWMLGDADPNFDRLIAECQQLKEERQVDPLNEDVLLAMEDMGL
DKEQTLQSLRSDAYDHYSALSLCDRHKRHKTLRLGALPSMPRALAFQAPVNIQAEQAG
TAMNISVPQVQLINPENQIVEPDGTLNLDSDGEDEEPSPEALVRYLSMRRHTVGVADPRTE
VMEDLQKLLPGFPVNPQAPFLQVAPNVNFMHNLLPMQNLQPTGQLEYKEQSLLQPPTLQ
LLNGMGPLGRRASDGGANIQLHAQQLLKRPRGPSPLVTMTPAVPAVTPVDEESSDGEPDQ
EAVQRYLANRSKRHTLAMTNPTAEIPDLQRLQGLQGFRRSRVWPPHLPDQHRSTYKDSN
TLHLPTERFSPVRRFSDGAASIQAFKAHLEKMGNNSSIKQLQCECEQLQKMYGGQIDERT
LEKTQQQHMLYQQEQHHQILQQQIQDSICPPQPSPLQAACENQALLTHQLQRLRIQPS
SPPNHPNNHLFRQPSNSPPPMSSAMIQPHGAASSSQFQGLPSRSAIFQQQPENCSPPN
VALTCLGMQQAQSQQVTIQVQEPVDMLSNMPGTAAGSSGRGISISPSAGQMOMQHRTNL
MATLSYGHRPLSKQLSADSAEASLNVNRFSPANYPDQHLHPLHFSQSRGSPSSYSPT
GVGFSPTQALKVPPLDQFPTFPFSAHQQPPHYTTTALQQALLSPTPPDYTRHQQVPHILO
GLLSPRHSLTGHSDIRLPPTFAQLIKRQQQQRQQQQQQQQQEQELFRHMNQGDAGSL
APSLGGQSMTERQALSQNADSYHHHTSPQHLLQIRAEQCVSQASSPTPPHGYAHQPALM
HSESMEEDCSCEGAKDGFQDSKSSSTLTGCHDSPLLLSTGGPGDPESLLGTVSHAQELG
IHPYGHQPTAAFSKNKVPSREPVIGNCMRSPGQAVELPDHNGLGYPARPSVHEHHRPR
ALQRHHTIQNSDDAYVQLDNLPGM SLVAGKALSSARMSDAVLSQSSLMGSQQFQDGENEE
CGASLGGHEHPDLSDGSLNNSCYPSTCITDILLSYKHPEVSFSMEQAGV

SEQ ID NO: 153_2R22-5-11_H
MTAVYMNGGLVNPYARWDRDVSSEGCQTESSKEGEEGQPRQLTPFEKLTQDMSQDEK
VVREITLGKRIGFYRIRGEIGSGNFSQVKLGHSITKEKVAIKILDKTCLDQKTQRLLSR
EISSMEKLHHPNIIRLYEVVETLSKLHLVMEYAGGGELFGKISTEGKLSEPESKLIFSQI
VSAVKHMHENQIIHRDLKAENVFYTSNTCVKVGDFGFSTVSKKGEMLNTFCGSPPYAAPE

FIGURE 1H

LFRDEHYIGIYVDI WALGVLLYFMVTGTMPFRAETVAKLKKSILEGTYSVPPHVSEPCHR
LIRGV LQQIPTERYGIDCIMNDEWMQGVPTPLEPFQLDPKHLSETSTLKEEENEVKST
LEHLGITEEHIRNNQGRDARSSITGVYRIILHRVQRKKALESVPVMMLPDPKERDLKKGS
RVYRGIRHTSKFCSIL

SEQ ID NO: 154_R31237_1_H, AAC33487

MSTRTP LPTVNERDTENHTSHGDGRQEVTSRTSRSGARCRNSIASCADQPHIGNYRLLK
TIGKGNFAKVKLARHILTGREVAIKIIDKTQLNPTSLOKLFREVRIMKILNHPNIVKLFE
VIETEKTLYLIMEYASGGEVFDYLVAHGRMKEKEARSKFRQIVSAVQYCHQKRIVHRDLK
AENLLLDADMNIKIADFGFSNEFTVGGKLDTF CGSPPYAAPELFQGGKYDGPEVDVWSLG
VILYTLVSGSLPFDGQNLKELRERVLRGKYRIPFYMSTDCENLLKRFLVLNPIKRGTL EQ
IMKDRWINAGHEEDELKPFVEPELDISDQKRIDIMVGMGYSQEEIQESLSKMKYDEITAT
YLLGRKSSSELDASDSSSSSNLSLAKVRPSSDLNNSTGQSPHHKVQSVSSSQKQRRYS
HAGPAIPSVVAYPKRSQTSTADGDLKEDGISSRKSSGSAVGGKGIAPASPM LGNASNP NK
ADIPERKKSSTVPSSNTASGGMTRNTYVCSERTTADRHSVIQNGKENSTIPDQRTPVAS
THS ISSAATPDRI RFPRGTASRSTFHGQPRERRATATYNGPPASPSLSHEATPLSQTRSRG
STNLF SKLTSKLTRSRNVSAEQDENKEAKPRSLRFTWSMKTTSSMDPGDMMREIRKVL D
ANNC DYEQRERFLLFCVHGDGHAENLVQWEMEVC KLPRLSLNGVRFKRISGTSIAFKNIA
SKIANELKL

SEQ ID NO: 155_W90839_M

KGPSWSSRSLGARCRNSIASCPEEQPHVGN YRLLRITIGKGNFAKVKLARHILTGREVAIK
IIDKTQLNPSSLQKLFREVRIMKGLNHPNIVKLFEVIETEKTLYLIMEYASAGEVFDYLV
SHGRMKEKEARAKFRQIVSAVHYCHQKNIVHRDLKAENLLLD AEANI KIADFGFSNEFTL
GSKLDTF CGSPPYAAPELFQGGKYDGPEVDIWSLG VILYTLVSGSLPFDGHN LKELRERV
LRGKYRVPFYMSTDCESILRRFLVLNPAKRCTLEQIMKDKWINIGYEGEELKPDTELKEE
RMPGRKASCSAVGSGSRGLPPSSPMVSSAHNP NKA EI PERRKDSTSTPNNLPPSMMTRRN
TYVCTERPGSERPSLLPNGKENSSGTSRVPPASPSHSLAPPSGERSRLARGSTIRSTFH
GGQVRDRRAGSGSGGVQNGPPASPTLAHEAAPLPSGRPRPTTNLFTKLTSKLTRRV TDE
PERIGGPEVTSCHLPWDKTETAPRLLRF PWSVKLTSSRPS

SEQ ID NO: 156_406786.5_H

MEVGGLTVFEEDQRCLSQSLPLPVSAEGPAAQT TAEP SRSFSSAHRHLSRRNGLSRLCQS
RTALSEDRWSSYCLSSLA AQNICTSKLHCPA APEHTDPSEPRGSVSCCSLLRGLSSGWSS
PLLPA PVCNPNKAI FTVD AKTTEILVANDKACGLLGYSSQDLIGQKLTQFFLRSDSDVVE
ALSEE HMEADGHA AVVFGTVVDI ITRSGEKI PVSVMKRM RQERRLCCVVLEPVERVST
WVAFQSDGTITSCDSLFAHLHG YVSGEDVAGQHITDLIPSVQLPPSGQHIPKNLKI QRSV
GRARDGTTFPLSLKLKSQPSSEEATTGEAAPVSGYRASVWVFCTISGLITLLPDGTIHGI
NHSFALT LFGYKTELLGKNITFLIPGFYSYMDLAYNSSLQLPDLASCLDVGNESGCGER
TLDPWQGDPAEGGQDPRIN VVL AGGHV VPRDEIRKLME SQDI FTGTQTELIAGGQLLSC
LSPQ PAPGV DNVPEGSLPVHGEQALPKDQQIT ALGREEPV AIESPGQDLLGESRSEPVDV
KPFASCEDSEAPVPAEDGGS DAGMCGLCQKAQLERMGVSGPSGSDLWAGAAVAKPQAKGQ
LAGGSLLMHCPCY GSEWGLW WRSQDLAPSPSGMAGLSFGTPTLDEPWLG VENDOR EELQTC
LIKEQLS QLSLAGALDVPHAELVPTECQAVTAPVSSCDLGGRDLCGGCTGSSSACYALAT
DLPGGLEAVEAQEVDVNSFSWNLKELFFSDQTDQTSSNCSCATSELRETPSSLAVGSDPD
VGS LQE QGSCVLD DRELLLLTGTCVDLQGGRFRFRES CVGHDPTEPLEVCLVSSEHYA ASD
RESPGHVPSTLDAGPEDTCPSAEEPRLNVQVTSTPVI VMRGAAGLQREIQEGAYSGSCYH
RDGLRLSIQFEVRRVELQGPTPLFCCWL VKDLLHSQRDSAARTRFLASLP GSTHSTAAE
LTGPSLVEVLRARPWFEPPKAVELEGLAAC EGEYSQKYSTMSPLGSGAFGFVWTA VDKG
KNKEVVVKFIKKEKVLED CWIEDPKLGKVTLEIAILSRVEHANI IKVLDIFENQGF FQLV

FIGURE 11

MEKHGSGLDLFAFIDRHPRLDEPLASYIFRQVRAGQSRLVSAVGYLRLKDI IHRDIK DEN
IVIAEDFTIKLIDFGSAAYLERGKLFYTF CGTIEYCAPEVLMGNPYRGPELEMWSLGVTL
YTLVFEENPFCELEETVEAAIHPPYLVSKELMSLVSGLLQPVPERRTTLEKLVTDPWVTQ
PVNLADYTWEVFRVKNKPESGVLSAASLEMGNRSLSDVAQAQELCGGPVPGEAPNGQGCL
HPGDPRLTS

SEQ ID NO: 157_AA544838_M 406786_M
TRPHPCLDPLASFIFRQLVSAVGYLHSQGI IHRDIK DENIVIAEDFTIKLIDFGSAAYL
ERGLFYTF CGTIEYCAPEVLIGNPYRGPELEMWSLGVTLTYTLIFEENPFCEVEETMEAV
IHPPFLVSQELMSLLSGLLQPCPEQRTTLEKLIRDPWVTQPVNLASYTWEVCRTNQ PES
GLLSAASLEIGSRSPSEMAQREGLCPPAPRETRGDQHCLHLKDPSLPVS

SEQ ID NO: 158_AA785735_H
MVMADGPRHLQRGPPVRVGFYDIEGTLGKGNFAVVKLGRHRITKTEVAIKI IDKSQLD AVN
LEKIYREVQIMKMLDHPHIIKLYQVME TKSMYLVTEYAKNGEIFDYLANHGRNLNESEAR
RKFWQILSAVDYCHGRKIVHRDLKAENLLLDNNMNIIADFGFGNFFKSGELLATWCGSP
PYAAPEVFEGQQYEGPQLDIWSMGVVLYVLVCGALPFDGPTLPILRQRVLEGRFRI PYFM
SEDCEHLIRMLVLDPSKRLTIAQIKEHKWMLIEVPVQRPVLYPQEQENEPSIGEFNEQV
LRLMHS LGIDQKXIESLQNKSYNHFAAIYFLLVERLKSHRSSFPVEQRLDGRQRRPSTI
AEQTVAKAQTVGLPVTMHS PNMRLLSALLPQASNVEAFSFPASGCQAEAAFMEEECVDT
PKVNGCLLDPVPPVLVRKGCQSLPSNMETS IDEGLETEGEAEEDPAHAFAEFQSTRSGQ
RRHTLSEVTNQLVVM PGAGKIFSMNDSPSLDSVDSEYDMGSVQRDNLNFLEDNPSLKDIML
ANQPSPRMTSPFISLRPTNPAMQALSSQKREVNHRSPVS FREGRRASDTSLTQGI VAFRQ
HLQNLARTKGILELNKVQLLYEQIGPEADPNLAPAAPQLQDLASSCPQEEVSQQQESVST
LPASVHPQLSPRQSLETQYLQHRLOKPSLLSKAQNTCQLYCKEPPRSLEQQQLQEHRLQOK
RLFLQKQSQLQAYFNQM QIAESSYPQPSQQLPLPRQETPPPSQQAPPFSLTQPLSPVLEP
SSEQMQYSPFLSQYQEMQLQPLPSTSGPRAAPPLPTQLQQQQPPPPPPPPPPRQPGAAPA
PLQFSYQTCELPSAASPADYPTPCQYPVDGAQQSDLTGPDCPRSPGLQEAPSSYDPLAL
SELPGLFDCEMLDAVDPQHNGYVLVN

SEQ ID NO: 159_AA207220_H
MESLVFARRSGPTPSAAELARPLAEGLIKSPKPLMKKQAVKRHHHKHNL RHRYEFLET LG
KGTYGKVKKARESSGRLVAIKSIRKDKI KDEQDLMHIRREIEIMSSLNHPHIIA IHEVFE
NSSKIVIVMEYASRGDLYDYI SERQQLSEREARHFFRQIVSAVHYCHQNRVVRDLKLEN
ILLDANGNIKIADFGLSNLYHQGFLOTF CGSPLYASPEIVNGKPYTGPEVDSWSLGVLL
YILVHGTMPFDGHDHKILVKQISNGAYREPPKPSDCLXGLIRWLLMVNPTRRATLEDVAS
HWWVNWGYATRVGEQEAPHEGGHPGSDSARASMADWLRRSSRPLENGAKVCSFFKQHAP
GGGSTTPGLERQHSLKKS RKENDMAQSLHSDTADDTAHRPGKSNLKL PKGILKKKVSASA
EGVQEDPPELSPIPASPGQAAPLLPKKGILKKPRQRESGYYSPEPSES GELL DAGDV FV
SGDPKEQKPPQASGLLLHRKGILKLNGKFSQTALELAAPTTFGSLDELAPPRPLARSRP
SGAVSEDSILSSESFDQLDLPERLPEPPLRGCVSVDNLTGLEPPSEGP GSCLRRWRQDP
LGDSFCFSLTDCQEV TATYRQALRVCSKLT

SEQ ID NO: 160_AA426580_H, MAK_V_H
MPAAAGDGLLGEPAAPGGGGGAEDAAPAAACEGSFLPAWVSGVPRERLRDFQHHKRVGN
YLIGSRKLGEFSFAKVREGLHVL TGEKVAIKVIDKKRAK KDTYVTKNLRREGQIQQMIRH
PNITQLLDILETENSYYLVMELCPGGNLMHKIYEKKRLEESEARRYIRQLISAVEHLHRA
GVVHRDLKIENLLLEDNNIKLIDFGLSNCAGILGYSDPFFSTQCGSPAYAAPELLARKKY
GPKIDVWSIGVNM YAMLTGTLPFTVEPFSRLALYQKMVDKEMNPLPTQLSTGAISFLRSL
LEPDPVKRPNIQQALANRWLNENYTGKVPCNVTPNRI SLEDLSPSVVLHMT EKLGYKNS

FIGURE 1J

DVINTVLSNRACHILAIYFLLNKKLERYLSGKSDIQDSLCKYKTRLYQIEKYRAPKESYEA
SLDTWTRDLEFHAVQDKKPKKEQKRGDFLHRPFSKKLDKNLPSHKQPSGSLMTQIQNTKA
LLKDRKASKSSFPDKDSFGCRNIFRKTSDSNCVASSSMEFIPVPPPTPRIVKKPEPHQP
GPGSTGIPHKEDPLMLDMVRSFESVDRDDHVEVLSPSHHYRILNSPVSLARRNSSERTLS
PGLPSGSMSPLHTPLHPTLVSAHEDKNSPKKEEGLCCPPVPSPNGPMQPLGSPNCVKSR
GRFPMMGIGQMLRKRHQSLOPSADRPLEASLPPLQPLAPVNLAFDMADGVKTQC

SEQ ID NO: 161_Z36720_H

MDTKLNLNEKVDQLLHFQEDVTEKLQSMCRDMGHLERGLHRLEASRAPGPGGADGVPHI
DTQAGWPEVLELVRAMQDAAQHGARLEALFRMVAADVRAIALVGATFQKSKVADFLMQG
RVPWRRGSPGDSPEEWVKEEEVCFMPPVPPAPGAAGQSLQDKGELSAEQGIWATLMTLV
IMVTAANKERVEEEGGKPKHVLSTSGVQSDAREPGEESQKADVLEGTAERLPPIRASGLG
ADPAQAVVSPGQGDGVPGPAQAFPGHLPLPTKVEAKAPETPSENLRGTGLELAPAPGRVNV
VSPSLEVAPGAGQGASSSRPDPEPLEEGTRLTPGPGPQCPGPPGLPAQARATHSGGETPP
RAALLKGAVAPGFSRRDLVFPSIFCACLGISIHQEMDTPGEMLMTGRGSLGPTLTTEAP
AAAQPGKQGPPTGRCLQAPGTEPGEQTPEGARELSPLQESSSPGGVKAEEEQRAGAEFG
TRPSLARSDDNDHEVGALGLQQGKSPGAGNPEPEQDCAARAPVRAEAVRRMPPGAEGSV
VLDDSPAPPAPFEHRVSVKETSISAGYEVQCQHEVLGGGRFGQVHRCTEKSTGLPLAAKI
IKVKSADREDVKNEINIMNQLSHVNLIQLYDAFESKHSCTLVMEYVDGGELFDRITDEK
YHLTELDVVLFTTRQICEGVHYLHQHYILHLDLKPENILCVNQTGHQIKIIDFGLARRYKP
REKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVIITYMLLSGLSPFLGETDAETMNFIV
NCSWDFDADTFEGLSEEAKDFVSRLLVKEKSCRMSATQCLKHEWLNLPKASRSKTRLK
SQLLLQKYIAQRKWKKHFFVVTAAANRLRKFTSP

SEQ ID NO: 162_SGK088_H

GEMALFECLVAGPTDVEVDWLRCGRLLQFALLKCKMHFDGRKCKLLLTSVHEDDSGVYTC
KLSTAKDELTC SARLTVRPSLAPLFTRLLEDVEVLEGRAARFDCKISGTPPPVVTWTHFG
CPMEESENRLRQDGGSLHSLHIAHVGSEDEGLYAVSAVNTHGQAHCSAQLYVEEPRTAAS
GPSSKLEKMPISIPPEPEQGELERLSIPDFLRPLQDLEVGLAKEAMLECQVTGLPYPTISW
FHNGHRIQSSDDRRMTQYRDVHRLVFPVAVGPQHAGVYKSVIANKLGAACYAHLYVTDVV
PGPPDGAPQVAVTGRMVTLTWNPPRSLDMAIDPDSLTYTVQHQLVGLSDQWTALVTGLRE
PGWAATGLRKGVQHIFRVLSTTVKSSSKPSPSEPQVQLLEHGPTLEEAPAMLDKPDIVYV
VEGQPASVTVTFNHVEAQVWVRSRGALLEARAGVYELSOPDDQYCLRICRVSRDMDGA
LTCTARNRHGTQTC SVTLELAEAPRFESIMEDVEVGAGETARFAVVVEGKPLPDIMWYKD
EVLLESSHVSFVYEENECSLVVLSTGAQDGGVYTCTAQNLAGEVSCKAELAVHSAQTAM
EVEGVGEDEDHRGRRLSDFYDIHQEIGRGAFSYLRRIVERSSGLEFAAKFIPSQAKPKAS
ARREARLLARLQHDCVLYFHEAFERRRGLVIVTELCTEELLERIARKPTVCESEIRAYMR
QVLEGIHYLHQSHVLHLDVKPENLLVWDGAAGEQQVRI CDFGNAQELTPGEPQYCQYGT
EFVAPEIVNQSPVSGVTDIWPVGVAFLCLTGISPFGENDRTTLMNIRNYNVAFEETTF
LSLSREARGFLIKVLVQDRLRPTAEETLEHPWFKTQAKGAEVSTDHLKLFLSRRRWQRSQ
ISYKCHLVLRPIPELLRAPPERVWVTMPRRPPPSGGLSSSSDSEEELEELPSVPRPLQP
EFSGSRVSLTDIPTEDALGTPETGAATPMDWQEQGRAPSQDQEAPSPALPSPGQEPAA
GASPRRGELRRGSSAESALPRAGPRELGRGLHKAASVELPQRRSPGPGATRLARGGLGEG
EYAQRLQALRQRLLRGGPEDGKVSGLRGPLESLGGRARDPRMARAASSEAPHHQPPLE
NRGLQKSSSFSQGEAEPRGRHRRAGAPLEIPVARLGARRLQESPSLSALSEAQPPSPARP
SAPKPSTPKSAEPSATTPSDAPQPPAPQPAQDKAPEPRPEPVASKPAPPPQALQTLALP
LTPYAQIIQSLQLSGHAQGPSQGAAPPSEPKPHA AVFARVASPPPGAPEKRVPSAGGPP
VLAEKARVPTVPPRPGSSLSSSIENLESEAVFEAKFKRSRESPLSLGLRLLSRSRSEERG
PFRGAEEEDGIYRPSAGTPELVRRPERSRSVQDLRAVGEPGLVRRLSLSLSQRLRRT
PAQRHPAWEARGGDGESSEGGSSARGSPVLAMRRRLSFTLERLSSRLQSRGSSSEDSSGAS

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FIGURE 1K

GRSTPLFGRLRRATSEGESLRRRLGLPHNQLAAQAGATTPSAESLGSEASATSGSSAPGES
 RSRLRWGFSRPRKDKGLSPPNLSASVQEELGHQYVRSESDFPVVFHIKLKDQVLLGEAA
 TLLCLPAACPAPHISWMKDKKSLRSEPSVIIVSCKDGRQLLSIPRAGKRHAGLYECSATN
 VLGSITSSCTVAVARVPGKLAPPEVTQTYQD TALVLWKPGDSRAPCTYTLERRVDGESVW
 HPVSSGIPDCYYNVTHLPVGVTVRFRVACANRAGQGPFNSSEKVFVRGTQDSSAVPSAA
 HQEAPVTSRPARARPPDSPTSLAPPLAPAAPTPPSVTVSPSSPPTPPSQALSSLKAVGPP
 PQTPRRHRGLQAARPAEPTLPSTHVTVPSEPKPFVLDGTGPIIPASTPQGVKPVSSSTPVY
 VVTSFVSAPPAPPEPPAPEPPPEPTKVTVQSLSPAKEVVSSPGSSPRSSPRPEGTTLRQGP
 PQKPYTFLEEKARGFRGVVRACRENATGRTFVAKIVPYAAEGKPRVLQOEYEVRLTLHHER
 IMSLHEAYITPRYLVLIAESCGNRELLCGLSDRFYSEDDVATYMVQLLOGLDYLHGHV
 LHLDIKPDNLLLAPDNALKIVDFGSAQPNPQALRPLGHRTGTLEFMAPEMVKGEPIGSA
 TDIWGAGVLTYYIMLSGRSPFYEPDPQETEARIVGGRFDAFQLYPNTS QSATLFLRKVLSV
 HPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLLR
 SYPGGP

SEQ ID NO: 163_AA542015_M SGK088_M
 ATDIWGAGVLTYYIMLSGYSPFYEPDPQETEARIVGGRFDAFQLYPNTS QSATLFLRKVLS
 VHPWSRPSLQDCLAHPWLQDAYLMKLRRQTLTFTTNRLKEFLGEQRRRRAEAAATRHKVLL
 RSYPGSP

SEQ ID NO: 164_R19772_H
 MKGGDRAYTRGPSLGLWFAKCCCCFPCRDAYSHSSSENGGKSESANLQAQPSLNFIHSS
 PGPKRSTNTLKKWLTSPVRLNSGKADGNIKKQKKVRDGRKSF DLGSPKPGDETTPOGDS
 ADESKKGWGEDEPDEESHTPLPPPMKIFDNDPTQDEMSSSLAARQASTEVP TAADLVNA
 IEKLVKNKLSLEGSSYRGS LKDPAGCLNEGMAPPTPPKNPEEEQKAKALGRMFVLNELV
 QTEKDYVKDLGIVVEGFMKRIEEKGVPEDMRGKDKIVFGNIHQIYDWHKDFFLAELEKCI
 QEQDRLAQLFIKHERKLHIYVWYCQNKPRSEYIVA EYDAYFEEVKQEINQRLTSLDFLIK
 PIQRITKYQLLLKDFLRYSEKAGLECS DIEKAVELMCLVPKRCNDMMNLGRLQGFEGTLT
 AOGKLLQODTFYVIELDAGMQSRTKERRVFLFEQIVIFSELLRKGS LTPGYMFKRSIKMN
 YLVLEENVNDNDPCKFALMNRETSE RVVLQAANADIQQAWVQDINQVLETQRDFLNALQSP
 IEYQRKERSTAVMRSQPARLPQASPRPYSSVPAGSEKPPKGSSYNPPLPPLKISTSNNGSP
 GFEYHQPGDKFEASKNDLGGCNGTSSMAVI KDYYALKENEICVSQGEVVQVLAVNQONMC
 LVYQPASDHSPAAEGWVPGSILAPLTKATAAESDGS IKKSCSWHTLRMRKRAEVENTGK
 NEATGPRKPKDILGNKVS VKETNSSESECEDDLDPNTSMEILNPNFIQEVAPFLVPLVD
 VTCLLGDTVILQCKVCGRPKPTITWKGPQDNI LDTDNSSATYTVSSCDSGEITLKI CNLM
 PQDSGIYTCIATNDHGTSTSATVKVQGVPAAPNRPIAQERSCTSVILRWLPPSSTGNCT
 ISGYTVEYREEGSQIWQOSVASTLD TYLVIEDLSPGCPYQFRVSASNPWGISLPSESEF
 VRLPEYDAAADGATISWKENFDSAYTELNEIGRGRFSIVKKCIHKATR KDVAVKVFVNKKM
 KKKEQAAHEAALLQHLQHPQYITLHDTYESPTS YILILELMDDGRLLDYLMNHDELMEEK
 VAFYIRDIMEALQYLHNCRV AHLDIKPENLLIDLRI PVPRVKLIDLEDAVQISGHFHIHH
 LLGNPEFAAPEVIQGI PVSLGTDIWSIGVLTYYMLSGVSPFLDESKEETCINVC RVDFS F
 PHEYFCGVSNAARDFINVI LQEDFRRRPTAATCLOHPWLQPHNGSYSKIPLDTSRLACFI
 ERRKHQNDVRPIPNVKSYIVNRVNQGT

SEQ ID NO: 165_5R72_8_2_H
 MADSGLDKKSTKCPDCSSASQKDVLCVCSKTRVPPVLV VEMSQTSSIGSAESLISLERK
 KEKNINRDITSRKDLPSRTSNVERKASQQQWGRGNFTEGKVPHIRIENGAAIEEYTFGR
 ILGKGSFGIVIEATDKETETKWA IKKVNKEKAGSSAVKLLEREVNILKSVKHEHIHLEQ
 VFETPKMYLVMELCEDGELKEILDRKGHFSENETRWI IQSLASAIAYLHNNDIVHRDLK
 LENIMVKSSLIDDNNEINLNIKVTD FGLAVKKQSRSEAMLQATCGTPIYMAPEVISAHDY

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FIGURE 1L

SQQCDIWSIGVVMYMLLRGEPFLASSEAKLFELIRKGELHFENAVWNSISDCAKSVLKQ
LMKVDPahrITAKELLDNQWLTGNKLSSVRPTNVLEMMKEWKNNPESVEENTTEEK NKPS
TEEKLKSYQPWGNVPETNYTSDEEEEEKQSTAYEKQFPATSKDNFDMCSSSFTSSKLLPAE
IKGEMEKTPTVTPSQGTATKYPAKSGALSRTKKKL

SEQ ID NO: 166_SGK309_H

MQCLAAALKDETMSGGGEQADILPANYVVKDRWKVLKKIGGGGFGEIYEAMDLLTREN
ALKVESAAQPKQVLKMEVAVLKKLQSGSLGQDGKEEMMKPGAKRGKDHVCRFIGCGRNE
KFNYVVMQLQGRNLADLRRSQPRGTFTLSTTLRLGKQILESIEAIHSGVFLHRDIKPSNF
AMGRLPSTYRKCYMLDFGLARQYTNTTGDVRPPRNVAGFRGTVRYASVNAHKNREMGRHD
DLWSLFYMLVEFAVGQLPWRKIKDKEQVGMIEKEYEHRMLLKHMPSEFHLFLDHIASLDY
FTKPDYQLIMSVFENSMKERGIAENEAFDWEKAGTDALLSTSTSTPPPAEHPADGSHVWG
GQCDASAWGPAPGEHRCATGRAPEXPGECTPNSAREALXGAGPQSPPCPPPRGSXGXSL
GGDRCQPEQTPDQHRQSNCRQGEGRWPFLSPPIPSLVPLPCSSXAPCPPPIISLLARPLF
PVPSPALASLCLPSSSSSVSFTLRRPSA

SEQ ID NO: 167_AA234451_H

MSGGGEQLDILSVGILVKERWKVLKIGGGGFGEIYDALDMLTRENVALKVESAAQPKQV
LKMEVAVLKKLQGDHVCRFICGRNDRFNYVVMQLQGRNLADLRRSQSRGTFTISTTLR
LGRQILESIESIHSGSXHRDIKPSNFAMGRFPSTCRKCYMLDFGLARQFTNSCGDVRPP
RAVAGFRGTVRYASINAHNRNEMGRHDDLWSLFYMLVEFVVGQLPWRKIKDKEQVGSIKE
RYDHRLMLKHLPPFEFSIFLDHISSLDYFTKPDYQLLTSVFDNSIKTFGVIESDPFDWEKT
GNDGSLTTTTTSTTPQLHTRLTPAAIGIANATPIPGDLLRENTDEVFPDEQLSDGENGIP
VGVSPDKLPGSLGHPRPQEKDVWEEMDANKNKIKLGICKAATEEENSHGQANGLLNAPSL
GSPIRVRSEITQPDRIPLVRKLRSIHSEFELEKRLTLEPKPDTDKFLETWYKIVYFSF

SEQ ID NO: 168_AA435956_H

TFTIFFEMTVFDLEAKSARGGSNLLMDSVSSFQLFMFQLLRGLAYIIHQHVLHRDLKPQN
LLISHLGELKLADFGARAKSIPSQTYSSVVTLWYRPPDALLGATEYSSELDIWGAGCI
FIEMFQGQPLFPGVSNILEQLEKIWEVLGVPTEDTWPGVSKLPNYPWFPLPTPRSLHV
VWNRLGRVPEAEDLASQMLKGFPRDRVSAQEALVHDYFSALPSQLYQLPDEESLFTVSGV
RLKPEMCDLLASYQKGHPAQFSKCW

SEQ ID NO: 169_AA626859_H

NGVADGVIKSVLWQTLQALNFCHIHNCIHRDIKPENILITKQGIKICDFGFAQILIPGD
AYTDYVATRWRAPPELLVGDTQYGSSVDIWAIGCVFAELLTGQPLWPGKSDVDQLYLIIR
TLGKLI PRHQSIFKSNGFFHGISIPEPEDMETLEEKFSVHPVALNFMKGCLKMNPDRL
TCSQLLESSYFDSFQEAQIKRKARNEGRNRRRQQNQLLPLIPGSHISPTPDGRKQVLQK
FDHLPNI

SEQ ID NO: 170_AA061797_M

KIALREIRMLKLKHPNLVNLIEVFRKRKMHLVFEYCDHTLLNELERNPNGVSDGVISV
LWQTLQALNFCHKHNCIHRDVKPENILITKQGMIKICDFGFARILIPGDAYTDYVATR
WRAPPELLVGDTKYGSSVDVWAVGCVFAELLTGQPLWPGKSDVDQLYLIIRTLGKLI
PRHQSIFRSNQFFRGISIPEDMETLEEKFSNVQPVALSFMKGCLKMNPDRLTCAQLLDSAYF
ESFQEDQMKRKARSEGRSRRRQQNQLLPLIPGSHISPTPDGRKQVVQLKFDHLPNI

SEQ ID NO: 171_AA397553_H

MPNSERHGGKKGSGGASGTLQPSGGGSSNSRERHRLVSKHKRHKSKHSDMGLVTPEA
ASLGTVIKPLVEYDDISSDSTFSDDMAFKLDRRENDERRGSDRSRDLHKHRRHQHRRSR

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FIGURE 1M

DLLKAKQTEKEKSQEVSSKSGSMKDRISGSSKRSNEETDDYGKAQVAKSSSKESRSSKLH
 KEKTRKERELKSGHKDRSKSHRKRETPKSYKTVDSPKRRSRSPHRKWSDDSSKQDDSPSGA
 SYGQDYDLSPSRSHTSNYDSYKKSPGSTSRQSVSPPYKEPSAYQSSTRSPSPYSRRQR
 SVSPYSRRRSSSYERSGSYGRSPSPYGRRRSSSPFLSKRSLRSPLPSRKSMKSRSRSP
 AYSRHSSSHSKKKRSSSRSRHSSIIPVRLPLNSSLGAELSRKKKERAAAAAAKMDGKES
 KGSPVFLPRKENSSEAKDSGLESKKLPRSVKLEKSAPDTELNVNTHLNTVKNSSDTGK
 VKLDENSEKHLVKDLKAQGTDRDCKPIALKEEIVTPKETETSEKETPPPLPTIASPPPLP
 TTTTPPQTPPLPPLPIPALPQQPPLPPSQPAFSQVPASSTSTLPPSTHSKTSAVSSQAN
 SQPPVQVSVKTQVSVTAAPHLKTSTLPLPLPPLPGGDDMDSPKETLPSKPVKKEKEQ
 RTRHLLTDLPLPPELPGGDLSPDSEPKAITPPQQPYKKRPKICCPRYGERRQTESDWG
 KRCVDKFDIIGIIGEGTYGQVYKARDKDTGELVALKKVRLDNEKEGFPITAIKILRQ
 LIHRSVVMKEIVTDKQDALDFKKDKGAFYLVFEYMDHDLMLGLESGLVHFSEDHIKFSM
 KQLMEGLECHYCHKNFLHRDIKCSNILLNNSGQIKLADFGGLARLYNSEESRPTYTNKVITLW
 YRPELLLGEEYTPAIDVWSCGILGELFTKKPIFQANLELAQLELISRLCGSPCPAVW
 PDVIKLPYFNTMKPKKQYRRRLREEFSFIPSAALDLDHMLTLDPSKRCTAEQTLQSDFL
 KDVELSKMAPDPLPHWQDCHLWSKKRRRQSQGVVVEPPPSKTSRKETTSGTSTEPVK
 NSSPAPPQPAPGKVESGAGDAIGLADITQQLNQSELAVLLNLLQSQTDLISIPQMAQLLNI
 HSNPEMQQLEALNQSISALTEATSQQQDSETEMAPEESLKEAPSAPVILPSAEQMTLEAS
 STPADMQNILAVLLSQLMKTQEPAGSLEENNSDKNSGPGQPRRTPTMPQEEAACPPHIL
 PPEKRPPPEPPPPPPPPPPPLVEGDLSSAPQELNPAVTAALLQLLSQPEAEPGHLPHHEH
 QALRPMEYSTRPRPNRTYGNTDGPETGFSADTDERNNGPALTESLVQTLVKNRTFSGSL
 SHLGESSYQGTGSVQFPQDQDLRFARVPLALHPVVGQPFLLKAEGSSNSVVAETKLQNY
 GELGPGTTGASSSGAGLHWGGPTQSSAYGKLYRGPTRVPPRGGGRGVVPY

SEQ ID NO: 172_AA789239_H

MEMYETLGKVGESYGTVMKCKHKNTGQIVAIKIFYERPEQSVNKIAMREIKFLKQFHHE
 NLVNLIEVFRQKKIHLVFEFIDHTVLDELQHYCHGLESKRRLKYLFQILRAIDYLHSNN
 VIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYTDYVATRWYRAPELVLKDTSYG
 KYVPVDI WALGCMIIEMATGNPYLPSSSDLDLLHKIVLKVXFMPELKAKLLQEAKVNSLI
 KPKESSKENELRKDERKT VYTNLTLLSSSVLGKEIEKEKKPKEIKVRVIKVKGGRGDI SEP
 KKKEYEGGLGQQDANENVHPMSPDTKLVTEPPNPINPSTNCGNGLKENPHCGGSVTMPPI
 NLTNSNLMAANLSSNLFHPSVRLTERAKKRTSSQSIGQVMPNSRQEDPGPIQSQMEKGI
 FNERTGHSDQMANENKRKLNF SRSDRKEFHFPPELPVTIQSKDTKGMEVKQIKMLKRESKK
 TESSKIPTLLNVDQNEKQEFIPLSLLSACCPIFTNICSQLTIRVEMAIARGRI

SEQ ID NO: 173_AA124976_M

LADIVHACLQIDPAERTSSTDLLRHDFTRDGFIEKFIPELRAKLLQEAKVNSFIKPEN
 FKENEPVRDEKKS VFTNTLLYGNPSLYGKEVDKRAKELKVRVIKAKGGKGDVPDQKKP
 EYEGDHRQQTADDTQPSSLDKKPSVLELTNPLNPSSENSDGVKEDPHAGGCMIMPPINLT
 SSNLLAANLSSNL SHPNSRLTERTKKRRTSSQTIGQTLNSNRQEDTGPTQVQTEKGAFNE
 RTGQNDQISSGNKRKLNF PKCDRKEFHFPPELPFTVQAKEMKGMEVKQIKVLKRESKKTDS
 SKIPTLLSMDPNQEKQEGGDGDCEGKNLKRNRFFFSR

SEQ ID NO: 174_AA575635_M CCRK_M

SASGQLKIADFGGLARVFS PDGGRLYTHQVATRWYRAPELLYGARQYDQGVLDLWAVGCIMG
 ELLNGSPLFP GENDIEQLCCVLRILGTPSPRVWPEITELPDYNKISFEEQAPVPLEEVL P
 DASPQALDLLGQFLLYPPRQRIAASQALLHQYFFTAPLPAHPSELPIPQRPGGPAPKAHP
 GPPHVHDFHVDRIEESLLNPELIRPFIPEG

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FIGURE 1N

SEQ ID NO: 175_AA631990_H

MITISISTEKSNGTHYPPMITTLQYYRGRGGKTAVVRHFS AEGPF AFAEMRHSKRTHCPDW
DSRESWGHE SYRGSHKRKRSHSSTQENRHCKPHHQFKESDCHYLEARSLNERDYRDDRY
VDEYRNDYCEGYVPRHYHRDIESGYRIHCSKSSVRSRRSSPKRKRNHRHCSSHQSRXS EIV
DTLGEGAFGKVVECIDHGMDGMHVAVKIVKNVGRYREAAARSEIQVLEHLNSTDPNSVFR C
VQMLEWFDHHGHVCIVFELLGLSTYDFIKENSFLPFQIDHIRQMAYQICQSINFLHHNKL
THTDLKPENILFVKSDYVVKYNSKMKRDERTLKN TDIKVVD FGSATYDDEHHSTLVSTRH
YRAPEVILALGWSQPCDVWSIGCILIEYYLGFTVFQTHDSKEHLAMMERILGP I PQHMIQ
KTRKRKYFHHNQLDWDEHSSAGRYVRRRCKPLKEFMLCHDEEHEKLF DLVRRMLEYDPTQ
RITLDEALQHPFFDLLKKK

SEQ ID NO: 176_AA557536_H

MCTVVDPRIVRRYLLRRQLGQGRTFREITLLQVSGLGPPVQSPCPGTDLSRQERNWPSWA
PEHSPSWPSSRLRLSPQEFGDHPNII SLLDVIRAENDRDIYLVFEFMDTDLNAVIRKGG L
LQDVHVRSIFYQLLRATRFLHSGHVVRDQKPSNVLLDANCTVKLCDFGLARSLGDLPEG
PEDQAVTEYVATR WYRAPEVLLSSHRYTASCPRYTLGVDMWSLGCILGEMLRGRPLFPGT
STLHQLELILETI PPPSEEXRPRQTL DALLPPDTSPEALDLLRLLVFAPDKRLSATQAL
QHPYVQRFHCPSDEWAREADV RPRAHEGVQLSVPEYRSRVYQ MILECGGSSGTSREKGPE
GVSPSQAHLHKPRADPQLPSRTPVQGP RP RPQSSPGHDPAEHES PRAAKNVPRQNSAPLL
QTALLGNGERPPGAKEAPPLTSLSVKPSGRGAAPSLTSQAAAQVANQALIRGDWNRGGGV
RVASVQVQPPRLPPEARPGRMFST SALQGAQG GARALLGGYSQAYGTVCHSALGHLPLL
EGHHV

SEQ ID NO: 177_N28606_H, MOK_H

MKNYKAIGKIGEGTFSEVMKMQSLRDGNY YACKQMKORFESIEQVNNLREIQALRRRLNPH
PNILMLHEVVFDRKSGSLALICELMDMNIYELIRGRRYPLSEKKIMHYMYQLCKSLDHIH
RNGIFHRDVKPENILIKQDVLKLGDFGSCRSVYSKQPYTEYISTRWYRAPECLLTDGFYT
YKMDLWSAGCVFYEIASLQPLFPGVNELDQISKIHDVIGTPAQKILT KFKQSRAMNDFDP
FKKSGSIPLLTTNLSPQCLSLHAMVAYDPDERIAAHQALQHPYFQEQRKTEKRALGSHR
KAGFPEHPVAPEPLSNSCQISKEGRKQKQSLKQEEDRPKRRGPAYVMELPKLKL SGVVRL
SSYSSPTLQSVLGS GTNGRVPVLRPLKCI PASKKTD PQKDLKPAPQQCRLPTIVRKGR

SEQ ID NO: 178_AB023153_H, ICK_H

MNRYTTIRQLGDGTYSVLLGRSIESGELIAIKMKRKFYSWEECMNQREVKSLKKLNHA
NVVKLKEVIRENDHLYFIFEYMKENLYQLIKERNKLPESAIRNIMYQILOGLAFI HKLG
FFHRDLKPENLLCMGP ELVKIADFGLAREIRSKPPYTDYVSTRWYRAPEVLLRSTNYSSP
IDVWAVGCIMAEVYTLRPLFPGASEIDTIFKICQVLGTPKKT DWPEGYQLSSAMNFRWPQ
CVPNNLKTLPNASSEAVQLLRDMLQWDPKKRPTASQALRYPYFQVGHPLGSTTQNLQDS
EKPQKGILERAGPPPYIKPVPPAQPPAKPHTRISSRQH QASQPPLHLTPYKAEVSR TDH
PSHLQEDKPSLLFP SLHNKHPQSKITAGLEHKNGEIKPKSRRRWGLISRSTKSDDDWAD
LDDLDFSPSLSRIDLKNKKRQSDDTLCRFESVLDLKPSEPVG TGNSAPTQTSYQRRDTPT
LRSAAKQHYLKHSRYLPGISIRNGILSNPGKEFIPPNPWSSSGLSGKSSG TMSVISKVNS
VGSSSTSSSGLTGNYVPSFLKKEIGSAMQRVHLAPI DPSPGYSSLKAMRPHPGRPFLDT
QPRSTPGLIPRPPAAQPVHGRTDWASKYPSRR

SEQ ID NO: 179_AA839940_M

SSNNGGMSAEEEIGPGAEPMRGPSLATRDWRDET VGT TD LQQGIDPGAVSPEPGKD HAAQ
GPGRTEAGRVSSAAEAAIVVLDDSAAPPAPFEHRVSIKDTLISAGYTVSQHEVLGGGRF
GQVHRCTERSTGLALAAKIIKVKNVKDREDVKNEVNIMNQLSHVNLIQLYDAFESKNSFT
LIMEYVDGGELFDRITDEKYHLTEL DVVLFTRQICEGVHYLHQHYILHLDLKPENILCVS

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FIGURE 10

QTGHQIKIIDFGLARRYKPREKLKVNFGTPEFLAPEVVNYEFVSFPTDMWSVGVITYMLL
SGLSPFLGETDAETMNFIVNCSWDFDADTFKGLSEEAKDFVSRLLVKEKSCRMSATQCLK
HEWLNHLPAKASGSNVRLRSQQLLQKYMAQSKWKKH FHVVA AVNRLRKFP TCF

SEQ ID NO: 180_AA460132_H

MAAARATTPADGEEPAPAEALAAARERSSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVDYASNCLYMEIEGVS
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVLDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 181_SGK034_H

QREKVNQGNMPLQSTFLAMDTEEGVEVVWNE LHFGDRKAFAAHEEKIQT VFEQLVLVDH
PNIVKLHKYWLDTSEACARVIFITEYVSSGSLKQFLKKTCKNHKAMNARAWKRWCTQILS
ALSFLHACSPPIIHGNLTSDTIFIQHNGLIKIGSVWHRIFSNALPDDLRSPIRAEREELR
NLHFFPPEYGEVADGTAVDIFSF GMCALEMAVLEIQ TNGDTRVTEEA IARARHSLSDPNM
REFILCCLARDPARRPSAHSLLFHRVLF EVHSLKLLAAHCFIQHQY LMPENVVEEKTAM
DLHAVLAELPRPRRPPLQWRYSEVSFMELDKFLEDVRNGIYPLMNFAATRPLGLPRVLAP
PPEEVQKAKTPTPEPFDSETRKVIQMOCNLERSEDKARWHLTLLLVL EDRLHRQLTYDLL
PTDSAQDLASELVHYGFLHEDDRMKLA AFLESTFLKYRG TQA

SEQ ID NO: 182_AA103218_M SGK034_M

HASAPEYGEVNDGTGFVDIFSF GMCALEMAVLEIQANGDTRVTEEA IARARHSLSDPNMR
EFILSCLARDPARRPSAHNLLFHRVLF EVHSLKLLAAHCFIQHQY LMPENVVEEKTAM
LHAVLAEMPQPHGPPMQWRYSEVSFLELDKFLEDVRNGIYPLMNFAAARPLGLPRVLAPP
PEEAQKAKTPTPEPFDSETRKVVQMOCNLERSEDKARWHLTLLLVL EDRLHRQLTYDLLP
TDSAQDLAELVHYGFLHEDDRTKLA AFLETTFLKYRG TQA

SEQ ID NO: 183_NEK7_H, N34132_H

MSGGAAEKQSSTPGSLFLSPAPAPKNGSSSDSSVGEKLGAAAADAVTGRTEEYRRRRHT
MDKDSRGAAATTTTTEHRFFRRSVICDSNATALELPGLPLSLPQPSIPAAVPQSAPPEPH
REETVTATATSQVAQQPPAAAAPGEQAVAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPP
ARSGSGGSAKEPQEERSQQQDDIEELET KAVGMSNDGRFLKFDIEIGRSFKTVYKGLD
TETTVEVAWCELODRKLT KSERQRFKEEA EMLKGLQHPNIVRFYDSWESTVKGKKCIVLV
TELMTSGTLKTYLKRFKVMKI KVLRSWCRQILKGLQFLHTRTPLI IHRDLKCDNIFITGP
TGSVKIGDLGLATLKRASF AKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCMLEMATSEY
PYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEIIEGCIRQNKDERYSIKDLLNHAFQ
EETGVRVELAEEDDGEKIAIKLWLRIEDIKKLKGKYKDNEAIEFCFDLERDVPEDVAQEM
VESGYVCEGDHKTMAKAIKDRVSLIKRKREQRQLVREEQENKKQEESLKKQVEQSSASQ
TGIKQLPSASTGIPTASTTSASVSTQVEPEEPEADQHQQQLQYQQPSISVLSDGTVDSGQG
SSVFTESRVSSQQT VSYGFPXHEQA HSTGTVP GHI PSTVQAQSQPHGVYPPSSVQQGIQQ
TAPPQQT VQYSLSQTSTSS EATTAQPV SQPQAPQVLPQVSAGKQSTQGV SQVAPAEPVAV
AQPPATQPTTLASSVDSAHSDVASGMSDGNENVPSSSGRHEGRTTKRHYRKSVRSRHE
KTSRPKLRILNVSNKGD RVVECOLETHNRKMVT FKF DL DGDNP EEIATIMVN NDFILAIE
RESFVDQVREIIEKADEMLSEDVSVEPEGDQGL ES LQ GKDDYGFSGS QKLEGEFKQPIPA
SSMPQQIGIPTSSLTQVVHSAGRRFIVSPVPESRLRESKVFPSEITDTVAASTAQSPGMN
LSHSASSLSLQQA FSELRR AQMTGEPNTAPPNFSHTGPTFPVVPFLSSIAGVPTTAAAT
APVPATSSPPNDISTSVIQSEVTVPTEEG IAGVATSTG VVTSGGLPIPPVSESPVLSSV
SSITIPAVVSISTTSPSLQVPTSTSEIVVSSTALYPSVTVSATSASAGGSTATPGPKPPA
VVSQQAAGSTTVGATLTSVSTTTSFPSTASQLSIQLSSSTSTPTLAETVVVSAHSLDKTS

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FIGURE 1P

HSSTTGLAFSLSAPSSSSSPGAGVSSYISQPGGLHPLVIPSVIASTPILPQAAGPTSTPL
LPQVPSIPPLVQPVANVPAVQQTLIHSQPQALLPNQPHTHCPEVDSDTQPKAPGIDDIK
TLEEKLRSLFSEHSSSGAQHASVSLETSLVIESTVTPGIPTTAVAPSKLLTSTTSTCLPP
TNLPLGTVALPVTVPVTPGQVSTPVSTTTSGVKPGTAPSKPPLTKAPVLPVGTLPAGTL
PSEQLPFPFPGPSLTQSQQPLEDLDAQLRRTLSPEMITVTSVAVGPVSMAAPTAITEAGTQP
QKGVSVQKEGPVLATSSGAGVFKMGRFQVSVAADGAQKEGKNKSEDAKSVHFESSTSESS
VLSSSSPESTLVKPEPNGITIPGISSDVPESAHTTASEAKSDTGQPTKVGRFQVTTTAN
KVGRFSVSKTEDKITDTKKEGPVASPPFMDLEQAVLPAVIPKKEKPELSEPSHLNGPSSD
PEAAFLSRDVGSGSPHSPHQLSSKSLPSQNLSQLSNSFNSSYMSSDNESDIEDDLK
LELRRLRDKHLKEIQDLQSRQKHEIESLYTKLGKVP PAVIIPPAAPLSGRRRRRPTKSKGS
KSSRSSSLGNKSPQLSGNLGQSAASVLHPQOTLHPPGNI PESGQNQLLQPLKPSPSDN
LYSAFTSDGAI SVPSLSAPGQGNKATIIVQKQ

SEQ ID NO: 184_BCON3_H

MSEGESQTVLSSGSDPKVESSSAPGLTSVSPPVSTTTSAASPEEEEESEDESEILEESP
CGRWQKRREEVNQRNVPGIDSAYLAMDTEEGVEVWNEVQFSEKKNYKLQEEKVRAVFDN
LIQLEHLNIVKFHKYWADIKENKARVIFITEYMSGSLKQFLKKTCKNHKTMNEKAWKRW
CTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIKIGSVAPDTINNHVKTCEEQKNL
HFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNGGESSYVPQEAISSAIQLLEDPLQ
REFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAAHCIVGHQHMI PENALEEITKNM
DTSAVLAEIPAGPGREPVTLYSQSPALEDKFLLEDVRNGIYPLTAFGLPRPQQPQQEEV
TSPVVPSPVKTPTPEPAEVETR KVVLQM CNIESVEEGVKHHLTLLLKLEDKLNRLHSCDL
MPNENIPELAAELVQLGFI SEADQSRLTSLLEETLNKFNFNARNSTLNSAAVTVSS

SEQ ID NO: 185_AA711829_M

LKQFLKKTCKNHKTMNEKAWKRWCTQILSALSYLHSCDPPIIHGNLTCDTIFIQHNGLIK
IGSVAPDTINNHVKTCEEQKNLHFFAPEYGEVTNVTTAVDIYSFGMCALEMAVLEIQNG
GESSYVPQEAISSAIQLLEDLQREFIQKCLQSEPARRPTARELLFHPALFEVPSLKLAA
AHCIVGHQHMI PENALEEITKNMDTSAVLAEIPAGPGREPVTLYSQSPALEDKFLLEDV
RNGIYPLTAFGLPRPQQPQQEEVTSPVVPSPVKTPTPEPAEVETR KVVLQM CNIESVEEG
VKHHLTLLLKLEDKLNRLHSCDLMPNESIPDLAAELVQLGFI SEADQSRLTSLLEETLNK
FNFNTRNSTLNTATVTVSS

SEQ ID NO: 186_AA099102_H

MSSCVSSQPSSNRAAPQDELGGRGSSSSSESQKPCEALRGLSSLSIHLGMESFIVVTECEP
GCAVDLGLARDRPLEADGQEVPLDTSGSQARPHLSGRKLSLQERSQGGLAAGGSLDMNGR
CICPSLPYSPVSSPQSSPRLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYG VVK
LAYNENDNTYYAMKVLSKKKLIRQAAPRRPPPRGTRPAPGGCIQPRGPIEQVYQEIAIL
KKLDHPNVVKLVEVLDDPNEDHLYMV FELVNQGPVMEVPTLKLPLEDQARFYFQDLIKGI
EYLHYQKI IHRDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNYVGTPAFMAPESLS
ETRKIFSGKAKDVWAMGVTLYCFVFGQCPFMDERIMCLHSKI KSQALEFPDQPDIAEDLK
DLITRMLDKNPESRIVVPEIKLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENS VKHIP S
LATVILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESLSELKEARQRRQP
PGRHPAPRGGGGSALVRGSPCVESCWAPAPGSPARMHPLRPEEAMEPE

SEQ ID NO: 187_5R69_17_2_H

MQEIPQEIQEIKKEQLSGSPWILLRENEVSTLYKGEYHRAPVAIKVFKKLQAGSIAIVR
QTFNKEIKTMKKFESPNILRIFGICIDETVTPPQFSIVMEYCELGT LRELLDREKDLTLG

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FIGURE 1Q

KRMVLVLGAARGLYRLHHSEAPELHGKIRSSNFLVTQGYQVKLAGFELRKTQTSM SLGTT
REKTRVKSTAYLSPQELEDVFYQYDVKSEIYSFGIVLWEIATGDIPFQGECECDWLSQW
L

SEQ ID NO: 188_H85811_H
MAPVYEGMASHVQVFSPTLQSSAFCSVKKLKIEPSSNWDMTGYGSHSKVYSQSKNIPLS
QPATTTVSTSLPVPNPSLPYEQTIVFPGSTGHI VVTSASSTSVTGQVLGGPHNLMRRSTV
SLLDTYQKCGLKRKSEEIENTSSVQIIEEHPPMIQNNASGATVATATTSTATSKNSGSNS
EGDYQLVQHEVLCSMTNTYEVLEFLGRGTFGQVVKCWKRGTEIVAIKILKNHPSYARQG
QIEVSILARLSTESADDYNFVRAYECFQHKHNTCLVFEMLEQNLYDFLKQNKFSPLPLKY
IRPVLQQVATALMKLKSGLIHADLKPENIMLVDPSPRQPYRVKVIDFGSASHVSKAVCST
YLQSRYYRAPEIILGLPFCEAIDMWSLGCVIAELFLGWPLYPGDSEYDQIRYISQTQGLP
AEYLLSAGTKTTRFFNRDTSFYPLWRLKTPDDHEAETGIKSKEARKYIFNCLDDMAQVN
MTTDLEGSMDLVEKADRRFIDLLKKMLTIDADKRITPIETLNHPFVTMTHLDFPHSTH
VKSCFQNMIEICKRRVNMVDTVNQSKTPFI THVAPSTSTNLMTFNNQLTTVHNQPSAASM
AAVAQRSMPLQTGTAQICARPDPFQALIVCPPGFQGLQASPSKHAGYSVRMENAVPIVT
QAPGAQPLQIQPGLLAQQAWPSGTQQILLPPAWQQLTG VATHTSVQHATVI PETMAGTQQ
LADWRNTHAHGSHYNPIMQQPALLTGHVTLPAQPLNVGVAVHVMRQOPTSTTSSRKSQKH
QSSVRNVSTCEVSSSQAISSPQRSKRKVENTPPRCAMVHSSPACSTSVTCGWGDVASSTT
RERQRQTIVIPDTPSPTVSVITISSDTDEEEEQKHAPTSTVSKQRKNVISCVTVHDSPTS
DSSNTSPYSVQQRAGHNNANAFDTKGSLENHCTGNPRTIIVPPLKTQASEVLVECDSLV
PVNTSHHSSSYKSKSSSNVTSTSGHSSGSSSGAITRQQRPQPHFQQQQPLNLSQAQQHI
TTDRTGSHRRQQAYITPTMAQAPYSFPHNSPSHGTVHPHLAAAAAAHLPTQPHLYTYTA
PAALGSTGTVAHLVASQGSARHTVQHTAYPASIVHQVPVSMGPRVLPSPTIHPSQYPAQF
AHQTYISASPASTVYTGYP LSPAKVNQYPYI

SEQ ID NO: 189_DYRK3_H
MMIDETKCPPCSNVLCNPSEPPPPRRLNMTAEQFTGDHTQHFLDGGEMKVEQLFQEFGNR
KSNTIQSDGISDSEKCSPTVSQGKSSDCLNTVKSNSSSKAPKVPLTPEQALKQYKHHLT
AYEKL E I INYPEIYFVGPNAKKRHGVI GGPNNGGYDDADGAYIHVPRDHLAYRYEVLKII
GKGSFGQVARVYDHKL RQYVALKMVRNEKRFHRAAEEIRILEHLKKQDKTGSMNVIHML
ESFTFRNHVCMAFELLSIDL YELIKKNKFQGFVSQVLVRKFAQSILQSLDALHKNKI IHCD
LKPENILLKHHGRSSTKVIDFGSSCFEYQKLYTYIQSRFYRAPEIILGSRYSTPIDIWSF
RCILAE LLTGQPLFPGEDEGDQLACMMELLGMPPPKLLEQSKRAKYFINSKGI PRYCSVT
TQADGRVVLVGGRSRRGKKRGPPGSKDWGTALKGCDYLFIEFLKRCLHWDPSARLT PAQ
ALRHPWISKSVPRLTTIDKVS GKR VVN PASAFQGLGSKLPPVVG IANKL KANLMSETNG
SIPLCSVLPKLIS

SEQ ID NO: 190_AA589241_M DYRK3_M
TRPELLGMPPQKLLEQSKRAKYFINSKGLPRYCSVSTQTDGRVLLGGRSRRGKKRGPPG
SKDWATA LKGCGDYLFIEFLKRCLQWDPSARLT PAQALRHPWISKSTPKPLTMDKVP GKR
VVNPTNAFQGLGSKLPPVVG IASKL KANLMSETSGSIPLCSVLPKLIS

SEQ ID NO: 191_5R72_16_2_H
MAGGRGAPGRGRDEPPESYPQRQDHELQALEAIYGADFQDLRPDACPVKPEPPEINLVLY
PQGLTGEEVYVKV DLRVKCPPTYPDVVPEIELKNAKGLSNESVNLLKSRLEELAKKHCGE
VMIFELAYHVQSFLSEHNKPPPKSFHEEMLERRAQEEQQRLLEAKRKEEQEQREILHEIQ
RRKEEIKEEKKRKEMAKQERLEIASLSNQDHTSKKDPGGHRTAAI LHGGSPDFVGN GKHR
ANSSGRSRRERQYSVCNSEDSPGSC EILYFNMGSPDQLMVHKGKICGSDEQLGKLVYNAL
ETATGGFVLLYEWVLQWQKMGPF L TSQEKEKIDKCKKQIQGTETEFNSLVKL SHPNVVR

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FIGURE 1R

YLAMNLKEQDDSIIVDILVEHISGVSLAAHLSHSGPIPVHQLRRYTAQLLSGLDYLHSNS
VVHKVLSASNVLVDAEGTVKITDYSISKRLADICKEDVFEQTRVRFSDNALPYKTGKKGD
VWRLGLLLLLSLQGECEYPTIPSDLPADFQDFLKKCVCLDDKERWSPQQLLKHSFIN
PQPKMPLVEQSPEDSGGQDYVETVIPSRLPSAAFFSETQRQFSRYFIEFEELQLLGKGA
FGAVIKVQNKLDGCCYAVKRI PINPASRQFRRIKGEVTLLSRLHHENIVRYNAWIERHE
RPAGPGTPPPDSGPLAKDDRAARGQPASDTDGLDSVEAAAPPPILSSSVIEWSTSGERSAS
ARFPATGPGSSDDEDDDEHGGVFSQSFLPASDSESIIFDNEDENSKSQNQDEDCNEK
NGCHESEPSVTTEAVHYLYIQMEYCEKSTLRDITDQGLYRDTVRLWRLFREILDGLAYIH
EKGMIHRDLKPVNIFLDSDDHVKIGDFGLATDHLAFSADSKQDDQTDGLIKSDPSGHLTG
MVG TALYVSPEVQGSTKSAYNQKVDLFSLGIIFFEMSYHPMVTASERIFVLNQLRDPTSP
KFPEDFDDGEHAKQKSVISWLLNHDPKRPTATELLKSELLPPQMEESELEHVLHHTLT
NVDGKAYRTMMAQIFSQRISPAIDYTYDSILKGNFSIRTAKMQQHVCETIIRIFKRHGA
VQLCTPLLLPRNRQIYEHNEAALFMDHSGMLVMLPFDLRIPFARYVARNNILNLKRYCIE
RVFRPRKLD RFHPKELLECAFDIVTSTTNSFLPTAEIITYTIYEIIQEFPALQERNYSIYL
NHTMLLKAILLHCGIPEDKLSQVYIILYDAVTEKLTRREVEAKFCNLSSLSSNLCLRYKF
IEQKGDQLDLMPTINSLIKQKTGIAQLVKYGLKDLLEEVVGLLKLGLIKLOVLINLGLVYK
VQQHNGIIFQFVAFIKRRQRAVPEILAAGGRYDLLIPQFRGPQALGPVPTAIGVSIADK
ISAAVLNMEESVTISSCDLLVSVSGQMSMSRAINLTQKLWTAGITAEIMYDWSQSQEELQ
EYCRHHEITYVALVSDKEGSHVKVKSFEKERQTEKRVLETELVDHVLOKLRTKVTDERNQ
READNLAVQNLKGSFSNASGLFEIHGATVVPVIVSVLAPEKLSASTRRRYETQVQTRLQT
SLANLHQKSSEIEILAVDLPKETILQFLSLEWDADEQAFNTTVKQLLSRLPKQRYLKLVC
DEIYNIKVEKKVSVLFLYSYRDDYYRILF

SEQ ID NO: 192_R43524_H, HRI_H
MLGGNSGVRKREEEGDGAGAVAAPPAIDFPAEGPDPEYDESDVPAEIQVLKEPLQQPTFP
FAVANQLLLVSLLEHLSHVHEPNPLRSRQVFKLLCQTFIKMGLLSSFTCSDEFSSRLRH
NRAITHLMRSAKERVRQDPCEDISRIQKIRSREVALEAQT SRYLNEFEELVILGKGGYGR
VYKVRNKLDGQYYAIKKILIKGATKTVCMKVLREVKVLAGLQHPNIVGYHTAWIEHVHVI
QPRADRAAIELPSLEVLSDQEEDREQCGVKNDSSSSSIIFAEPTPEKEKRFGESDTENQ
NNKSVKYTTNLVIRESGELESTLELQENGLAGLSASSIVEQQPLRRNSHLEESFTSTEE
SSEENVNFLGQTEAQYHLMLHIQMQLCELSLWDWIVERNKRGREYVDESACPYVMANVAT
KIFQELVEGVFYIHNMGIVHRDLKPRNIFLHGPDQQVKIGDFGLACTDILQKNTDWTNRN
GKRTPHTTSRVGTCLYASPEQLEGSEYDAKSDMYSGLGVVLELFPFGTEMERAEVLTGL
RTGQLPESLRKRCPVQAKYIQHLTRRNSSQRPSAIQLLQSELFQNSGNVNLTLQMKIIEQ
EKEIAELKKQLNLLSQDKGVRDDGKGGVG

SEQ ID NO: 193_17000057519457_H
MAAARATTPADGEEPAPAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRTVQEARALLRCRRAGISAPVVFFVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFI SALPEDKGVLDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

SEQ ID NO: 194_AA013524_M
LVQQGAEARVFRGRFQGRAAVVKHRFPKSYRHPELEARLGRRTVQEARALLRCRRAGIA
APVVFFVDYASNCLYMEEIEDSVTVRDYIQSTMETEKDPQCLLDLARRMGQVLAMHDQD
LIHGDLTTSNMLLRPLAQLHIVLIDFGLSFSVGLPEDKGVLDLYVLEKAFLSTHPHTETA
FEAFLKSYGASSKKSSPVLKKLDEVRLRGRKRSMVG

FIGURE 1S

SEQ ID NO: 195_17000139801197_H, IRAKM_H
MAGNCGARGALSAHTLLFDLPALLGELCAVLDS CDGALGWRGLAERLSSSWLDVRHIEK
YVDQKGSGTRELLWSWAQKNKTIGDLLQVLQEMGHRRAIHLITNYGAVLSPSEKSYQEGG
FPNILFKETANVTVDNVLIPHEHNEKGVLLKSSISFQNIIEGTRNFHKDFLIGEGEIFEVY
RVEIQNLTYAVKLFKQEKMQCKKHWKRFLLSELEVLLLFHHPNILELAAYFTETEFKCLI
YPYMRNGTLFDRLQCVGDTAPLPWHIRIGILIGISKAIHYLHNVQPCSVICGSISSANIL
LDDQFQPKLTDFAMAHFRSHLEHQSTINMTSSSSKHLWYMPEEYIRQGKLSIKTDVYSF
GIVIMEVLTGCRVVLDDPKHIQLRDLRELMEKRGDLSCLSFDDKKVPPCPRNFSAKLFC
LAGRCAATRALKRPSMDEVLTNTLESTQASLYFAEDPPTSLKSFRCPSPLFLENVPSIPVE
DDESQNNNLLPSDEGLRIDRMTQKTPFECSQSEVMFLSLDKKPESKRNEEACNMPSSSCE
ESWFPKYIVPSQDLRPYKVNIDPSSEAPGHSCSRPVESSCSSKFSWDEYEQYKKE

SEQ ID NO: 196_AA840598_M IRAKM_M
MWKRFLSELEVLLLFRRHPHILELAAYFTETEFKLCVYPYMSNGTLFDRLQCTNGTTPLSW
HVRISVLIGIAKAIQYLHNTQPCAVICGNVSSANILLDDQLQPKLTDFAAAHFRPNLEQQ
SSTINMTGGGRKHLWYMPEEYIRQGRLSVKTVDVYSFGIVIMEVLTGCKVVLDDPKHVQLR
DLLMELMEKRGDLSCLSFDRKIPPCPRNFSAKLFSLAGRCVATKAKLRPTMDEVLSLE
STQPSLYFAEDPPTSLKSFRCPSPLFLDNVPSIPVEDDENQNNHVSPPKEVLGTDRVTQK
TPFECSQSEVTLGLDRNRGNRGSEADCNVPSSSHEECWSPELVAPSQDLSPTVISLGGSS
WEVPGHSYGSKPMEKRCSSGLFCSEHEQSKKQ

SEQ ID NO: 197_AA088547_H
MASAVRGSRPWPRLGLQLQFAALLGLTSPQVHTLRPENLLLSTLDGSLHALSKQTGDL
KWTLRDDPVIEGPMYVTEMAFLSDPADGSLYILGTQKQGLMKLPFTIPELVHASPCRSS
DGVFYTGRRQDAWFVDPESGETQMTLTTEGPSTPRLYIGRTQYTVTMHDPRAPALRWNT
TYRRYSAPPMDGSPGKYM SHLASCGMGLLLTVDPGSGTVLWTQDLGVPVMGVYTWHDGL
RQLPHLT LARDTLHFLALRWGHIRLPASGPRDTATLFTSLDTQLLMTLYVGKDETGFYVS
KALVHTGVALVPRGLTLAPADGPTTDEVTLQVSGEREGSPSTAVRYPGSGVALPSQWLLI
GHHELPPVLHTTMLRVHPTLGSGTAETRPENTQAPAFFLELLSLSREKLWDSELHPEEK
TPDSYLG LGPQDLLAASLTAVLLGGWILFVMRQVVEKQOETPLAPADFAHISQDAQSLHS
GASRRSQKRLQSPSKQAQPLDDPEAEQLTVVGKISFNPKDVLGRGAGGTFVFRGQFEGRA
VAVKRLRLRECFLVRREVQLLQESDRHPNVLRYFCTERGPQFHYIALELCRASLQEYVEN
PDLDRGGLEPEVVLQQLMSGLAHLHSLHIVHRDLKPGNILITGPD SQGLGRVVLSDFGLC
KKLPAGRCFSLSHSGIPGTEGWMAPELLQLLPDSPTS AVDIFSAGCVFYVLSGGSHPF
GDSLYRQANILTGAPCLAHLEEEVHDKVVARDLVGAMLSPLPQPRPSAPQVLAHPFFWSR
AKQLQFFQDVSDWLEKESEQEPLVRALEAGGCAVVRDNWHEHISMPLOTDLRKFRSYKGT
SVRDLLRAVRNKKHHYREL PVEVRQALGQVPDGFVQYFTNRFPRLLLHTHRMRSCASES
LFLPYYPDPSEARRPCPGATGR

SEQ ID NO: 198_HGP_6644466
MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTGVNVYLMKRSRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGE
KSLNDLIEERYKASQDPFPAAILKVALNMARGLKYLHQEKLLHGDIKSSNVVIKGDFFE
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVI TDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDDEDKTFDESDFDDEAYYAALGTRPPINMEELDES YQKVIELFSVC
TNEDPKDRPSAAHIVEALET DV

SEQ ID NO: 199_AA449542_M
SPRGLSHSPWAVKKISLLCDDHYRTVYQKRLTDEAKILKLNHPNIIGYRAFTEASDGSL
CLAMEYGGESLNDLIEERNKDSGSPFPAAVILRVALHMARGLKYLHQEKLLHGDIKSS

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FIGURE 1T

NVVIKGFETIKICDVGVSLPLDENMTVTDPEACYIGTEPWKPKEALEENGIITDKADV
AFGLTLWEMMTLCIPHVNLPDDVDDEATFDESDFDDEAYYAALGTRPSINMELDDSYQK
AIELFCVCTNEDPKDRPSAAHIVEALELDGQCCGLSESKH

SEQ ID NO: 200_5R57_10_2_M TESK2_M
LLDSDLYLPWTVRVKLAYGIAVGLSYLHFKGIFHRDLTSKV

SEQ ID NO: 201_AA232253_H
MSSLGASFVQIKFDDLQFFENC GGSGSVYRAKWISQDKEVAVKLLKIEKEAEILSVL
SHRNIIQFYGVILEPPNYGIVTEYASLGSLYDYINSNRSEEMDMDHIMTWATDVAKGMHY
LHMEAPVKVIHRDLKSRNVVIAADGVLKICDFGASRFHNHTTHMSLVGTFFPWMAPEVIQS
LPVSETCDTYSYGVVLWEMLTREVFPKGLEGLQVAWLVEKNERLTIPSSCPRSFAELLH
QCWEADAKKRPSFKQIIISILESMSNDTSLPDKNSFLHNKAEWRCIEATLERLKKLERD
LSFKEQELKERERRLKMWEQKLTEQSNTPLLPSFEIGAWTEDDVYCWVQQLVRKGDSSAE
MSVYASLKFENNITGKRLLLLLEEDLDKDMGIVSKGHIHFKSAIEKLTHDYINLFHFPPL
IKDSGGEPEENEEKIVNLELVFGFHLKPGTGPQDCKWKMYMEMDGDIEAITYIKDVTFTNT
NLPDAEILKMTKPPFVMEKWI VGI AKSQTVECTVYESDVRTPKSTKHVHLIQWSRTKPQ
DEVKAVQLAIQTLFTNSDGNPGSRSDSSADCQWLDTLMRQIASNTSLQRSQSNPILGSP
FFSHFDGQDSYAAAVRRPQVPIKYQQITPVNQSRSSSPTQYGLTKNFSSLHLNSRDSGFS
SGNTDTSSERGRYSDRSRNKYGRGSI SLNSSPRGRYSGKSQHSTPSRGRYPGKFYRVSQS
ALNPHQSPDFKRSPRDLHQPNITPGMPLHPETDSRASEEDSKVSEGGWTKVEYRKKPHRP
SPAKTNKERARGDHRGWRNF

SEQ ID NO: 202_AI375137_H
MGNYKSRPTQTCTDEWKKVSESYVITIERLEDDLQIKEKELTELNRNIFGSDEAFSKVNL
NYRTENGLSLLHLCCICGKKSHIRTLMLKGLRPSRLTRNGFTALHLAVYKDNAELITSL
LHSGADIQQVGYGGLTALHIATIAGHLEAADVLLQHGANVNIQDAVFFTPLHIAAAYGHE
QVTRLLLKFGADVNVSGEVGDRPLHLASAKGFLNIAKLLMEEGSKADVNAQDNEDHVPLH
FCSRFGHHDIVKYLLQSDLEVQPHVVNIYGDTPHLACYNKGFEVAKEIIQISGTESLTK
ENIFSETAFHSACTYGKSIDLKFLLDQNVININHQGRDGHTGLHSACYHGHIRLVQFLL
DNGADMNLVACDPSRSSGEKDEQTCMLWAYEKGHDAIVTLLKHYKRPQDELPCNEYSQPG
GDGSYVSVPSPLGKIKSMTKEKADILLRAGLP SHFHLQLSEIEFHEIIGSGSFGKVYKG
RCRNKIVAIKRYRANTYCSKSDVDMFCREVSILCQLNHPCVIQFVGACLN DPSQFAIVTQ
YISGGSFLSLLHEQKRILDLQSKLIIAVDVAKGMEYLHNLTQPIIHRDLNSHNILLYEDG
HAVVADFGESRFLQSLDEDNMTKQPGNLRWMAPEVFTQCTRYTIKADVFSYALCLWEILT
GEIPFAHLKPAAAAADMAYHHIRPPIGYSIPKPISSLLIRGWNACPEGRPEFSEVVMKLE
ECLCNIELMSPASSNSSGSLSPSSSSDCLVNRGGPGRSHVAALRSRFELEYALNARSYAA
LSQSAGQYSSQGLSLEEMKRSLQYTPIDKYGYVSDPMSSMHFHSRNSSSSFEDSS

SEQ ID NO: 203_H97685_H
MESERSPLYRQLIDLGYLSSSHWNCGAPGQDTKAQSMLEQSEKLRHLSTFSHQVLQTRL
VDAAKALNLVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMNIANRKQEE
MKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEVGTREIKCCIRQIQELIISRLNQA
VANKLISSVDYLRESFVGTLERCLQSLEKSQDVSVHITSNYLKQIILNAAHYHVEVTFHSGS
SVTRMLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAKSICSQFRTRLNS
SHEAFAASLRQLEAGHSGRLEKTEDLWLRVRKDHAPRLARLSLESRLQDVLHLHRKPKLG
QELGRGQYGVVYLCDNWGGHFPKALKSVVPPDEKHWNDLALFHYMRSLPKHERLVDLHG
SVIDYNYGGGSSIAVLLIMERLHRDLTYTGLKAGLTLETRLQIALDVVEGIRFLHSQGLVH
RDIKLNVLDDKQNRKITDLGFCCKPEAMMSGSI VGTPIHMAPELFTGKYDNSVDVYAFG

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FIGURE 1U

ILFWYICSGSVKLPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDGDPLK
RPLLGI VQ PMLQGIMNRLCKSNSEQPNRGLDDST

SEQ ID NO: 204_W20810_M

DVNLKASKASDVYSFGILVWAVLAGREAELVDKTSLIRETVCDRQSRPPLTELPPGSPET
PGLEKLKELMIHCWGSQSENRP SFQDCEPKTNEVYNLVKDKVDAVSEVKHYLSQHRSSG
RNLSAREPSQRGTEMDCPRETMVSKMLDRHLHEEPSGVPVPGKCPERQAQDTSVGPATPAR
TSSDPVAGTPQIPHTLPFRGTTGPGVFTETPGPHQQRNQGDRHGTPWYPWTPPNPMTGP
PALVFNNCSEVQIGNYNLSLVAPPRTTASSSAKYDQAQFGRGRGWQPFHK

SEQ ID NO: 205_AA744236_H

MGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYKRENEDKVNKAAKHLKTL
RHPCLLRFLSCTVEADGIHLVTERVQPLEVALETLSAEVCAGIYDILLALI FLHDRGHL
THNNVCLSSV FVSE DGHWKLGGMETVCKVSOATPEFLRSIQSIRDPASIPPEEMSPEFTT
LPECHGHARDAFSFGTLVESLLTILNEQVSADVLSSFQOTLHSTLLNPI PKCRPALCTLL
SHDFFRND FLEV NFLKSLTLKSEEEKTEFFKFLDRVSC LSEELIASRLVPLLLNQLVF
AEPVAVKSFLPYLLGPKKDH AQGETPCLLSPALFQSRVIPVLLQLFEVHEEHVRMVLLSH
IEAYVEHFTQEQLKKVILPQVLLGLRDTSDSIVAITLHSLAVLVSLLGPEVVVGGERTKI
FKRTAPSFTKNTDLSLEGDPFSQPIKFPINGLSDVKN TSEDS ENFPSSSKKSEEPDWSE
PEEPENQTVNIQIWPREPCDDVKSQCTTLDVEESSWDDCEPSSLDTKVNPGGGITATKPV
TSGEQKPIPALLSLTEESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSELG
LGEEFTIQVKKKPKVDPEMDWFADMIPEIKPSAAFLILPELRTMVPKDDVSPVMQFSS
KFAAAEITEGEAEGWEEEGELNWNEDNNW

SEQ ID NO: 206_AI052250_H

MESMLNKLKSTVTKVTADVTSAVMGIPVTREFDVGRHIASGCNGLAWKIFNGTKKSTKQE
VAVFVFDKKLIDKYQKFEDQIIDSLKRGVQQLTRLRHPRLTLVQHPLEESRDCLAFCTE
PVFASLANVLGNWENLPSPISPDIKDYKLYDVETKYGLLQVSEGLSFLHSSVKMVHGNIT
PENIILNKSGAWKIMGFDFCVSSTNPSEQEPKFPCKEWDPNLP SLCLPNPEYLAPEYILS
VSCETASDMSYSLGTVMYAVFNKGKPIFEVNKQDIYKFSRQLDQLSRLGSSSLTNIPEEV
REHVKLLLNVTPTVRPDADQMTKIPFFDDVGAVTLQYFDTL FQRDNLQKSQFFKGLPKVL
PKLPKRIVIVQRILPCLTSEFVNPDMPFVLPNVLLIAEECTKEEYVKLILPELGPVFKQQ
EPIQILLIFLQKMDLLLTKTPDEIKNSVLP MVYRALEAPSIQIQELCLNI IPTFANLID
YPSMKNALIPRIKNACYKHLPLRFV

SEQ ID NO: 207_AA278842_H

MWFFARDPVRDFFELIPEPPEGGLPGPWALHRGRKKATGSPVSI FVYDVKPGAEEQTQV
AKAAFKRFKTLRHPNILAYIDGLETEKCLHVTEAVTPLGIYLKARVEAGGLKELEISWG
LHQIVKALSFLVNDCSLIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQNGGGPPRKGIPE
LEQYDPPELADSSGRVVREKWSADMWRLGCLIWEVFNGLPLPRAAALRNPGKIPKTLVPHY
CELVGANPKVRPNPARFLQNCRAPGGFMSNRFVETNLFLEEIQIKEPAEKQKFFQELSKS
LDAFPEDFCRHKVLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYQOKIIPVVVKMFSS
TDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGF LDTNPAIREQTVKSMLLLAPKLN
EANLNVELMKHFARLQAKDEQGPIRCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPF
APSRVAGVLGFAATHNLYSMNDCAQKILPVLCGLTVDP EKSVRDQAFKAIRSFLSKLESV
SEDPTQLEEVEKDVAHAASSPGMGGAASWAGWAVTGVSSLT SKLIRSHPTTAPTETNIPQ
RPTPEGVPAPAPTVPATPTTSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVL
AQQDDWSTGGQVSRASQVSNSDHKSSKSPESDWSSWEAEGSWEQGWQEPSSQEP PPDGTR
LASEYNWGGPESD KGD PFATLSARPSTQPRPDSWGEDNWEGLETD SRQVKAELARKKRE
ERRREMEAKRAERKVAKGPMKLGARKLD

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FIGURE 1V

SEQ ID NO: 208_AA599286_H

MAFMEKPPAGKVLLDDTVPLTAAIEASQSLQSHTEYIIRVQGGISVENSWQIVRRYSDFD
LLNNSLQIAGLSLPLPPKKLIGNMDREFIAERQKGLQNYLNVITTNHILSNCELVKKFLD
PNNYSANYTEIALQQVSMFFRSEPKWEVVEPLKDIGWRIRKKYFLMKIKNQPKERLVLSW
ADLGPDKYLSKDFQCLIKLLPSCLPYIYRVTFATANESSALLIRMFNEKGTLKDLIYK
AKPKDPFLKKYCNPKKIQGLELQQIKTYGRQILEVLKFLHDKGFPYGHLSASNVMLDGD
CRLLDLENSLLGLPSFYRSYFSQFRKINTLESVDVHCFGHLLYEMTYGRPPDSVPVDSFP
PAPSMVAVVLESTLSCEACKNGMPTISRLLQMPFLSDVLLTTSEKPQFKIPTKLKEALR
IAKECIEKRLIEEQQIHHQRRRLTRAQSHHGSEEERKKRKILARKKSKRSALENSEEHS
KYSNSNNSAGSGASSPLTSPSSPTPPSTSGISALPPPPPPPPPPAAPLPAPASTEAPQALS
SQAVNGMSRGALLSSIQNFQKGTLRKAKPVITVLRSAEASCLHLEGKVLFYSSPLPPN
YPLPGKVIAEPVQPQTVLFCRCCKQLFERNNSLSRIKLGWHAKKKKKK

SEQ ID NO: 209_AA425725_H

MSASTGGGGDSGGSGSSSSSQASCPRESSGSELALATPVPQMLQGLLGSDDEEQEDPKD
YCKGGYHPVKIGDVFNTRYHVVRKLGWGHFSTVWLCWDIQRKRFVALKVKSAGHYTETA
VDEIKLLKCVRDSDPSDPKRETIVQLIDDFRISGVNGVHVCMVLEVLGHQLLKI I KSNY
QGLPVPVKSIVRQVLHGLDYLHTKCKI IHTDIKPENILLCVGDYAIRRLAAEATEWQQA
GAPPPSRISIVSTAPQEVLTGKLSKNKRKKMRKRKQKRLLEERLRDLQRLEAMEAATQA
EDSGLRLDGGSGSTSSSGFSGLSPASCSILSGSSNQRETGGLLSPSTPFGASNLLVNP
LEPQNADKIKIKIADLGNACWVHKHFTEDIQTRQYRAVEVLIGAEGPPADIWSTACMAF
ELATGDYLFEPHSGEDYSRDEDHIAHIVELLGDI PPAFALSGRYSREFFNRRGELRHIHN
LKHGGLYEVLMEKEYEWPLEQATQFSAFLLPMMEYIPEKRASAADCLQHPWLN

SEQ ID NO: 210_SGK022_H

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSCKKHQRKVAIKVIDKMGGPSEFIQRFLPRELQ
IVRTL DHKNI IQVYEMLESADGKICLVMELEAGGDVFDVNLGGPLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFPAKVLPSKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLSISADCQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 211_AA060026_M SGK022_M

MEDFLLSNGYQLGKTIGEGTYSKVKEAFSCKKHQRKVAIKI IDKMGGPEEFIQRFLPRELQ
IVRTL DHKNI IQVYEMLESADGKI YLMELAEAGGDVFDVNLGGPLPESRAKALFRQMV
AIRYCHGCGVAHRDLKCENALLQGFNLKLTDFGFPAKVLPSKSHRELSQTFCGSTAYAAPEV
LQGI PHDSKKGDVWSMGVVLYVMLCASLPFDDTDIPKMLWQQQKGVSPFTHLGISTECQD
LLKRLLEPDMILRPSIEEVSWHPWLAST

SEQ ID NO: 212_AA399669_H

MGKGDVLEAAPT TTTAYHSLMDEYGYEVGKAIGHGSYGSVYEAFTKQKVMVAVKIISKKK
ASDDYLNKFLPREIQQVMKVL RHKYLINFYRAIESTSRVYIILELAQGGDVLEWIQRYGA
CSEPLAGKWFSQTLGLIAYLHKSIVHRDLKLENLLLDKWENVKISDFGFPAKVMVPSNQPV
GCSPXYRQVNCFSHLSQTYCGSFAYACPEILRGLPYNPFLSDTWSMGVILYTLVVAHLPF
DDTNLKKLLRETQKEVTFPANHTISQECKVQLLIACVAQWRKTQARPLSPLL

SEQ ID NO: 213_AA758539_H

MDDATVLRKKGYIVGINLGKGSYAKVKSAYSERLKFNVAVKIIDRRKTPTDFVERFLPRE
MDILATVNHGSIKTYEIFETSDGRIYIIMELGVQGDLLFEIKCQGALHEDVARKMFRQL
SSAVKYCHDLDIVHRDLKCENLLLDKDFNIKLSDFGFSKRCLRDSNGRIILSKTFCGSAA

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FIGURE 1W

YAAPEVLQSI PYQPKVYDIWSLGVILYIMVCGSMPYDDSDIRKMLRIQKEHRVDFPRSKN
LTCECKDLIYRMLQPDVSQLHIDEILSHSWLQPPKPKATSSASFKEGEGKYRAECKLD
TKTGLRPDHRPDHKLGAKTQHRLLVVPENENRMEDRLAETSRAKDHHS GAIEVGKAST

SEQ ID NO: 214_AA883975_H

MSGDKLLSELGYKLGRTIGEGSYSKVKVATSKKYKGTVAIKVVDRRRAPPDFVNKFLPRE
LSILRGVRPHPHIVHVFIEVCNGKLYIVMEAAATDLLQAVQRNGRIPGVQARDLFAQIA
GAVRYLHDHHLVHRDLKCENVLLSPDERRVKLTDFGFGRAHGYPDLSSTTYCGSAAYASP
EVLLGIPYDPKKYDVWSMGVVLVYVMVTGCMFPDDSDIAGLPRRQKRGVLYPEGLELSERC
KALIAELLQFSPSARPSAGQVARNCWLRAGDSG

SEQ ID NO: 215_AA905446_H

VGRQETGVRRWAFLICQPI SPPLTSSEFIQRFLPRELQIVRTL DHKNI IQVYEMLESADG
KICLVMELAEAGGDVFDVCLNGGPLPESRAKALFRQMVEAIRYCHGCGVAHRDLKCENALL
QGFNLKLTDFGFAKVLPKSHRELSQTF CGSTAYAAPEVLQGI PXKMLWQQQKGVSFPTH
SISADCQDLLKRLLEPDMILRPSIEEVS WHPWLAST

SEQ ID NO: 216_H29974_H

YSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVELALAEFWALTSLKRRHQNV
VQFEECVLQRNGLAQRM SHGNKSSQLYLRLVETSLKGERILGYAEPCYLWFMVMEFCEGG
DLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLKPDNILITERSGTPILKVAD
FGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYMAPEVWEGHYTAKADIFALG
IIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLENPKMELHIPQKRRTSMSEG
IKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 217_AA498104_M H29974_M

PLLLPPPPAAMETGKENGARRGTKSPERKRRSPVQRVLCEKLRPAAQAMDPAGAEVPGEA
FLARRRPDGGGGDVPARPRYSLLAIEIGRGSYGVVYEAVAGRSGARVAVKKIRCDAPENVE
LALAEFWALTSLKRRHQNVQFEECVLQRNGLAQRM SHGNKNSQLYLRLVETSLKGERIL
GYAEPCYLWFMVMEYCEGGDLNQYVLSRRPDPATNKSFMLQLTSAIAFLHKNHIVHRDLK
PDNILITERSGTPILKVADFGLSKVCAGLAPRGKEGNQDNKNVNVN KYWLSSACGSDFYM
APEVWEGHYTAKADIFALGIIIWAMIERITFIDSETKKELLGTIYIKQGT EIVPVGEALLE
NPKMELHIPQKRRTSMSEGVKQLLKDMLAANPQDRPD AFELETRMDQVTCAA

SEQ ID NO: 218_AA215311_H

MVSSQPKYDLIREVGRGSYGVVYEAVIRKTSARVAVKKIRCHAPENVELALREFWALSSI
KSQHPNVIHLEECILQKDMVQKMSHGSNSSLYLQLVETSLKGEIAFDPRSAYYLWFMVMD
FCDGGDMNEYLLSRKPNRKTNTS FMLQLSSALAFHKNQIIHRDLKPDNILISQTRLDT
DLEPTLKVADFGLSKVCSASGQNPEEPVSVNKCFLSTACGTDFYMAPEVWEGHYTAKADI
FALGIIIWAMLERITFIDTETKKELLGSYVKQGT EIVPVGEALLENPKMELLI PVKKKSM
NGRMKQLIKEMLAANPQDRPD AFELELRVLVQIAFKDSSWET

SEQ ID NO: 219_AA018361_H

MRAAFPAGGAGGSVEPPSARPAPQAGTAARSEEAPARAQAAGMAGPGWGPPRLDGFILT
ERLGS GTYATVYKAYAKD TREVVAIKCVAKKSLNKASVENLLTEIEILKGI RHPHIVQL
KDFQWSDNIYLIMEFCAGGDL SRFIHTRRILPEKVARVFMQQLASALQFLHERNISHLD
LKPQNILLSSLEKPHLKLADFGFAQHMS PWDEKHVLRGSPLYMAPEMVCQRQYDARVDLW
SMGVILYEALFGQPPFASRSFSELEEKIRSNRVIELPLRPLLSRDCRDLLQRLLERDPSR
RISFQDFFAHPWVDLEHMPSGESLGRATALVVQAVKKDQEGDSAAALS LYCKALDFFVPA

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FIGURE 1X

LHYEVDAQRKEAIKAKVGQYVSRAEELKAIVSSSNQALLRQGTSARDLLREMARKDKPRLL
AALEVASAAMAKEEAAGGEQDALDLYQHSLGELLLLLRSPRAGGGSCFTLRFRTSWPEN
T

SEQ ID NO: 220_AA311714_H

MENFILYEEIGRGSKTIVYKGRRKGTINFVAILCTDKCRRPEITNWVRLTREIKHKNIVT
FHEWYETSNHLWLXENLPEDVVREFGIDLISGLHHLHKLGLFCDISPRKILLEGPGTL
KFSNFCLAKVEGENLEEFFALVAAEEGGDNGENVLKKSMKSRVKGSPVYTAPEVVRGAD
FSISSDLWSLGCCLLYEMFSGKPPFFSESVSELTEKILCEDPLPPIPKDSSRPKASSDFIN
LLDGLLQORDPQKRLTWTRLLQHSFWKKAFAAGADQESSVEDLSLSRNTMECSGPQDSKELL
QNSQSRQAKGHKSGQPLGHSFRLENPTFRPKSTLEGQLNESMFLSSRPTPTSTAVEV
SPGEDMTHCSPQKTSPLTKITSGHLSQODLESQMRELIYTDSDLVVTPIIDNPKIMKQPP
VKFDAKILHLPTYSVDKLLFLKDQDWNDFLQQVCSQIDSTEKSMGASRAKLNLLCYLCVV
AGHQEVATRLLHSPFLFQLLIQHLRIAPNWDIRAKVAHVIGLLASHTTELQENTPVVETTS
SIGIGILNCLVQHSTPVPQRQCLVYV

SEQ ID NO: 221_SGK384_H

SLAHVLRARQILTEPEVRDYLRLGLVSGRLRYLHQRCILHR

SEQ ID NO: 222_AA210451_M SGK384_M

MGQQHGTNRNGLTHRELPRGVGLLLAMALMNVALYLCLDQLFISPRSTADSRRCPGYYFR
MGRMRNCSRWLSCEELRTEVRQLKRVGEGAVKRVFLSEWKEHKVALSRLTRLEMKEDFLH
GLQMLKSLQSEHVVTLVGYCEEDGTILTEYHPLGSLSNLEETLNLISKYQDVNTWQHRLQL
AMEYVSIINYLHHSPLGTRVMCDSDNDLPKTLISQYLLTSNFSIVANDLDALPLVDHDSGV
IKCGHRELHGDFVAPEQLWPYGEDTPFQDDLMPSYNEKVDIWKIPDVSSFLLGHVEGSDM
VRFHLFDIHKACKSQIPAERPTAQNVLDAYQRVFHSRLRDTVMSQTKEML

SEQ ID NO: 223_SGK071_2_H

EVVAVQMMVECMDDHYASQALEELMPLLLKLRHAHISVYQELFITWNGEISSLYLCLVMEF
NELSFQEVIEDKRKAKKIIDSEWMQNVLGQVLDALAYLHHLDIHRNLKPSNIIILISSDH
CKLQDLSSNVLMTDKAKWNIRAEEDPFRKSWMAPEALNFSFSQKSDIWSLGCIIIDMTSC
SFMDGTEAMHLRKSRLRQSPGSLKAVLKTMEEKQIPDVETFRNLLPLMLQIDPSDRITIKD
VVHITFLRGSFKSSCVSLTLHRQMVPAITDMLLEGNVASILGDAGDTKGERALKLLSMA
LASYCLVPEGSLFMPLALLHMHQDQWLSQDQDRVPGKRDFAVLGKLGLLGPPIPKGLPWPP
ELVEVVVTTMELHDRVLDVQLCACSLLLHLLGQALVHHPEAKAPCNQAITSTLLSALQSH
PEEEPLVMVYSLLAITTTQESSESLSEELQNALGLEHILEHLNSSLERDVCASGLGLLW
ALLLDDPILALQRPRKKRAPNHGKPGKPKNPASTQSIIVNKAPLEKVPDLISQVLATYPA
DGEMAEASCGVFWLLSLLGCIKEQQFEQVVALLLQSIRLCQDRALLVNNAYRGLASLVKV
SELAAFKVVVQEEGSGLSLIKETYQLHRDDPEVVENVGMLLVHLASYEEILPELVSSSM
KALLQEIKERFTSSLVSDSSAFSKPGLPPGGSPQLGCTTSGGLE

SEQ ID NO: 224_AA118352_M SGK071_M

EEDPCQKSWMAPEALKFSFSTKSDIWSLGCIIIDMATCSFLNDTEAMQLRKAIRHHPGSL
KPIILKTMEEKQIPGTDVYYLLLPFMLHINPSDLAIKDVMQVTFMNSFKSSSVLNMQR
QKVPIFITDVLLEGNMANILGSWLCASFVNDNRHCDSGIGSQRLGDFQSVSWTEHPLKD
VMQNFSSRPEVQLRAINKLLTMPEDQLGLPWPTELLEVISIIKQHGRILDILLSTCSLL
LRVLGQALAKDPEAEIPRSSLIISFLMDTLRSHPNSERLVNVVYNVLAIISSQGQISEEL
EEEGFLQLAQENLEHFQEDRDICLSILSLLWSLLVDVVTVDKEPLEQLSGMVTWVLATHP
EDVEIAEAGCAVLWLLSLLGCIKESQFEQVVVLLLSIQLCPGRVLLVNNAFRGLASLAK

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FIGURE 1Y

VSELVAFRIVVLEEGSSGLHLIQDIYKLYKDDPEVVENLCMLLAHLTSYKEILPEMESGG
IKDLVQVIRGRFTSSLELISYADEILQVLEANAQPGLOEDQLEPPAGQEAPLQGEPLFRP

SEQ ID NO: 225_018653.9_H

GRGRGAGHARGLGRGPAGRRAEPPRSLSRPGPGPGSRAGPAGRGEESDAAPAGGSGRGFL
RLLPAGLRPQRALRSGSEPPRPGQSPEPSAPGAGRRGGRGELARQIRARYEEVQRYSRG
GPGPGAGRPERRRMLDLAPGGPGLPRPRPPWARPLSDGAPGWPPAPGPGSPGPGPRLGCA
ALRNVSGAQYMGSGYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGVRRGCYRLAA
HKLLKEMVLLERLRHPNVLQLYGYCYQDSEDIPTLTITITELGAPVEMIQLLQTSWEDRF
RICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVDGELKVTDLDDARVEETPCAGSTDCI
LEFPARNFTLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSIVNATGE
LAWGVDETLAQLEKVLHLYRSGQYLQNSTASSSTEYQCIPDSTIPQEDYRCWPSYHHGSC
LLSVFNLAEADVCESHAQCRAFFVTNQTWTGRQLVFFKTGWSQVVPDPNKTTYVKASG

SEQ ID NO: 226_AA396601_M

TRPGCAALRNVSGAQYVGSYTKAVYRVRLPGGAVALKAVDFSGHDLGSCVREFGARRG
CYRLAAHKLLKEMVLLERLRHPNVLQLYGYCYQDSEGIPTLTITITELGAPVEMIQLLQTS
SWEDRFRICLSLGRLLHHLAHSPLGSVTLLDFRPRQFVLVNGELKVTDLDDARVEETPCT
SSADCTLEFPARNFSLPCSAQGWCEGMNEKRNLYNAYRFFFTYLLPHSAPPSLRPLLDSI
VNATGELAWGVDETLAQLETALHLFRSGQYLQNSTSSRAEYQRIIPDSAITQEDYRCWPSY
HHGGCLLSVFNLAEAIDVCESHAQCRAFFVTNQTWTGRKL VFFKTGWNQVVPDAGKTTY
VKAPG

SEQ ID NO: 227_VRK3_H

MISFCPCGKSIQAAFKFCPYCGNSLPVEEHVGSQTFVNPHVSSFQGSKRGLNSSFETSP
KKVKWSSTVTSRPLSLFSDGDSSEEDTLSSSERSKSGSGSRPPTPKSSPQKTRKSPQVTR
GSPQKTSCSPQKTRQSPQTLKRSRVTTSLALPTGTVLTDKSGRQWKLSFQTRDNQGIL
YEAAPTSTLTCDSGPQKQKFSKLDAKDGRLFNEQNFFQRAAKPLQVNWKKLYSTPLLA
IPTCMGFGVHQDKYRFLVLP SLGRSLQSA LDVSPKHVLSERSVLQVACRLLDAL EFLHEN
EYVHGNVTAENIFVDPEDQSQVTLGAGYGAFRYCPSGKHVAYVEGSRSPHEGDLEFI SMD
LHKGCGPSRRSDLQSLGYCMLKWLYGFLPWTNCLPNTEDIMKQKQKFVDKPGPFVGP CGH
WIRPSETLQKYLKVVMALTYEEKPPYAML RNNLEALLQDLRVSPYDPIGLPMVP

SEQ ID NO: 228_S71575_M VRK3_M

IPTCIGFGIHQDKYRFLVFP SLGRSLQSA LDDNPKHVVSERCVLQVACRLLDAL EY LHEN
EYVHGNLTAENVFVN PEDLSQVTLVGYGFTYRYCPGGKHVAYKEGSRSPHDGDLEFI SMD
LHKGCGPSRRSDLQTLGYCMLKWLYGSLPWTNCLPNTTEKITRQKQKYLDSPERLVGLCGR
WNKASETLREYLKVVMALNYEEKPPYATLRNSLEALLQDMRVSPYDPLDLQ MVP

SEQ ID NO: 229_AA45427_H

MGHALCVCSRGTVIDNKR YLF IQKLGE GGF SYVDLVEGLHDGHFYALKRILCHEQQDRE
EAQREADMHRLFNHPNILRLVAYCLRERGAKHEAWLLL PFFKRGTLWNEIERLKDKGNFL
TEDQILWLLGICRGLEAIHAKGYAHRDLKPTNILLGDEGQPVLM DLGSMNQACIHVEGS
RQALTLDWAAQRCTISYRAPELFSVQSHCVIDERTDVWSLGCVL YAMMFGE GPYDMVFQ
KGDSVALAVQNQLSIPQSPRHSSALRQLLNSMMTVDPHQRP H I PLLLSQLEALQPPAPGQ
HTTQI

SEQ ID NO: 230_H05721_H

MAVRQALGRGLQLGRALLLRFTGKPGRAYGLGRPGPAAGCVRGERPGWAAGPGAEP RRVG
LGLPNRLRFFRQSVAGLAARLQRQFVVRAGCAGPCGRAVFLAFLGLGLIEEKQAESRR

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FIGURE 1Z

AVSACQEIQAIF TQKSKPGPDPLDTRRLQGFRLEEYLIQSIGKGCSAAVYEATMPTLPQ
 NLEVTKSTGLLPGRGP GTSAPGEGQERAPGAPAFPLAIKMMWNI SAGSSSEAILNTMSQE
 LVPASRVALAGEYGAVTYRKS KRGPKQLAPHPNIIRVLRAFTSSVPLLPGALVDYDPVLP
 SRLHPEGLGHGRTLFLVMKNYPCTLRQYLCVNTSPRLAAMMLLQ LLEGVDHLVQQGIAH
 RDLKSDNILVELDPDGCPWLVIADFGCCLADESIGLQLPFSSWYVDRGNGCLMAPEVST
 ARPGPRAVIDYSKADAWAVGAIAYEIFGLVNPFGYQGKAHLESRSYQEAQLPALPESVPP
 DVRQLVRALLQREASKRPSARVAANVLHLSLWGEHILALKNLKLDKMVGWLLQQSAATLL
 ANRLTEKCCVETKMKMLFLANLECETLCQAALLLCSWRAAL

SEQ ID NO: 231_AI086865_H

MEKYERIRVVGRGAFGIVHLCLRKADQKLVIIKQIPVEQMTKEERQAAQNECQVLKLLNH
 PNVEYYENFLEDKALMIAMEYAPGGTLAEFIQKRCNSLLEEETILHFFVQILLALHHVH
 THLILHRDLKTQNILDKHRMVVKIGDFGISKILSSKSTPCYISP ELCEGKPYNQKSDIW
 ALGCVLYELASLKRAFEANLPALVLKIMSGTFAPISDRYSPELRQLVLSLLSLEPAQRP
 PLSHIMAQPLCIRALLNLHTDGREVRGPQQHREQDHQCPLQ RGIIMTFGSGSNGCLGHGS
 LTDISQPTIVEALLGYEMVQQVEEALSFTLLGSAPLDQEPLLSIDLGTAHSAAVTGEEDL
 GSGDVNRLPSWERGHLLAGVASSTDVSTFSEGDCKEPDKCCWRHKQCTGHI IYPFASDCV
 RHSLHLHSVNHNCNSRLKDSSSEDSSSSRGAGPTCSHVIESPCFELTPEEEHVERFRYGW
 CKSYRPVSVAVIHHPLYHECGADDLNXXKKRKRKRKRKSKPPIPTQVGPATASPD LGTSMAT
 GTPDSTAPITITWRSESPTGKGQGSKVIKKVKKKKEKEKDKEEMDEKAKLKKKAKKGQLTK
 KKSPVKLEPSPPDVSRSL SARQLARMSESSPESREELESEDSYNGRGQGE LSSSEDIVESS
 SPRKRENTVQAKKTGAKPSQARKVNKRKSPPGSNPNLS

SEQ ID NO: 232_AA836348_H

MSVLGEYERHCDSINSDFGSESGCGDSSPGPSASQGP RAGGAAEQEELHYIPIRVLGR
 GAFGEATLYRRTEDDSL VVWKEVDLTRLSEKERRDALNEI VILALLQHDNI IAYYNHFM D
 NTTLLIELEYCNGGNLYDKILRQKDKLFEEMVWYLFQIVSAVSCIHKAGILHRDIKTL
 NIFLTKANLIKLG DYGLAKKLNSEYSMAETLVGTPY YMSPELCQGVKYNFKSDIWAVGCV
 IFELLTLKRTFDATNPLNLCVKIVQGIRAMEVDSSQYSLELIQMVHSCLDQDPEQRPTAD
 ELLDRPLLKRKRSSSTVTEAPIAVVTSRTSEVYVWGGGKSTPQKLDVIKSGCSARQVCAG
 NTHFAVVTEKELYTWVNMQGGTKLHGQLGHGDKASYRQPKHVEKLQ GKAIRQVSCGDDF
 TVCVTDEGQLYAFGSDYYGCMGV DKVAGPEVLEPMQLNFFLSNPVEQVSCGDNHVVLTR
 NKEVYSWGCGEYGRGLDSEEDYTPQKVDVPKALII VAVQCGCDGTFLLTQSGKVLACG
 LNEFNKLGLNQCMGSIINHEAYHEVPYTTSTFLAKQLSFYKIRT IAPGKTHTA AIDERGR
 LLTFGCNKCGQLGVGN YKKRLGINLLGGPLGGKQVIRVSCGDEFTIATDEKVLNSKTIR
 SNSSGLSIGTVFQSSSPGGGGGGGGGEEEDSQQES ETPDPSSGGFRGTMEADRGMEGLISP
 TEAMGNSNGASSSCPGWLRKELENAEFIPMPDSPSPLSAAFSESEKDTLPYEELQGLKVA
 SEAPLEHKPQVEASVTELF AFESQLV TSAESCSNLCWEGNTTDSSCVCVQLSAGG

SEQ ID NO: 233_R86668_H, MKK6_H

MNLLLSYRDVDYSAIIELVETLQALPTCDVAEQHNVC FHYTFALNRRNRPGDRAKALSV
 LLPLVQLEGSVAPDLYCMCGRIYKDMFFSSGFQDAGHREQAYHWYRKAFDVEPSLHSGIN
 AAVLLIAAGQH FEDSKELRLIGMKLGCLLARKGCVEKMQYYWDVGFYLG AQIILANDPTQV
 VLAAEQLYKLNAPIWYLVSVMETFLLYQHFRPTPEPPGPPRRAHFWLHFL LQSCQPFKT
 ACAQGDQCLVLVLEMNKVLLPAKLEVRGTD PVSTVTLSSLLEPETQDIPSSWTFPVASICG
 VSASKRDERCCFLYALPPAQDVQLCFPSVGHCQWFCGLIQAWVTNPDSTAPAEAEAGAGE
 MLEFDYETETGERLVLGKGT YGVYAGRDRHTRVRIAIKEI PERDSRFSQPLHEEIALH
 RRLRHKNIVRYLGSASQGGY LKIFMEEVPGGSLSSLLRSVWGPLKDNESTISFYTRQILQ
 GLGYLHDNHIVHRDIKGD NVLINTFSGLLKISDFGT SKRLAGITPCTETFTGT LQYMAPE
 IIDQGPRGYGKAADIWSL GCTVIEMATGRPPFHELGSPOAAMFQVGM YKVHPPMPSSLSA

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FIGURE 1AA

EAQAFLLRTFEPDPRLRASAQTL LGDPFLQPGKRSRSPSSPRHAPRPSDAPSASPTPSAN
STTQSQTFFPCPQAPSQHPPSPKRCLSYGGTSQ LRVPEEPAAEEPASPEESSGLSLLHQE
SKRRAMLA AVLEQELPALAENLHQEQKQEQGARLGRNHVEELLRCLGAHIHTPNRRQLAQ
ELRALQGRRLRAQGLGPALLHRPLFAFPDAVKQILRKQIRPHWMFVLDSLLSRAVRAALG
VLGPEVEKEAVSPRSEELSNEGDSQQSPGQQSPLPVEPEQGPAPLMVQLSLLRAETDRLR
EILAGKEREYQALVQRALQRLNEEARTYVLAPEPPTALSTDQGLVQWLQELNVDSGTIQM
LLNHSFTLHTLLTYATRDDL IYTRIRGGMVCRIWRAILAQ RAGSTPVTSGP

SEQ ID NO: 234_PAK6_H

MFGKKKKKIEISGPSNFEHRVHTGFD PQEQKFTGLPQQWHSLLADTANRPKPMVDPSCIT
PIQLAPMKTIVRGNKPKCKETSINGLLED FDNISVTRSNSLRKESPTPDQGASSHGPGHA
EENGFITFSQYSSSESDTTADYTTEKYREKSLY GDDLDPYRGSHA AKQNGHVMKMKHGEA
YYSEVKPLKSDFARFSADYHSHLDSLKPSEYSD LKWEYQRASSSSPLDYSFQFTPSRTA
GTSGCSKESLAYSESEWGPSLDDYDRRPKSS YLNQTS PQPTMRQRSRSGSGLQEPMPFPG
ASAFKTHPQGHSYNSYTYPRLSEPTMCIPKVDY DRAQMVLSPPLSGSDTYPRGPAKL PQS
QSKSGYSSSSHQYPSGYHKATLYHHPSLQSS SQYISTASYLSSLSSSTYPPPSWGSSS
DQQPSRVSHEQFRAALQLVVS PGDPREYLANFIKIGEGSTGIVCIATEKHTGKQVAVKKM
DLRKQQRRELLFNEVVIMRDYHHDNVDMYSS YLVGDELWVMEFLEGGALTDIVTHTRM
NEEQIATVCLSVLRALS YLHNQGVHRDIKSDS ILLTSDGRIKLSDFGFCAQVSKEVPKR
KSLVGTPTYWMAPEVISRLPYGTEVDIWSL GIMVIEMIDGEPPYFNEPPLQAMRRIRD SLP
PRVKDLHKVSSVLRGFLDLMLVREPSQRATAQ ELLGHPFLKLAGPPSCIVPLMRQYRHH

SEQ ID NO: 235_SURTK106_H

MNDRNEIQMEAKLQSLTIIAQEI LCRFFITLRRHARFLLTKLGRQGMARSGITHSCAVCI
LCGPSREGDSPVAMGMTRMLLECSLSDKLCV IQEKQYEVIIIVPTLLVTIFLILLGVILWL
FIREQRTQQQRSGPQGIAPVPPPRDLSWEAGH GGNVALPLKETSVENFLGATT PALAKLO
VPREQLSEVLEQICSGSCGPIFRANMNTGDPS KPKSVILKALKEPAGLHEVQDFLGRIQF
HQYLKGKHNVLVQLEGCCTEKLPLYMVLEDVA QGDLLGFLWTCRRDVMTMDGLLYDLTEKQ
VYHIGKQVLLALEFLQEKHLFHGDVAARNIL MQSDLTAKLCGLGLAYEVYTRGAISSTQT
IPLKWLAPERLLLRPASIRADVWSFGILLYE MVTLGAPPYPEVPPTSILEHLQRRKIMKR
PSSCTHTMYSIMKSCWRWREADRSPRELRLR LEAAIKTADDEAVLQVPELVVPELYAAV
AGIRVESLFYNYSML

SEQ ID NO: 236_AA098024_M

LQEKHLFHGDVAARNILIQSDLT PKLCHLGLAYEVHAHGAISSARSSTIPLKWLAPERLL
LRPASIRGDIWSFGILLYEMVT LGAPPYPEVPPTSILQYLQRKKIMKRPSSCSHAMYNIM
KCCWRWSEDSRPLL VQLLQRLEAASRSADDKAVLQVPELVVPELYADVAGIRAESISYSF
SVL

SEQ ID NO: 237_SGK2ALPHA_H

MNSSPAGTPSPQPSRANGNINLGPSANPNAQPTDF LKLVIGKGNYGKVLLAKRKSDGAF
YAVKV LQKKSILKKKEQSHIMAERSVLLKNVRHPFLVGLRYSFQTPEKLYFVL DYVNGGE
LFFHLQRRERFLEPRARFYAAEVASAI GYLHSLNIIYRDLKPENILLDCQGHVVLTD FGL
CKEGVEPEDTTSTFCGTPEYLAPEVLRKEPYDRAVDWWCLGAVLYEMLHGLPPFYSQDVS
QMYENILHQPLQIPGGRTVAACDLLQSLLHKDQRQRLGSKADFLEIKNHVFFSPINWDDL
YHKRLTPPFNPNTGPADLKHFDPEFTQEAVSKS IGCTPDTVASSSGASSAFLGFSYAPE
DDDILDC

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FIGURE 1BB

SEQ ID NO: 238_CCRK_H

MDQYCILGRIGEGAHGIVFKAKHVETGEI IALKKVALRRLEDGFPNQALREI KALQEMED
NQYVVQLKAVFPHGGGFVLA FEFMLSDLA EVVRHAQRPLAQAQVKS YLQMLLKGVAFCHA
NNIVHRDLKPANLLISASGQLKIADFG LARVFS PDGSRLYTHQVATRSVGCIMGELLNGS
PLFPGKNDIEQLCYVLRLGTNPQVWPEL TELPDYNKISFKEQVMPLEEVLPDVSPQA
LDLLGQFLLYPPHQRIAASKALLHQYFFTAPLPAHPSELPIPQRLGGPAPKAHPGPPHIH
DFHVDRPLEGVAVEPRADSALHPGGVRSWPWSRLPAPQDHSVHLFLCHLPGFTLQGLPMA
TVGPHHTLPLSPCEGWSRGRGHVPSQEYENIQSSRGDSWPVLGEPYLLCATDVPIRTVSS
AASQGLHMQNDDACLGAASPECCLLVKEKCRE

SEQ ID NO: 239_TESK2_H

MDRSKRNSIAGFPPRVERLEEFEGGGGGEGNV SQVGRVWPSSYRALISAFSRLTRLDDFT
CEKIGSGFFSEVFKVRHRASGQVMALKMNTLSSNRANMLKEVQLMNRLSHPNILRYINSG
NLEQLLDSNLHLPWTVRVKLAYDIAVGLSYLHFKGIFHRDLTSKNCLIKRDENGYS AVVA
DFGLAEKIPDVSMGSEKLAVVGSPFWMAPEVLRDEPYNEKADVFSYGIILCEI IARIQAD
PDYLPRTENFGLDYDAFQHMVGDCPPDFLQLTFNCCNMDPKLRPSFVEIGKTL EEILSRL
QEEEQERDRKLQPTARGLLEKAPGVKRLSSLD DDKIPHKSPCPRRTIWLSRSQSDIFSRKP
PRTVSVLDPYYRPRDGAARTPKVNPFSARQDLMGGKIKFFDLPSKSVISLVFDLDAPGPG
TMPLADWQEPLAPPIRRWRS LPGSPEFLHQEACPFVGREESLSDGPPPRLLSSLKYRVKEI
PPFRASALPAAQAHEAMDCSILQEENGFGSRPQGTSPCPAGASEEMEVEER PAGSTPATF
STSGIGLQTQ GKQDG

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FIGURE 2A

SEQ ID NO: 1_X69117_H BARK2_H

ATGGCGGACCTGGAGGCCGTGCTGGCCGATGTCAGTTACCTGATGGCCATGGAGAAGAGC
AAGGCGACCCCGGCCGCCGCCAGCAAGAGGATCGTCCTGCCGGAGCCAGTATCCGG
AGTGTGATGCAGAAGTACCTTGCAGAGAGAAATGAAATAACCTTTGACAAGATTTTCAAT
CAGAAAATTGGTTTCTTGCTATTTAAAGATTTTTGTTTGAATGAAATTAATGAAGCTGTA
CCTCAGGTGAAGTTTTATGAAGAGATAAAGGAATATGAAAACTTGATAATGAGGAAGAC
CGCCTTTGCAGAAGTCGACAAATTTATGATGCCTACATCATGAAGGAACCTCTTTCTGT
TCACATCCTTTCTCAAAGCAAGCTGTAGAACACGTACAAAGTCATTTATCCAAGAAACAA
GTGACATCAACTCTTTTTTCAGCCATACATAGAAGAAATTTGTGAAAGCCTTCGAGGTGAC
ATTTTTCAAAAATTTATGGAAAGTGACAAGTTCAGTAGATTTTGTGAGTGGAAAAACGTT
GAATTAAATATCCATTTGACCATGAATGAGTTCAGTGTGCATAGGATTATTGGACGAGGA
GGATTCCGGGGAAGTTTATGGTTGCAGGAAAGCAGACACTGGAAAAATGTATGCAATGAAA
TGCTTAGATAAGAAGAGGATCAAAATGAAACAAGGAGAAACATTAGCTTTAAATGAAAGA
ATCATGTTGTCTCTTGTGTCAGCACAGGAGACTGTCCTTTCATTGTATGTATGACCTATGCC
TTCCATACCCCGAGATAAACTCTGCTTCATCCTGGATCTGATGAACGGGGGCGATTGTCAC
TACCACCTTTCACAACACGGTGTGTTCTCTGAGAAGGAGATGCGGTTTTATGCCACTGAA
ATCATTCTGGGTCTGGAACACGTGCACAATCGGTTTGTGTCTACAGAGATTTGAAGCCA
GCAAATATTCTCTTGGATGAACATGGACACGCAAGAATATCAGATCTTGGTCTTGCCTGC
GATTTTTTCAAAAAGAAGCCTCATGCGAGTGTGGCACCCTATGGGTACATGGCTCCCGAG
GTGCTGCAGAAGGGGACGGCCTATGACAGCAGTGCCGACTGGTTCTCCCTGGGCTGCATG
CTTTTCAAACCTTCTGAGAGGTACAGCCCTTTCAGACAACATAAAACCAAAGACAAGCAT
GAAATTGACCGAATGACACTCACCGTGAATGTGGAACCTCCAGACACCTTCTCTCCTGAA
CTGAAGTCCCTTTTGGAGGGCTTGCTTCAGCGAGACGTTAGCAAGCGGCTGGGCTGTCAC
GGAGGCGGCTCACAGGAAGTAAAAGAGCACAGCTTTTTCAAAGGTGTTGACTGGCAGCAT
GTCTACTTACAAAAGTACCCACCACCCTTGATTCTCTCCCGGGGAGAAGTCAATGCTGCT
GATGCCTTTGATATTGGCTCATTTGATGAAGAGGATACCAAAGGGATTAAGCTACTTGAT
TGCGACCAAGAACTCTACAAGAACTTCCCTTTGGTCATCTCTGAACGCTGGCAGCAAGAA
GTAACGGAAACAGTTTATGAAGCAGTAAATGCAGACACAGATAAAATCGAGGCCAGGAAG
AGAGCTAAAAATAAGCAACTTGGCCACGAAGAAGATTACGCTCTGGGGAAGGACTGTATT
ATGCACGGGTACATGCTGAACTGGGAAACCCATTTCTGACTCAGTGGCAGCGTCGCTAT
TTTTACCTCTTTCAAATAGACTTGAATGGAGAGGAGAGGGAGAGTCCCGGCAAAATTTA
CTGACAATGGAACAGATTCTCTCTGTGGAAGAACTCAAATTAAGACAAAAAATGCATT
TTGTTTCAAGATAAAAGGAGGGGAAACAATTTGTCTTGCAATGTGAGAGTGATCCAGAGTTT
GTGCAAGTGAAGAAAGAGTTGAACGAAACCTTCAAGGAGGCCAGCGGCTATTGCGTCGT
GCCCCGAAGTTCTCTCAACAAACCTCGGTACAGTACTGTGGAGCTCCCAAAGCCATCCCTC
TGTCACAGGAACAGCAACGGCCTCTGA

SEQ ID NO: 2_AA144574_M BARK2_M

CTGCTTCGTAGTCTACAGAGACCTGAAGCCTGCGAACATCCTCCTAGATGAATATGGGCA
CGTGAGGATATCGGATCTCGGCCTTGCTGTGATTTCTCAAAAAGAAGCCTCATGCCAG
CGTGGGCACCCATGGGTACATGGCTCCCGAGGTGTTGCAGAAGGGAACGTGCTATGACAG
CAGCGCCGACTGGTTCTCCCTGGGCTGTATGCTCTTCAAACCTTCTGCGGGGCCACAGCCC
CTTCAGGCAGCATAAAACCAAAGACAAGCATGAGATAGACCGAATGACCCTGACCGTGAA
CGTGCAGCTTCCAGATGCCTTCTCCCTGAGCTGAGGTCCCTCTTAGAGGGTTTGCTCCA
GCGGGACGTGAGCCAGCGGCTGGGCTGCGGAGGAGGAGGGGCAGAGAGTTGAAGGAGCA
CATCTTCTTCAAGGGCATTGACTGGCAGCATGTGTACTTACGGAAGTACCCGCCACCCCT
AATCCCTCCTCGGGGAGAGGTCAACGCTGCAGATGCCTTCGATATCGGCTCCTTCGATGA
GGAAGACACCAAAGGCATTAAGCTGTTGGACTGTGACCAGGACCTCTATAAGAACTTCCC
ACTGGTGATCTCCGAGCGCTGGCAGCAAGAAGTGGTGGAGACCATCTATGACGCCGTCAA
TGCTGATACTGATAAAATCGAGGCCAGGAAGAAGGCTAAAAATAAGCAACTTGGTCAAGA

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FIGURE 2B

GGAAGATTACGCTATGGGGAAGGACTGCATCATGCACGGGTACATGCTGAAGCTGGGGAA
CCCCTTTCTCACACAGTGGCAAAGACGCTATTTTTACCTGTTCCCCAACAGACTGGAGTG
GAGAGGAGAGGGCGAGTCTCGGCAAAGTCTACTGACCATGGAACAGATCATGTCTGTGGA
GGAGACCCAGATTAAAGACAGAAAGTGCATCTTACTCAGGATAAAGGGAGGGAAGCAATT
TGTCTTGCAATGTGAGAGTGACCCCGAGTTTGCACAGTGGCTGAAGGAGCTGACCTGCAC
CTTCAATGAGGCCCAGAGACTGCTGCGCCGTGCCCCCAAATTCCTCAACAAACCACGGGC
CGCCATCCTGGAGTTCTCCAAGCCACCACTGTGTACAGAAATAGCAGCGGCCTCTGAAC
CACAGAGCAGCGGGGCTGAAGGAGGGGCCCCAGCTCTTCAGCCCAGGAGTGGAACGAAG
CCACGGGGAACCGTGTGGGGCTAAGACACAGTGTCTTCTGAGCACTGACGGGGCTGCTCCA
AGCCGAGGAGGCTCAGGACACCAGGGCGGCCTTCTGGGAGCTGGGACATCCTCGGGGCTG
TCCTATCCACACTCGAAATTACTGAAGAAGCAGAGGCATTCTGCTGTG

SEQ ID NO: 3_AA826850_H

GAAGAGGATGGGCTCGTCCATGTCGGCGGCCACCGCGCGGAGGCCGGTGTGTTGACGACAA
GGAGGACGTGAACTTCGACCACTTCAGATCCTTCGGGCCATTGGGAAGGGCAGCTTTGG
CAAGGTGTGCATTGTGCAGAAGCGGGACACGGAGAAGATGTACGCCATGAAGTACATGAA
CAAGCAGCAGTGCATCGAGCGCGACGAGGTCCGCAACGTCTTCCGGGAGCTGGAGATCCT
GCAGGAGATCGAGCACGTCTTCTGGTGAACCTCTGGTACTCCTTCCAGGACGAGGAGGA
CATGTTTCATGGTTCGTGGACCTGCTACTGGGCGGGGACCTGCGCTACCACCTGCAGCAGAA
CGTGACAGTTCTCCGAGGACACGGTGAGGCTGTACATCTGCGAGATGGCACTGGCTCTGGA
CTACCTGCGCGGCCAGCACATCATCCACAGAGATGTCAAGCCTGACAACATTCTCCTGGA
TGAGAGAGGACATGCACACCTGACCGACTTCAACATTGCCACCATCATCAAGGACGGGGA
GCGGGCGACGGCATTAGCAGGCACCAAGCCGTACATGGCTCCGGAGATCTTCCAXTCTTT
TGTC AACGGCGGGACCGGCTACTCCTTCGAGGTGGACTGGTGGTTCGGTGGGGGTGATGGC
CTATGAGCTGCTGCGAGGATGGAGGCCCTATGACATCCACTCCAGCAACGCCGTGGAGTC
CCTGGTGCAGCTGTTTACGACCCGTGAGCGTCCAGTATGTCCCCACGTGGTCCAAGGAGAT
GGTGGCCTTGCTGCGGAAGCTCCTCACTGTGAACCCCGAGCACCGGCTCTCCAGCCTCCA
GGACGTGCAGGCAGCCCCGGCGCTGGCCGGCGTGTGTGGGACCACCTGAGCGAGAAGAG
GGTGGAGCCGGGCTTCGTGCCCAACAAAGGCCGTGTGCACTGCGACCCACCTTTGAGCT
GGAGGAGATGATCCTGGAGTCCAGGCCCTGCACAAGAAGAAGAAGCGCCTGGCCAAGAA
CAAGTCCCGGGACAACAGCAGGGACAGCTCCAGTCCGAGAATGACTATCTTCAAGACTG
CCTCGATGCCATCCAGCAAGACTTCGTGATTTTTTAACAGAGAAAAGCTGAAGAGGAGCCA
GGACCTCCCGAGGGAGCCTCTCCCCGCCCTGAGTCCAGGGATGCTGCGGAGCCTGTGGA
GGACGAGGCGGAACGCTCCGCCCTGCCATGTGCGGCCCATTTGCCCCCTCGGCCGGGAG
CGGCTAGGCCGGGATGCCCGTGGTCTCACCCCTTGAGCTGCTTTGGAGACTCGGCTGCC
AGAGGGAGGGCCATGGGCGGAGGCCTGGCATTACGTTCCACCCAGCCTGGCTGGCGGT
GCCCCAGTGCCCCGGACACATTTACACCTCAGGCTCGTGGTGGTGCAGGGGACAAGAG
GCTGTGGGTGCAGGGGACACCTGTGGAGGGCATTTCCTGGGGCCCCGAGACCCGCCTA
GATGGAGGAAGCGCTGCTGGGCGCCCTCTTACCGCTCACGGGGAGCTGGGGCCATGGATG
GGACAGGAGTCTTTGTCCCTGCTCAGCCCCGAGGCTGTGCACGGCCCTCGTCACAAGGTG
ACCCTTGACGACAGGCCGCGGGTGCCCCAGGCTCGGCTCAGTTCTTGGAGGTCAAGGGC
ATGGGTTGGGGTAGTGGGTGGGGAGGTGAATGTTTTCTAGAGATTCAAAGTCTCCAGCA
ATTTCTGTATAGTTTTACCTCTGAGAATTACAATGTGAGAACCGCTC

SEQ ID NO: 4_AA960957_H

GTCCCACATCCCGCATCCGGCATCCAGCGGCCGGGCATGTAGCAGCGGCAGCAACGGCG
GAATATGGGCGGGAACCACTCCACAAGCCCCCGTGTGTTGACGAGAATGAGGAAGTCAA
CTTTGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCAT
CGTGCAGAAGCGAGACACTAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTG
CATCGAGAGGGATGAGGTTTCGGAATGTTTTCCGGGAGCTGCAGATCATGCAAGGGCTGGA

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FIGURE 2D

SEQ ID NO: 5_TBK1_H

TCCTGAGTCTCGAGGAGGCCGCGGGAGCCCGCGGCGGTGGCGCGGCGGAGACCCGGCTG
GTATAACAAGAGGATTGCCTGATCCAGCCAAGATGCAGAGCACTTCTAATCATCTGTGGC
TTTTATCTGATATTTTAGGCCAAGGAGCTACTGCAAATGTCTTTCGTGGAAGACATAAGA
AAACTGGTGATTTATTTGCTATCAAAGTATTTAATAACATAAGCTTCCTTCGTCCAGTGG
ATGTTCAAATGAGAGAATTTGAAGTGTGAAAAAACTCAATCACAAAAATATTGTCAAAT
TATTTGCTATTGAAGAGGAGACAACAACAAGACATAAAGTACTTATTATGGAATTTTGTG
CATGTGGGAGTTTATACACTGTTTTAGAAGAACCCTTCTAATGCCTATGGACTACCAGAAT
CTGAATTCTTAATTGTTTTGCGAGATGTGGTGGGTGGAATGAATCATCTACGAGAGAATG
GTATAGTGCACCGTGATATCAAGCCAGGAAATATCATGCGTGTTATAGGGGAAGATGGAC
AGTCTGTGTACAACTCACAGATTTTGGTGCAGCTAGAGAATTAGAAGATGATGAGCAGT
TTGTTTCTCTGTATGGCACAGAAGAATATTTGCACCCTGATATGTATGAGAGAGCAGTGC
TAAGAAAAGATCATCAGAAGAAATATGGAGCAACAGTTGATCTTTGGAGCATTGGGGTAA
CATTTTACCATGCAGCTACTGGATCACTGCCATTTAGACCCTTTGAAGGGCCTCGTAGGA
ATAAAGAAGTGATGTATAAAAATAATTACAGGAAAGCCTTCTGGTGCAATATCTGGAGTAC
AGAAAGCAGAAAATGGACCAATTGACTGGAGTGGAGACATGCCTGTTTCTTGCACTCTTT
CTCGGGGTCTTCAGGTTCTACTTACCCCTGTTCTTGCAAACATCCTTGAAGCAGATCAGG
AAAAGTGTGGGGTTTTGACCAGTTTTTTGCGAGAACTAGTGATATACTTCACCGAATGG
TAATTCATGTTTTTTCGCTACAACAAATGACAGCTCATAAGATTTATATTCATAGCTATA
ATACTGCTACTATATTTTCATGAAGTGGTATATAAACAACCAAAATTTCTTCAAATC
AAGAACTTATCTACGAAGGGCGACGCTTAGTCTTAGAACCTGGAAGGCTGGCACAACATT
TCCCTAAAACCTACTGAGGAAAACCTATATTTGTAGTAAGCCGGAACCTCTGAATACCA
TAGGATTAATATATGAAAAAATTTCCCTCCCTAAAGTACATCCACGTTATGATTTAGACG
GGGATGCTAGCATGGCTAAGGCAATAACAGGGGTTGTGTGTTATGCCTGCAGAATTGCCA
GTACCTTACTGCTTTATCAGGAATTAATGCGAAAGGGGATACGATGGCTGATTGAATTAA
TTAAAGATGATTACAATGAACTGTTCAAAAAAGACAGAAGTTGTGATCACATTGGATT
TCTGTATCAGAAACATTGAAAAAACTGTGAAAGTATATGAAAAGTTGATGAAGATCAACC
TGGAAGCGGCAGAGTTAGGTGAAATTTAGACATACACACCAAAATTGTTGAGACTTTCCA
GTTCTCAGGGAACAATAGAAACCAGTCTTCAGGATATCGACAGCAGATTATCTCCAGGTG
GATCACTGGCAGACGCATGGGCACATCAAGAAGGCACTCATCCGAAAGACAGAAATGTAG
AAAAACTACAAGTCCTGTAAATTGCATGACAGAGATTTACTATCAGTTCAAAAAAGACA
AAGCAGAACGTAGATTAGCTTATAATGAAGAACAAATCCACAAATTTGATAAGCAAAAAC
TGTATTACCATGCCACAAAAGCTATGACGCCTTTACAGATGAATGTGTTAAAAAGTATG
AGGCATTTTTGAATAAGTCAGAAGAATGGATAAGAAAGATGCTTCATCTTAGGAAACAGT
TATTATCGCTGACTAATCAGTGTTTTGATATTGAAGAAGAAGTATCAAAATATCAAGAAT
ATACTAATGAGTTACAAGAACTCTGCCTCAGAAAATGTTTACAGCTTCCAGTGGAATCA
AACATACCATGACCCCAATTTATCCAAGTTCTAACACATTAGTAGAAATGACTCTTGGTA
TGAAGAAATTAAAGGAAGAGATGGAAGGGGTGGTTAAAGAACTTGCTGAAAATAACCACA
TTTTAGAAAGGTTTGGCTCTTTAACCATGGATGGTGGCCTTCGCAACGTTGACTGTCTTT
AGCTTTCTAATAGAAAGTTTAAAGAAAGTTTCCGTTTGCACAAGAAAATAACGCTTGGGCA
TTAAATGAATGCCTTTATAGATAGTCACTGTTTCTACAATCCAGTATTTGATGTGGTCG
TGTAATATGTACAATATTGTAAATACATAAAAAATATACAAATTTTTGGCTGCTGTGAA
GATGTAATTTTATCTTTTAACATTTATAATTATATGAGGAAATTTGACCTCAGTGATCAC
GAGAAGAAAGCCATGACCGACCAATATGTTGACATACTGATCCTCTACTCTGAGTGGGGC
TAAATAAGTTATTTTCTCTGACCGCCTACTGGAAATATTTTTAAGTGGAACCAAAATAGG
CATCCTTACAAATCAGGAAGACTGACTTGACACGTTTGTAAATGGTAGAACGGTGGCTAC
TGTGAGTGGGGAGCAGAACCGCACCCTGTTATACTGGGATAACAATTTTTTTGAGAAGG
ATAAAGTGGCATTATTTTATTTTACAAGGTGCCCAGATCCCAGTTATCCTTGTATCCATG
TAATTTTCAAGATGAATTATTAAGCAAACATTTTAAAGTGAATTCATTATTAATAAACTATTC
ATTTTTTCTCTTTGGCCATAAATGTGTAATTGTCATTAAATTTCTAAGGTCATTTCAACT

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FIGURE 2C

GCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGACATGTTTCATGGT
GGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTTCAC
AGAGGGGACTGTGAAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAG
GTACCACATCATCCACAGAGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACA
TGTTTCACATTACAGACTTCAACATAGCGACGGTAGTGAAAGGAGCAGAAAGGGCTTCCTC
CATGGCTGGCACCACCAAGCCCTACATGGCTCCAGAAGTATTCCAGGTGTACATGGACAGAGG
CCCCGGATACTCGTACCCTGTCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCT
GCGGGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTCAACAT
GTTCAAGGTGGAGCGTGTCCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCT
GAGGAAGCTCCTGACCAAGGATCCTGAGAGCCGCGTGTCCAGCCTTCATGACATACAGAG
CGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGCACTGATGCCCGG
CTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCCACATTTGAGCTTGAAGAGATGAT
TCTAGAATCCAAGCCACTTCACAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGA
TGGCACAAGGACAGCTGCCCGCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCG
GGAGGAATTCATCATATTCAACAGAGAGAAGCTCAGGAGGCAGCAGGGACAGGGCAGCCA
GCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCTCCAGGACGGGTG
CAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCACACTTG
TTGCTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCTCTTTGTGC
CCTGATGGTCCCTGTCTCACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGG
GCTGGGAAGCCTGGGTTCTGGTCCCATCTCCATGACTGATTCACGTGTGACCTCAGACAA
GTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTAAACACTTCTGCC
CCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTT
TGATATTTATAAAATCATTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCC
ATTCCCCAAAGCAATCAAACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGA
GGGCACTTCCGAAAAACACAGCCCTGACAGCAAAATAAAGGTCTGATATGTTGGCCCTT
CTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTTCATGTGCATTCT
CTGGCAGGCCACAGTCCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCCTCATTTAAGAAGACTATCCTTACCTTTT
AGTTTCAGCAGTCCTCACCACCACCATATCCCCAGTGCTGGGATGGCACACAGGTGTCCA
TTCAGATGAGAGTTGGGTGCTGAGCATTGGTTACTCCTGCAGAGTGTAATCAGACCCCC
ATCCAATGGCCCCGAAAGCCCAGACCTGCAGCAGAACTCTCCAATCTCTATCAGCTTTC
AGGGTTTTCTCTCCTGGGAAGGGTGTAATAATCAGCTTGTCAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATACAATAGGAAGCATGGGTGCTTAG
AAAGTTTATTTTCAGGAGGAAAATGGGTTACACAAAAAGCAAACCTACATTCTGATCTGCT
CAGGGAGAAGCTTGCCCTTGAAGTGAAGATGTTGGGATGAGCAGGGAAAGCTTAGACTT
TGGAGTCAGGTTTGTGTTTCAAGATCCAGCCCTGCTGGCTACTAACTAACTGGGAGACCTT
AGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTG
GATGACTCATAGAATGGCCTTTTTTGTGAGCATAATCGTCATCATTTATTTAGATACTTTC
TTCCTTCACTCACCCAGCAGGTGAGTTTCTGTGCAACAAACCTGTTTAGGATTCTTCC
AAATGTTCTTCCTGGGGTCTTTGATATTTGTTTGTACATCCTGCTGAAGTTCGACTGTG
TTTTTATTTTTTTCATCCAATTCATTTTTTACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCTCTTAGATTTCTTAAAAGACATTTTAAATGTATGGTTAGGTTTTAT
ATTTTTATTTTTTAAAAAAGAAATAGTCAGTGTTCCTCCTTCAACCGAGACTATTTTC
TGGATTGTGTGCTCCTCGTCAGTTGACTTGTTCGACACTTTTCTTTACTTCATGTCCC
CATCAACAACCGTCCTGCTCCCCACCTCCCCAGGAAATAAGGGGCCTGCTCCTCTCCCT
ACTGTGACCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTTATTGGGCTGAGTTCACGA
ATTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGTTCTGTTCAAGT
TGGCATTCTTGTGTTGGAATAAACTATTTCTTGGACATTCCTTC

FIGURE 2E

GTTTTAAGCTGTATATTTCTTTAATTCTGCTTACTATTTTCATGGAAAAAATAAATTTCT
CAATTTTAAAAAA

SEQ ID NO: 6_AA305176_H

TGGCTGCTCGCGGAGGGGCAGTGTACGCGGGGCCGCTGTAGGCTGTCCAGCGATGGATCC
CACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGAGGGCGTGAATAG
GATCGCAGTGCCAAAACCGCCCTCCATTGAGGAATTCAGCATAGTGAAGCCCATAGCCG
GGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTATGCAGTAAAGGT
TGTTAAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCAAGCTGAGAGAGA
TGCACTGGCACTAAGCAAAAGCCCATTTCATTGTCCATTTGTATTATTCACTGCAGTCTGC
AAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAAGTCTCTCCTACA
TATATATGGTTATTTTGATGAAGAGATGGCTGTGAAATATATTTCTGAAGTAGCACTGGC
TCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACCGGACAATATGCT
TATTTCTAATGAGGGTCATATTAAACTGACGGATTTTGGCCTTTCAAAGTTACTTTGAA
TAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAAACCTAGACAAGA
TTATTTCAAGAACCCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGGATTTAACACACC
AATTGCAGAAAAAATCAAGACCCTGCAAACATCCTTTCAGCCTGTCTGTCTGAAACATC
ACAGCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAGGACACTACGCCTTA
TTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCCAGGAATGCCTGT
GAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCACATCCAGTGCCAG
TAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAGCAGTCCCAAATG
GGAAAAAGATTGCCAGGTTTGAGGGACATTTATCTTAATGAAAATCAATTATGTATGTCA
AATGAATGTGAGAAATATTATACCTTTTCATATAAATTCATATAAGAAATGAAATTGTTA
CATGAATGGCAGTCATAGTATTAATCAGAAATTCATTTTCTGCACATTCTGTCAAATTC
TTTTGAAATATTTTCAATTTCTCATTCAATTGTGACATTGTTCTTACTTGATTATATAATGA
GATTCTTGCAAGTAAATTGATAATAAATGCTTGGCTTCTGTGTATCTAGGTGGACCTCACT
TGTTTTTAGAAGTCCTTCCCATGATACAGACATTGGCTTGTTGGTTTTGTTTTATTTTGT
TTTAAACATATGTCATTTAAAAACTCATATTACCTCCTTTT

SEQ ID NO: 7_AA116841_M

CCACGCGTCCGATCCCATGGCCAGAAGGCGAAGAAAAGCTATCTGATAATGCTCAAAGTG
CAATGGACATGCTTTTAACCATTGATGATTCAAAGAGAGCTGGAATGAGAGAACTAAAC
AGCATCCTCTCTTCAGTGAAGTGGACTGGGAAAATCTGCAGCATCAGACTATGCCTTTTCG
TACCCCAACCAGACGACGAAACAGATACATCCTATTTTGAAGCCAGAAATAATGCTCAAC
ATCTGACCGTATCTGGGTTTAGTCTGTAGCACATGCGTGTCAATTTTTATCTAACTTGTGA
TATAGAATTAAGTTTTACAGTAATATGCTACTTAATACTAGATTGGTCTAAATGGGATAA
AAGTCATTATTTTACCCAGACTGAACAGCTTTTAATTACTAAGTACAACAGTTTTTACAG
AATTAAAATACTATAAGCAATATAATCAGTAATTAATCTTTACCTTAGAACTGTATATAA
GCCATAATAGCTTTTTTTCATCTTATTTATTCACTGCACTTTATGAAGAGCAAAGTATCAA
TAACTAAACACTACCACTCTAAATAGAGGGAGTGAGCCGT

SEQ ID NO: 8_AA256100_H

AGGGAGCTGACGGGCGCCCGGCCGGCTGCGGTCCGTGCGGAGGCTGAGCCGGCGCGGGC
GCGACCGGAGGCAGTTTCCGTTACTATGGCAATGACGGCAGGGACTACAACAACCTTTCC
TATGAGCAACCATAACCCGGGAAAGAGTGACTGTAGCCAAGCTCACATTGGAGAATTTTTA
TAGCAACCTAATTTTACAGCATGAAGAGAGAGAAACCAGGCAGAAGAAATTAGAAGTGGC
CATGGAAGAAGAAGGATTAGCAGATGAAGAGAAAAAGTTACGTCGATCACAACACGCTCG
CAAAGAAACAGAGTTCTTACGGCTCAAAGGACCAGACTTGGCTTGGATGACTTTGAGTC
TCTGAAAGTTATAGGAAGAGGAGCTTTTGGAGAGGTGCGGTTGGTCCAGAAGAAAGATAC
AGGCCATATCTATGCAATGAAGATATTGAGAAAGTCTGATATGCTTGAAAAGAGCAGGT

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FIGURE 2F

GGCCCATATCCGAGCAGAAAGAGATATTTTGGTAGAAGCAGATGGTGCCTGGGTGGTGAA
GATGTTTTTACAGTTTTTCAGGATAAGAGGAATCTTTATCTAATCATGGAATTTCTCCCTGG
AGGTGACATGATGACATTGCTAATGAAGAAAGACACCTTGACAGAAGAGGAAACACAGTT
CTACATTTTCAGAGACTGTTCTGGCAATAGATGCGATCCACCAGTTGGGTTCATCCATCG
GGATATTAAGCCAGACAACCTTTTTATTGGATGCCAAGGGTCATGTAAAATTATCTGATTT
TGGTTTTATGTACGGGATTAAAGAAAGCTCACAGGACTGAATTTTTATAGAAATCTCACACA
CAACCCACCAAGTGACTTCTCATTTTCAGAACATGAACTCAAAGAGGAAAGCAGAAACTTG
GAAGAAGAACAGGAGACAACCTGGCATATTCCACAGTTGGGACACCAGATTACATTGCTCC
AGAAGTATTCATGCAGACTGGTTACAACAAATTGTGTGACTGGTGGTCTTTGGGAGTGAT
TATGTATGAAATGCTAATAGGATATCCACCTTTCTGCTCTGAAACACCTCAAGAAACATA
CAGAAAAGTGATGAACTGGAAAGAACTCTGGTATTTCTCCAGAGGTACCTATATCTGA
GAAAGCCAAGGACTTAATTCTCAGATTTTGTATTGATTCTGAAAACAGAATTGGAAATAG
TGGAGTAGAAGAAATAAAAGGTCATCCCTTTTTTGAAGGTGTCGACTGGGAGCACATAAG
GGAAAGGCCAGCAGCAATCCCTATAGAAATCAAAGCATTGATGATACTTCAAATTTTGA
TGACTTCCCTGAATCTGATATTTTACAACCAGTGCCAAATACCACAGAACCGGACTACAA
ATCCAAAGACTGGGTTTTTCTCAATTATACCTATAAAAGGTTTGAAGGGTTGACTCAACG
TGGCTCTATCCCCACCTACATGAAAGCTGGGAAGTTATGAATGAAGATAACATTCACCCA
TAACCAAGAGAACTCAGGTAGCTGCATCACCAGGCTTGCTTGGCGTAGATAACAATACAC
TGAAATACTCCTGAAGATGGTGGTGGCTTATTGACTACAAGAGGAAATTCTACAGGATTAG
GATTTCTAAGACTACTATAGGAATTGGTTGGCAGTGCCAGCTGGCTCTTTTTTTTAATAT
TTTATTATTTTTTGTTAACTTTATTATATGAAGGTAAGGTAATAAAGGAACAGACATCCC
TTTCTAACTGCACTGCCTACATGCGTATTAAGGTCCATTCTGCCTGTGTGTGCTGTGGCT
TTGAAGTGTAAACACCTCTAATCAATTCAGGAGAAACACATATCATTTAAAGCAACATAGG
CTAACCTGTAGGTAACACTGCAGTATTGATGTTTTTACTGCAAATCTTATGGGTCTAGATA
ATCAGTAAAAGCCATCTTCCATAGTTGGTGTTAGAACATTGCCCTATTGGTTTGGACATC
TGTAGAATATATATGAAGACAATTTCTGTAATGGTTTTAAGAGATTTAAAAAGAAATTCA
CTGGTTCTTTACAAAATAGAATTTATCATCAAGTTATTACACAACTTCACAGTAAGGAG
TGACAAGTTTATAATAAGGAAGACAAAGTTTAACACCTTCACTCAAGCACTCCACTAATA
TATTTACGTTGCATTACAGAAATACTGATGACCTTCATATACGTAGTCTGTATACTCATAG
GGAGATGTACTGTATTATATAACATGTAAAGTTGATTTTCTTGTGACAAGAGAACTTCTT
TTTTTAAACAAGAGGACATGGCATTATTTTAAATTTGATTATGGTGAGTTGAATTTAAGACA
TGACCATGAAGGCTGCTTGTAGAATTAGTGTATTTTTATTAACTATTTTTTTTAAATGTC
AACTTCTATCATGTAAATGGACTTATAGAGAACAAAAGCTATTTACTTTGGTTTTCTA
GAAAGTTGTTACATATCATGGCTGGTTAACTTTTTATTTCTTTTGATGAAAATTTTTCTT
TGATAGTACTTGTATTATTGTGCCATTATTTTCTTATGCTCCAAATGTACCAAAGATCTT
GAACAGAGTGGAATGTTCACAACTGAGTAGAATTTTCCTTTCTGTGGGCATGCTGTATTC
AGACCTGACAGATCTTTGATAGAGGTCAGCTTATTAAAGGGCAATATTGTTCTTGTTTAG
CTACATCACTGTGGTGAATATAGATGGAATTAAGGAAGTAAATGCAGGCCAGGGGGTTGT
GATGAGAGGATAGGGGAGATAATATCAGCATCAAATCTTTGGGTATCTCTCTAAGAATT
AAATAATCTTTTCTAGCTTAATATTTTAATTCTAATTCAAACAACCTCTGAGGTTTTGTT
TCATTAGTAATAGTTGAGGAATAATATACTAGCAAAGAATGGCCTAATGTTTGTCTATAAC
TGTTAATGGATGAAATTTTTTAAAGATACAACCATGATAACCATTATAAATGATCTATGA
TCAAATCTAAAGTGATGAATTATTTGTAGGAATGTCCTTCTAATGGGGAAGAATTGCAT
AGGAGCATTATGCAAATCTACACAAGCTTTTATAAATGTTGCTGCTGGGTAGCTCCACAG
TGTTTCATAAGGCCATCCTGTTTCCCCCACTCCCCCATTTTTGGTTTTGTTCTTTTTAA
ATATTTGTTGAGTACTTACGTGTTTATCTAACAGTTCACCTCCATTTTTCTAGTCTGGAT
TTTTTGAGTATTTAGGAAAGAGAGCTATTAAAACTCTGGGGATTTCTCAATGTGACTAA
CTCTAATTTTTCTAATTATAACTGCCTTTAATTAACATAATATTAACTTTTGCTGAGGTT
TATGAGATTTTCTACCCCCACATCGCTCCCTTTTTTTTAAAGGACTGTTTTGCTAGTG
TGATAATGAATAGGTAAGATATGAGATAATTGCAACATTGTCCTAGTTCCTAGTATGGTAA

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FIGURE 2G

CTATTCTTGAAATGGTATTGAAAAATACCGTTAATTCAAATTGACAGAGATTGATAAAAA
GAAACTGATTTACCTAAGTTTACTTTTTTAATTGCATAATAGAGCATTTTTTTGTTTTGAGT
TCCCTCATTCTTATTACCAGAAAGAGCTTGCAAATAGTTTTACTTTCTTGGCACTGGAAG
GGTAGTTCTGGAAAGCTACTTTGTTGAGAGTCTCATTCTTCCCTGGAGTTAATAGAGTGA
TTCACAATCTTTGGGGTTTTCTCCTCATCAAAGCATTTCCTTAAGTGCCTATCTAAAAGC
AATTAAAGACTGTGTCTGCCCTTTAGAAGCTAAGAATTTGATTTCATGATGCAAATTAAT
AGATAATTTGCAAAGTACCCTTGAGATTGAATTTTCTCTATTATATATTTCCCATATTTT
AGGTGAATAATTTAATTTAAATGACAAAACCTATCTAGTCAACTGGGCATAATGACATT
TTCTTTAAATTAGACTCTATTTTGAATTTAAAGAGTTTTATTATAAACCGTGTGTTTTTG
GTTTTTCTAAGTATATAGAAAGCTTGTATAATTCAGATTTATCAATTTCTGATTTAATG
TAGACTTTGACTTTTTTTATTAAAAACCTTTGTATTAAAGCAAGTTATGTTATTTTTCTTT
TATGCATTTATTACTAACATAGCTTTAAATCTTTAAATGTATTGAAGCATTGTGCTGTCT
GAAAATAAGGAATTGCTTATAAACCCAGCCACTTCTGAATACAATATGTAGCTGATTTAAT
AAGCTAGTTAGTGAATGGAAAATAAGTGTGGAGTATTAAAAATGTTCTTTGGTTGGTAAG
GCCTAAGATAGGGTTTTCATTTATTTCTATACTTTTTCTGTTTTTTAAACACCTGCATATT
TTTATGTAAATCTCTAAATTTAAAATATTTTAAAGTACATTTATTTTTGGTGTTTTTATTGT
ATAAAACCTTAGACAATCAATCAGTCAGTCTTTACTGACAGGAGCAGCAGCTATCTGTCT
TTTGCTGATCTACAAATAAATGAATTGAGAATTTAGTCCATAGAGGTCCCTGGCTACCAA
ACACATTCTCCTTTGAATTGTTAAAATTCAGAACATTCAAATAACTGTTTTGCTACAAC
CCATGATTATTTTCTGTTGTGTTTATTTAAATTTACTTTCTCTTTAGAAGTGCACCTTAT
TTCTGAAAAATCTTAATGAAACAAACGCTTAGAACAAATATAAATATGAGACACTTGGA
CTACTAGAGATATTTTAGATTTTTATGAAAAAATGTGAGGGGATATTGCTGCTTTAAAA
AGGAATAAAGTAATAAAAAATATATCTCAGCTATTTTTTTAAAGCAATATAATTGAGCAAT
TGTCTAGAAAAGTAATCATGAGGCTACTGAGTTTGGTGTTCAGTTACTGAGTTTCAAAAA
TGTTTTGGTGGCATGAGGACAAAATTTCAATTGAAGGTAAGATAAGAATAAAAACTATGTT
TAC

SEQ ID NO: 9_AA210825_H

CACGAGGGCTACTGGCGCCTGGCGACCCTCCCTGCCCCCACCCAACCCCGCTCCGGCAA
CGCCCCCTTCTCAGGCTCCCGACCGAACTTTTCTCCAACCTTCTGCGACTCGTGAGATT
CCCTTCTACCCACTCCGGCCCTCGGGACCCCTCTGCCCATCCCTGGCCGGTCCGGTCCC
TGCGAACCCTTTATCTCTGGAATCCACTCGGTCCCCGACTCAGAGACTCCTGCCCTCCA
CCCCAAGGACCCCGCCATCCTCAGGTCCCCTCCGCTGCCAGATCTTTTCTCGGATCCC
CGCTCTCCACACCTGCTCACGAGATCCCGCGGATCTAGAACCCAGGGTCCCCCGGGGC
CCCCCGGCGGGTCCCGGGTGGGCTCCAGGCGGGCGGTCCCCGGCTCCCCCATGGCCAC
CGCCCCCTCATTATCCCGCCGGGTCCCTGGCTCTCCCGGCGGGGTCTCCTCCGCCCC
CCGGCGGCCTAGAGCTGCAGTCGCCGCCACCGCTACTGCCCCAGATCCCGGCCCCGGGT
CCGGGGTCTCCTTTACATCCAGATCGGGCTGACCCGCGAGTTCTGTGCTGTTGCCCGCCG
CCTCCGAGCTGGCTCATGTGAAGCAGCTGGCCTGTTCCATCGTGAGACAGAAAGTTCCCTG
AGTGTGGCTTCTACGGCCTTTACGACAAGATCCTGCTTTTCAAACATGACCCACGTCGG
CCAACCTCCTGCAGCTGGTGGCTCGTCCGGAGACATCCAGGAGGGCGACCTGGTGGAGG
TGGTGTGTCGGCCTCGGCCACCTTCGAGGACTTCAGATCCGCCCCGACGCCCTCACGG
TGCACTCCTATCGGGCGCCTGCCTTCTGTGATCACTGCGGGGAGATGCTCTTCGGCCTAG
TGCGCCAGGGCCTCAAGTGCGATGGCTGCGGGCTGAACCTACCACAAGCGCTGTGCCTTCA
GCATCCCCAACAACTGTAGTGGGGCCCGCAAACGGCGCCTGTATCCACGTCTCTGGCCA
GTGGCCACTCGGTGCGCCTCGGCACCTCCGAGTCCCTGCCCTGCACGGCTGAAGAGCTGA
GCCGTAGCACCACCGAACTCCTGCCTCGCCGTCCCCCGTCATCCTCTTCTCTCTCTG
CCTCATCGTATACGGGCCGCCCATTTAGAGCTGGACAAGATGCTGCTCTCCAAGGTCAAGG
TGCCGCACACCTTCTCATCCACAGCTATACACGGCCACCGTTTGCCAGGCTTGCAAGA
AACTCCTCAAGGGCCTCTTCCGGCAGGGCCTGCAATGCAAAGACTGCAAGTTTAACTGTC

FIGURE 2H

ACAAACGCTGCGCCACCCGCGTCCCTAATGACTGCCTGGGGGAGGCCCTTATCAATGGAG
ATGTGCCGATGGAGGAGGCCACCGATTTTCAGCGAGGCTGACAAGAGCGCCCTCATGGATG
AGTCAGAGGACTCCGGTGTTCATCCCTGGCTCCCACTCAGAGAATGCGCTCCACGCCAGTG
AGGAGGAGGAAGGCGAGGGAGGCAAGGCCAGAGCTCCCTGGGGTACATCCCCCTAATGA
GGGTGGTGCATCGGTGCGACACACGACGCGGAAATCCAGCACCCACGCTGCGGGAGGGTT
GGGTGGTTTATTACAGCAACAAGGACACGCTGAGAAAGCGGCACTATTGGCGCCTGGACT
GCAAGTGTATCACGCTCTTCCAGAACAACACGACCAACAGATACTATAAGGAAATTCCGC
TGTGAGAAATCCTCACGGTGGAGTCCGCCAGAACTTCAGCCTTGTGCCGCCGGGCACCA
ACCCACACTGCTTTGAGATCGTCACTGCCAATGCCACCTACTTCGTGGGCGAGATGCCTG
GCGGGACTCCGGGTGGGCCAAGTGGGCAGGGGGCTGAGGCCGCCCGGGGGCTGGNNGAGA
CAGCCATCCGCCAGGCCCTGATGCCCCTCATCCTTCAGGACGCACCCAGCGCCCCAGGCC
ACGCGCCCCACAGACAAGCTTCTCTGAGCATCTCTGTGTCCAACAGTCAGATCCAAGAGA
ATGTGGACATTGCCACTGTCTACCAGATCTTCCCTGACGAAGTGCTGGGCTCAGGGCAGT
TTGGAGTGGTCTATGGAGGAAAACACCGGAAGACAGGCCGGGACGTGGCAGTTAAGGTCA
TTGACAAACTGCGCTTCCCTACCAAGCAGGAGAGCCAGCTCCGGAATGAAGTGGCCATTC
TGCAGAGCCTGCGGCATCCCGGGATCGTGAACCTGGAGTGCATGTTTCGAGACGCCTGAGA
AAGTGTGTTGTGGTGATGGAGAAGCTGCATGGGGACATGTTGGAGATGATCCTGTCCAGTG
AGAAGGGCCCGCTGCCCTGAGCGCCTCACCAAGTTCCTCATCACCCAGATCCTGGTGGCTT
TGAGACACCTTCACTTCAAGAACATTGTCCACTGTGACTTGAAACCAGAAAACGTGTTGC
TGGCATCAGCAGACCCATTTCCCTCAGGTGAAGCTGTGTGACTTTGGCTTTGCTCGCATCA
TCGGCGAGAAGTCGTTCCGCCGCTCAGTGGTGGGCACGCCGGCCTACCTGGCACCCGAGG
TGCTGCTCAACCAGGGCTACAACCGCTCGCTGGACATGTGGTCAGTGGGCGTGATCATGT
ACGTCAGCCTCAGCGGCACCTTCCCTTTCAACGAGGATGAGGACATCAATGACCAGATCC
AGAACGCCCGCTTCATGTACCCGCCAGCCCCTGGAGCCACATCTCAGCTGGAGCCATTG
ACCTCATCAACAACCTGCTGCAGGTGAAGATGCGCAAACGCTACAGCGTGGACAAATCTC
TCAGCCACCCCTGGTTACAGGAGTACCAGACGTGGCTGGACCTCCGAGAGCTGGAGGGGA
AGATGGGAGAGCGATACATCACGCATGAGAGTGACGACGCGCGCTGGGAGCAGTTTGCAG
CAGAGCATCCGCTGCCCTGGGTCTGGGCTGCCACGACAGGGATCTCGGTGGGGCCTGTC
CACCACAGGACCACGACATGCAGGGGCTGGCGGAGCGCATCAGTGTCTCTGAGGTCCTG
TGCCCTCGTCCAGCTGCTGCCCTCCACAGCGGTTCTTCACAGGATCCCAGCAATGAACTG
TTCTAGGGAAAGTGGCTTCCCTGCCCAAACCTGGATGGGACACGTGGGGAGTGGGGTGGGG
GAGCTATTTCCAAGGCCCTCCCTGTTTCCCCAGCAATTAAACGGACTCATCTCTGGCC
CCATGGCCTTGATCTCAGCAAAA

SEQ ID NO: 10_AA127299_H

ATTCAATTTCATAATTGTTGGTGCAAAAGATTTGCTTGCTATGGATTCAAATGGTCTTTCT
GATCCTTACATCAAAATCACAAATCTTTCTCAAAAACGAAAGTGATTAAGAAAACCTTG
ACTCCAACCTTGAATGAAACTTTTTTTGTGCATTTTCCAGAAAAACAACCCTTGAATTA
GAATGTTGGGACCACGATACTTTTTTCAGATGATTTTATTGGCAAGGCTTCCATTTCTTG
GCAGAGATTCCAGCTTTGGCAGAAGTTGATATGTGGATAGATATGAAAACGAAAAAGGA
GAATTTGCAGGAAAA

SEQ ID NO: 11_AA316804_H

ATGTCTGCAATAATTCCCCTCCATCAGCCCAGAAGTCTGTATTACCCACAGCTATTCCT
GCTGTGCTTCCAGCTGCTTCTCCGTGTTCAAGTCCTAAGACGGGACTCTCTGCCCCACTC
TCTAATGGAAGCTTCAGTGCACCATCACTACCAACTCCAGAGGCTCAGTGCATACAGTT
TCATTTCTACTGCAAAATGGCCTCACACGGGAGAGTGTTACCATTGAAGCCCAGGAACTG
TCTTTATCTGCTGTCAAGGATCTTGTGTGCTCCATAGTTTATCAAAAGTTTCCAGAGTGT
GGATTCTTTGGCATGTATGACAAAATCTTCTCTTTTCGCCATGACATGAACTCAGAAAAC
ATTTTGCAGCTGATTACCTCAGCAGATGAAATACATGAAGGAGACCTAGTGGAAGTGGTT

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FIGURE 2I

CTTTCAGCTTTAGCCACAGTAGAAGACTTCCAGATTCGTCCACATACTCTCTATGTACAT
TCTTACAAAGCTCCTACTTTCTGTGATTACTGTGGTGAGATGCTGTGGGGATTGGTACGT
CAAGGACTGAAATGTGAAGGCTGTGGATTAAATTACCATAAACGATGTGCCTTCAAGATT
CCAAATAACTGTAGTGAGTAAGAAAGAGACGTCTGTCAAATGTATCTTTACCAGGACCC
GGCCTCTCAGTTCCAAGACCCCTACAGCCTGAATATGTAGCCCTTCCCAGTGAAGAGTCA
CATGTCCACCAGGAACCAAGTAAGAGAATTCCTTCTTGGAGTGGTCGCCCCAATCTGGATG
GAAAAGATGGTAATGTGCAGAGTGAAAGTTCCACACACATTTGCTGTTCACTCTTACACC
CGTCCCACGATATGTCAGTACTGCAAGCGGTTACTGAAAGGCCTCTTTCGCCAAGGAATG
CAGTGTAAGATTGCAAATTCAACTGCCATAAACGCTGTGCATCAAAAGTACCAAGAGAC
TGCCTTGGAGAGGTTACTTTCAATGGAGAACCCTCCAGTCTGGGAACAGATACAGATATA
CCAATGGATATTGACAATAATGACATAAATAGTGATAGTAGTCGGGGTTTGGATGACACA
GAAGAGCCATCACCCCCAGAAGATAAGATGTTCTTCTTGGATCCATCTGATCTCGATGTG
GAAAGAGATGAAGAAGCCGTTAAACAATCAGTCCATCAACAAGCAATAATATTCCGCTA
ATGAGGGTTGTACAATCCATCAAGCACACAAAGAGGAAGAGCAGCACAATGGTGAAGGAA
GGGTGGATGGTCCATTACACCAGCAGGGATAACCTGAGAAAGAGGCATTATTGGAGACTT
GACAGCAAATGTCTAACATTATTTTCAAGATGAATCTGGATCAAAGTATTATAAGGAAATT
CCACTTTTCAAGAAATTCCTCCGCATATCTTACCACGAGATTTTCAACAACATTTTCAAGGC
AGCAATCCACACTGTTTTTGAATCATTACTGATACTATGGTATACTTCGTTGGTGAGAAC
AATGGGGACAGCTCTCATAATCCTGTTCTTGCTGCCACTGGAGTTGGACTTGATGTAGCA
CAGAGCTGGGAAAAGCAATTCGCCAAGCCCTCATGCCTGTTACTCCTCAAGCAAGTGTT
TGCATTCTCCAGGGCAAGGGAAAGATCACAAAGATTTGTCTACAAGTATCTCTGTATCT
AATTGTCAGATTCAGGAGAATGTGGATATCAGTACTGTTTACCAGATCTTTGCAGATGAG
GTGCTTGGTTTCAAGGCCAGTTTGGCATCGTTTATGGAGGAAAACATAGAAAGACTGGGAGG
GATGTGGCTATTAAAGTAATTGATAAGATGAGATTCCCCACAAAACAAGAAAGTCAACTC
CGTAATGAAGTGGCTATTTTACAGAATTTGCACCATCCTGGGATTGTAAACCTGGAATGT
ATGTTTGAACCCCAAGACGAGTCTTTGTAGTAATGGAAAAGCTGCATGGAGATATGTTG
GAAATGATTCTATCCAGTGAGAAAAGTCGGCTTCCAGAACGAATTACTAAATTCATGGTC
ACACAGATACTTGTGTGCTTTGAGGAATCTGCATTTTAAGAATATTGTGCACTGTGATTTA
AAGCCAGAAAATGTGCTGCTTGCATCAGCAGAGCCATTTCTCAGGTGAAGCTGTGTGAC
TTTGGATTGTGACGCATCATTGGTGAAAAGTCATTCAAGGAGATCTGTGGTAGGAAGTCCA
GCATACTTAGCCCCCTGAAGTTCTCCGGAGCAAAGGTTACAACCGTTCCCTAGATATGTGG
TCAGTGGGAGTTATCATCTATGTGAGCCTCAGTGGCACATTTCTTTTAAATGAGGATGAA
GATATAAATGACCAAATCCAAATGCTGCATTTATGTACCCACCAAATCCATGGAGAGAA
ATTTCTGGTGAAGCAATTGATCTGATAACAATCTGCTTCAAGTGAAGATGAGAAAACGT
TACAGTGTGACAAATCTCTTAGTCATCCCTGGCTACAGGACTATCAGACTTGGCTTGAC
CTTAGAGAATTTGAAACTCGCATTTGGAGAACGTTACATTACACATGAAAGTGATGATGCT
CGCTGGGAAATACATGCATACACACATAACCTTGTATACCCAAAGCACTTCATTATGGCT
CCTAATCCAGATGATATGGAAGAAGATCCTTAA

SEQ ID NO: 12_PKNBETA_H

ATGGAGGAGGGGGCGCCGCGGCAGCCTGGGCGGAGCCAGTGGCCCCCAGAGGATGAGAAG
GAGGTGATCCGCCGGGCCATCCAGAAAGAGCTGAAGATCAAGGAGGGGGTGGAGAACCTG
CGGCGCGTGCCACAGACCGCCGCACTTGGGCCATGTGCAGCAGCTGCTGCGGTCTCTCC
AACCGCCGCCTGGAGCAGCTGCATGGCGAGCTGCGGGAGCTGCACGCCCCGAATCCTGCTG
CCCGGCCCTGGGCCTGGCCCAGCTGAGCCTGTGGCCTCAGGACCCCGCCGTGGGCAGAG
CAGCTCAGGGCTCGGCACCTAGAGGCTCTCCGGAGGCAGCTGCATGTGGAGCTGAAGGTG
AAACAGGGGGCTGAGAACATGACCCACACGTGCGCCAGTGGCACCCCAAGGAGAGGAAG
CTCCTTGACAGCTGCCAGCAGATGCTGCGGGACAGCCAGCTGAAGGTGGCCCTGCTGCGG
ATGAAGATCAGCAGCCTGGAGGCCAGTGGGTCCCCGGAGCCAGGGCCTGAGCTACTGGCG
GAGGAGCTACAGCATCGACTGCACGTTGAGGCAGCGGTGGCTGAGGGGCGCCAAGAAGCTG

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FIGURE 2J

GTGAAACTGCTTAGTAGCCGGAGAACACAGGACCGCAAGGCACTGGCTGAGGCCAGGQC
CAGCTACAGGAGTCCTCTCAGAACTGGACCTCCTGCGCCTGGCCTTGGAGCAGCTGCTG
GAGCAACTGCCTCCTGCCACCCCTTTGCGCAGCAGAGTGACCCGAGAGTTGCGGGCTGCG
GTGCCTGGATACCCCCAGCCTTCAGGGACACCTGTGAAGCCACCGCCCTAACAGGGACA
CTGCAGGTCCGCTCCTGGGCTGTGAACAGTTGCTGACAGCCGTGCCTGGGCGCTCCCCA
GCGGCCGCACTGGCCAGCAGCCCCCTCCGAGGGCTGGCTTCGGACCAAGGCCAAGCACCAG
CGTGGCCGAGGCGAGCTTGCCAGTGAGGTGCTGGCTGTGCTAAAGGTGGACAACCGTGTT
GTGGGGCAGACGGGCTGGGGGCAGGTGGCCGAACAGTCCTGGGACCAGACCTTTGTATC
CCTACTGGAGCGAGCCCGTGAGCTGGAGATTGGGGTACACTGGCGGGACTGGCGGCAGCTA
TGTGGCGTGGCCTTCTGAGACTTGAAGACTTCCTGGACAATGCCTGTCACCAACTGTCC
CTCAGCCTGGTACCGCAGGGACTGCTTTTGGCCAGGTGACCTTCTGCGATCCTGTCTATT
GAGAGGCGGCCCCGGCTGCAGAGGCAGGAACGCATCTTCTCTAAACGCAGAGGCCAGGAC
TTCTTGAGGCGTTCGCAGATGAACCTCGGCATGGCGGCCTGGGGGCGCCTCGTCATGAAC
CTGCTGCCCCCTGCAGCTCCCCGAGCACAATCAGCCCCCTAAAGGATGCCCTCGGACC
CCAACAACACTGCGAGAGGCCTCTGACCCTGCCACTCCAGTAATTTCTTGCCCAAGAAG
ACCCCTTGCGTGAAGAGATGACACCCCCACCCAAGCCCCACGCCTCTACCTCCCCAG
GAGCCAACATCCGAGGAGACTCCGCGCACCAACCGTCCCATATGGAGCCTAGGACTCGA
CGTGGGCCATCTCCACCAGCCTCCCCACCAAGAACCCCTCGGCTTCAGGACTTCCGC
TGCTTAGCTGTGCTGGGCCGGGGACACTTTGGGAAGGTCTCTGGTCCAGTTCAAGGGG
ACAGGGAAATACTACGCCATCAAAGCACTGAAGAAGCAGGAGGTGCTCAGCCGGGACGAG
ATAGAGAGCCTGTACTGCGAGAAGCGGATCCTGGAGGCTGTGGGCTGCACAGGGCACCCCT
TTCTTGCTCTCCCTCCTTGTCTGCTTCCAGACCTCCAGCCATGCCCCGCTTTGTGACTGAG
TTTGTGCTGCTGGTGGTGACCTCATGATGCAGATCCACGAGGATGTCTTCCCCGAGCCCCAG
GCCCCGCTTCTACGTGGCTTGTGTTGTCTGGGGCTGCAGTTCTTACACGAGAAGAAGATC
ATTTACAGGGACCTGAAGTTGGATAACCTTCTGCTGGATGCCCAGGGATTCTTGAAGATC
GCAGACTTTGGAAGCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGT
GGCACCCCGGAGTTCTTGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGCCGCTC
GACTGGTGGGCGCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCCA
GGGGACACAGAGGAAGAGGTGTTGACTGCATCGTCAACATGGACGCCCCCTACCCCGGC
TTTCTGTGCGGTGCAAGGGCTTGAGTTTATTGAGAAGCTCCTCCAGAAGTGCCCGGAGAAG
CGCCTCGGGGACGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACC
ACCAACTGGCAAGCCCTGCTCGCCCGCACCATCCAGCCCCCTTCGTGCCTACCCTGTGT
GGCCCTGCGGACCTGCGCTACTTTGAGGGCGAGTTTACAGGGCTGCCGCCTGCCCTGACC
CCACCTGCACCCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGAC
TTTGTGTCAGAGCGATTCTTGAACCCCTGA

SEQ ID NO: 13_AI021023_M PKNBETA_M

GCTGAAGTGGGATAACCTTCTGCTGGATGCCCAGGGATTCTTGAAGATCGCAGACTTTGG
ACTCTGCAAGGAAGGGATCGGCTTCGGGGACCGGACTAGCACCTTCTGTGGCACCCCGGA
GTTCTTGCTCCCGAGGTGCTGACCCAGGAGGCATACACAGGGCTGTGGACTGGTGGGG
GCTGGGTGTGCTGCTCTACGAGATGCTGGTGGGTGAGTGCCCGTTCCAGGGGACACAGA
GGAAGAGGTGTTTGAAGTGCATCGTCAACATGGACGCCCCCTACCCCGGCTTTCTGTGCGT
GCAAGGGCTTGAGTTTATTGAGAAGCTCCTCCAGAAGTGCCCGGAGAAGCGCCTCGGGGC
GGGTGAGCAGGATGCCGAGGAGATCAAGGTCCAGCCATTCTTCAGGACCACCAACTGGCA
AGCCCTGCTCGCCCGCACCATCCAGCCCCCTTTGTGCCTACCCTGTGTGGCCCTGCGGA
CCTGCGCTACTTTGAGGGCGAGTTTACAGGGCTGCCGCCTGCCCTGACCCACCTGCACC
CCACAGCCTCCTCACTGCCCGCCAACAGGCCGCCTTCCGGGACTTCGACTTTGTGTGAGA
GCGATTCTTGAACCCCTGAGGGCATCTCCTGGCACCTCTGTCCCTTCCCCACAGACTG
TTAGAGCCTCTGCTCGTTTACCCCGTGCGCCCTGCCTGGAGGTCCAGGCCTTGCTGGGTAC
TTCTGAGCCCTTGGGATTCAAAGTGGCAGCCATGGGGCCACTGTTGTGGGCTTTGTCTCAG

FIGURE 2K

TGTCAC TGGGCAAAGTGTGTCCCTTCCCCCTCCAGCTCGCCCTCTTCTACCTCCCAGCGA
GACCTGGCCCAGAAAGGGTGCCGCAGCAAGGAGTGATATGGTTTGTCTTTTAAAGACTGG
ACTTGCTTTATATTAAATTTGTAAAAGTG

SEQ ID NO: 14_H19102_H

GGTGGCAACATCCGGGGTCCCTGGGCCCCGAGGCTGGAAGAGCCTCTGGACAGGTTTGGGA
ACCATCAGGTCAGATCTGGAAGAACTCTGGGAAC TACGGGGGCACCACTATCTGCACCAG
GAATCCCTAAAGCCAGCCCCAGTACTGGTAGAGAAGCCTCTGCCAGAGTGCCAGTGCCT
CAGTTCATCAACCTCTTTCTACCAGAGTTTCCCATTAGGCCCATTAGGGGGCAGCAGCAG
CTGAAGATTTTAGGCCCTCGTGGCTAAAGGCTCCTTTGGAAGTGTCTTCAAGGTGCTAGAT
TGCACCCAGAAAGCTGTATTTGCAGTGAAGGTGGTGCCCCAAGGTAAAGTCTTACAGAGG
GATACCGTGAGGCAGTGCAAAGAGGAGGTAGCATCCAGCGACAGATCAACCATCCCTTT
GTACACAGCTTGGGGGACAGCTGGCAGGGAAAACGGCACCTTTTCATTATGTGTAGCTAC
TGCAGCACAGATCTGTACTCCCTTTGGTTCGGCTGTTGGCTGCTTTCCTGAGGCTTCCATC
CGTCTCTTTGCTGCCGAGTTGGTGCTGGTACTGTGTTATCTCCATGACTTGGGCATCATG
CATCGAGATGTGAAGATGGAGAATATTCTTCTAGATGAACGAGGCCATCTGAAACTGACA
GACTTTGGTCTGTCCCGCCACGTGCCCCAGGGAGCTCAAGCCTACACTATCTGTGGCACT
CTTCAGTACATGGCCCCAGAGGTCTTAAGTGGAGGACCTTACAACCATGCTGCTGATTGG
TGGTCCCTGGGTGTCTTGCTTTTCTCTCTGGCGACTGGAAAGTTTCCAGTGGCTGCAGAG
AGAGATCATGTGGCCATGTTGGCAAGTGTGACCCACAGTGAAGTCTGAGATCCCAGCTTCT
CTTAACCAGGGCCTCTCACTCCTGCTCCATGAGCTCTTATGCCAGAACCCCCCTCCATCGT
CTACGTTATCTGCATCACTTCCAGGTCCACCCTTTCTTTTCGGGGTGTGGCCTTCGACCCA
GAGCTCCTACAGAAGCAGCCAGTGAAGTGTGTCACGGAGACACAAGCTACCCAGCCCAGT
TCAGCGGAGACCATGCCCTTTGACGACTTTGACTGTGATCTGGAGTCCTTCTTGCTCTAC
CCTATCCCTGCTTGA

SEQ ID NO: 15_AA476563_H

ATGGAATTCTTTAGGATAGACAGTAAGGATAGCGCAAGTGAAGTCTTGGGACTTGACTTT
GGAGAAAAATTGTATAGTCTAAATCAGAACCTTTGAAACCATTCTTTACTCTTCCAGAT
GGAGACAGTGCTTCTAGGAGTTTAAATACTAGTGAAAGCAAGGTAGAGTTTAAAGCTCAG
GACACCATTAGCAGGGGCTCAGATGACTCAGTGCCAGTTATTTTCGTTTAAAGATGCTGCT
TTTGATGATGTCAGTGGTACTGATGAAGGAAGACCTGATCTTCTTGTAATTTACCTGGT
GAATTGGAGTCAACAAGAGAAGCTGCAGCAATGGGACCTACTAAGTTTACACAACTAAT
ATAGGGATAATAGAAAATAAACTCTTGGAAGCCCCCTGATGTTTTATGCCTCAGGCTTAGT
ACTGAACAATGCCAAGCACATGAGGAGAAAGGCATAGAGGAACTGAGTGATCCCTCTGGG
CCCAAATCCTATAGTATAACAGAGAAACACTATGCACAGGAGGATCCCAGGATGTTATTT
GTAGCAGCTGTTGATCATAGTTCAGGAGATATGTCTTTGTTACCCAGCTCAGATCCT
AAGTTTCAAGGACTTGGAGTGGTTGAGTCAGCAGTAACTGCAAACAACACAGAAGAAAGC
TTATTCGGTATTTGTAGTCCACTCTCAGGTGCTAATGAATATATTGCAAGCACAGACACT
TTAAAAACAGAAGAAGTATTGCTGTTTACAGATCAGACTGATGATTTGGCTAAAGAGGAA
CCAACTTCTTTATTCCAGAGAGACTCTGAGACTAAGGGTGAAAGTGGTTTAGTGCTAGAA
GGAGACAAGGAAATACATCAGATTTTTTGAGGACCTTGATAAAAAATTAGCACTAGCCTCC
AGGTTTTTACATCCCAGAGGGCTGCATTCAAAGATGGGCAGCTGAAATGGTGGTAGCCCTT
GATGCTTTACATAGAGAGGGAATTGTGTGCCGCGATTTGAACCCAAACAACATCTTATTG
AATGATAGAGGACACATTCAGCTAACGTATTTTAGCAGGTGGAGTGAGGTTGAAGATTCC
TGTGACAGCGATGCCATAGAGAGAATGTACTGTGCCCCAGAGGTGGAGCAATCACTGAA
GAACTGAAGCCTGTGATTGGTGGAGTTTGGGTGCTGTCTCTTTGAACTTCTCACTGGC
AAGACTCTGGTTGAATGCCATCCAGCAGGAATAAATACTCACACTACTTTGAACATGCCA
GAATGTGTCTCTGAAGAGGCTCGCTCACTCATTCAACAGCTCTTGCAAGTTCAATCCTCTG

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FIGURE 2L

GAACGACTTGGTGCTGGAGTTGCTGGTGTGGAAGATATCAAATCTCATCCATTTTTTTACC
CCTGTGGATTGGGCAGAACTGATGAGATGA

SEQ ID NO: 16_AA626690_H

ATGCTACCATTCGCTCCTCAGGACGAGCCCTGGGACCGAGAAATGGAAGTGTTTCAGCGGC
GGCGGCGCGAGCAGCGGCGAGGTAAATGGTCTTAAAATGGTTGATGAGCCAATGGAAGAG
GGAGAAGCAGATTCTTGTCATGATGAAGGAGTTGTAAAGAAATCCCTATTACTCATCAT
GTTAAGGAAGGCTATGAGAAAGCAGATCCTGCACAGTTTGAGTTGCTCAAGGTTCTTGGT
CAGGGGTCAATTTGGAAAGGTTTTTCTTGTTAGAAAGAAGACCGGTCCTGATGCTGGGCAG
CTCTATGCAATGAAGGTGTTAAAAAAGCCTCTTTAAAAGTTTCGAGACAGAGTTTCGGACA
AAGATGGAGAGGGATATACTGGTGGAAAGTAAATCATCCATTTATTGTCAAATTCGACTAT
GCCTTTTCAGACTGAAGGGAACTGTACTTAATACTGGATTTTCTCAGGGGAGGAGATGTT
TTCACAAGATTATCCAAAGAGGTTCTGTTTACAGAGGAAGATGTGAAATTCTACCTCGCA
GAACTGGCCCTTGCTTTGGATCATCTGCACCAATTAGGAATTGTTTATAGAGACCTGAAG
CCAGAAAACATTTTGGCTTGATGAAATAGGACATATCAAATTAACAGATTTTGGACTCAGC
AAGGAGTCAGTAGATCAAGAAAAGAAGGCTTACTCATTTTGTGGTACAGTAGAGTATATG
GCTCCTGAAGTAGTAAATAGGAGAGGCCATCCCAGAGTGCTGATTGGTGGTCATATGGT
GTTCTTATGTTTGAAATGCTTACTGGTACTCTGCCATTTCAAGGTAAAGACAGAAATGAG
ACCATGAATATGATATTAAAAGCAAACTTGGAATGCCTCAATTTCTTAGTGCTGAAGCA
CAAAGTCTTCTAAGGATGTTATTCAAAGGAATCCAGCAAATAGATTGGGATCAGAAGGA
GTTGAAGAAATCAAAGACATCTGTTTTTGGCAAATATTGACTGGGATAAAATTATATAAA
AGAGAAGTTCAACCTCCTTTCAAACCTGCTTCTGGAAAACCAGATGATACTTTTTGTTTT
GATCCTGAATTTACTGCAAAAACACCTAAAGATTCTCCCGGTTTGCCAGCCAGTGCAAAT
GCTCATCAGCTCTTCAAAGGATTCAGCTTTGTTGCAACTTCTATTGCAGAAGAATATAAA
ATCACTCCTATCACAAGTGCAAATGTATTACCAATTGTTTCAGATAAATGGAAATGCTGCA
CAATTTGGTGAAGTATATGAATTGAAGGAGGATATTGGTGTGCTCCTACTCTGTTTGC
AAGCGATGCATACATGCAACTACCAACATGGAATTTGCAGTGAAGATCATTGACAAAAGT
AAGCGAGACCCTTCAGAAGAGATTGAAATATTGATGCGCTATGGACAACATCCCAACATT
ATTACTTTGAAGGATGTCTTTGATGATGGTAGATATGTTTACCTTGTTACGGATTTAATG
AAAGGAGGAGAGTTACTTGACCGTATTCTCAAACAAAAATGTTTCTCGGAACGGGAGGCT
AGTGATATACTATATGTAATAAGTAAGACAGTTGACTATCTTCATTGTCAAGGAGTTGTT
CATCGTGATCTTAAACCTAGTAATATTTTATACATGGATGAATCAGCCAGTGAGATTCA
ATCAGGATATGTGATTTTGGGTTTGCAAAACAACCTTCGAGGAGAAAATGGACTTCTCTTA
ACTCCATGCTACACTGCAAACTTTGTTGCACCTGAGGTTCTTATGCAACAGGGATATGAT
GCTGCTTGTGATATCTGGAGTTTAGGAGTCCTTTTTTACACAATGTTGGCTGGCTACACT
CCATTTGCTAATGGCCCCAATGATACTCCTGAAGAGATACTGCTGCGTATAGGCAATGGA
AAATTCTCTTTGAGTGGTGGAACTGGGACAATATTTTCAGACGGAGCAAAGGATTTGCTT
TCCCATATGCTTCATATGGACCCACATCAGCGGTATACTGCTGAACAAATATTAAAGCAC
TCATGGATAACTCACAGAGACCAGTTGCCAAATGATCAGCCAAAGAGAAATGATGTGTCA
CATGTTGTTAAGGGAGCAATGGTTGCAACATACTCTGCCCTGACTCACAAGACCTTTCAA
CCAGTCCTAGAGCCTGTAGCTGCTTCAAGCTTAGCCCAGCGACGGAGCATGAAAAAGCGA
ACATCAACTGGCCTGTAA

SEQ ID NO: 17_AA215680_H

ATGAGCCTGGTGGCCTGTGAGTGCCCTGCCCAGCCCCGGCCTGGAGCCTGAGCCTTGCTCA
CGAGCACGGTCCCAAGCTCACGTGTACCTGGAGCAGATTCGCAACAGGGTGGCTCTGGGA
GTGCCTGACATGACAAAACGTGACTATCTGGTGGATGCGGCCACGCAGATCCGGCTGGCC
CTGGAGCGCGATGTTAGTGAGGACTATGAGGCGGCCTTCAACCACTATCAGAATGGCGTG
GACGTGCTGCTCCGTGGCATAACGTTGACCCCAACAAGGAGCGACGTGAGGCTGTGAAG
CTGAAAATTACCAAATACCTGCGGCGGGCAGAGGAGATCTTCAACTGCCACCTGCAGCGG

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FIGURE 2M

CCGCTGAGCAGTGGAGCCAGCCCCAGCGCGGGTTTCAGCAGCCTGAGGCTCCGGCCCCATT
CGCACGCTGAGCTCTGCCGTGGAGCAGCTGAGGGGCTGCAGGGTGGTCGGGGTTCATCGAG
AAGGTGCAGCTGGTCCAGGACCCGGCAACCGGAGGGACCTTTGTGGTGAAGAGCCTACCC
AGGTGCCACATGGTGAAGCAGGGAGCGGCTGACCATCATCCACACGGAGTCCCCCTACATG
ACGAAGCTGCTCAGGTACTTTGTGAGCGAGGACTCCATCTTCCTGCACCTGGAGCATGTG
CAAGGAGGCACTCTCTGGTCCCACCTGCTCTCCCAGGCGCACTCCCGACATTCTGGGCTC
AGCTCTGGCTCTACCCAGGAGAGGATGAAGGCTCAGCTCAACCCCCACCTCAACCTCCTG
ACCCCAGCGAGGCTTCCCTCAGGCCATGCCCTGGCCAGGACAGAATCGCCCTGGAGCCT
CCTAGGACTTCTCCGAACCTTCTCCTAGCTGGGGAGGCCCCATCCACCAGACCCCAGAGG
GAGGCTGAAGGTGAACCCACAGCCAGGACCAGACCTCTGGCTCCTCGGACCTTCCAAAG
GCCCCAGGTGGCCACCTGCACCTTCAAGCTAGGAGGGCTGGCCAGAATCAGACGCTGGG
CCCCCTCGGGGGCTCACTTGGGTTCTGAGGGGGCGGCCCGGTGCTAGGGGGCTGTGGC
CGAGGCATGGATCAGAGCTGCCTGTCAGCAGATGGGGCCGGCCGGGGCTGTGGCAGGGCC
ACCTGGAGTGTGAGAGAGGAGCAGGTGAAGCAGTGGGCGGCAGAGATGCTGGTAGCGCTG
GAGGCGCTGCACGAGCAGGGGGTGTGTGCCGGGACCTCCACCCCGGGAACCTGCTCCTG
GACCAGGCAGGTCACATCCGGCTCACATATTTGGCCAGTGGTCAGAGGTGGAGCCCCAG
TGCTGCGGGGAGGCCGTGGACAATCTCTACAGCGCCCCAGAGGTGGGTGGGATTTCCGAG
CTGACGGAAGCCTGTGACTGGTGGAGCTTTGGGTCTCTACTGTATGAACTGCTGACGGGA
ATGGCACTGTCCCAGAGCCACCCTTCAGGAATCCAGGCCACACCCAGCTCCAGCTGCCC
GAGTGGCTCAGTCGCCCAGCGGCCTCTCTGCTGACTGAGCTGCTGCAGTTCGAGCCTACC
CGGCGCCTGGGCATGGGAGAAGGTGGTGTGAGCAAACTCAAGTCCCATCCCTTTTTTCAGT
ACCATCCAATGGAGCAAGCTGGTGGGGTAA

SEQ ID NO: 18 SGK_H

ATGACGGTGAAACTGAGGCTGCTAAGGGCACCCCTCACTTACTCCAGGATGAGGGGCATG
GTGGCAATTCTCATCGCTTTCATGAAGCAGAGGAGGATGGGTCTGAACGACTTTATTTCAG
AAGATTGCCAATAACTCCTATGCATGCAAACACCCTGAAGTTCAGTCCATCTTGAAGATC
TCCCAACCTCAGGAGCCTGAGCTTATGAATGCCAACCCCTTCTCCTCCACCAAGTCCTTCT
CAGCAAATCAACCTTGGCCCGTCGTCCAATCCTCATGCTAAACCATCTGACTTTCACCTC
TTGAAAGTGATCGGAAAGGGCAGTTTTTGAAAGGTTCTTCTAGCAAGACACAAGGCAGAA
GAAGTGTTCTATGCAGTCAAAGTTTTACAGAAGAAAGCAATCCTGAAAAGAAAGAGGAG
AAGCATATTATGTCGGAGCGGAATGTTCTGTTGAAGAATGTGAAGCACCCCTTTCCTGGTG
GGCCTTCACTTCTCTTTCCAGACTGCTGACAAATTTGTACTTTGTCTTAGACTACATTAAT
GGTGGAGAGTTGTTCTACCATCTCCAGAGGGAACGCTGCTTCTGGAACCACGGGCTCGT
TTCTATGCTGCTGAAATAGCCAGTGCCTTGGGCTACCTGCATTCACTGAACATCGTTTAT
AGAGACTTAAAACCAGAGAATATTTTGCTAGATTACAGGGACACATTGTCCTTACTGAT
TTCGGACTCTGCAAGGAGAACATTGAACACAACAGCACAAATCCACCTTCTGTGGCAGG
CCGGAGTATCTCGCACCTGAGGTGCTTCATAAGCAGCCTTATGACAGGACTGTGGACTGG
TGGTGCCCTGGGAGCTGTCTTGTATGAGATGCTGTATGGCCTGCCGCCTTTTTATAGCCGA
AACACAGCTGAAATGTACGACAACATTCTGAACAAGCCTCTCCAGCTGAAACCAAATATT
ACAAATTCCGCAAGACACCTCCTGGAGGGCCTCCTGCAGAAGGACAGGACAAAGCGGCTC
GGGGCCAAGGATGACTTCATGGAGATTAAGAGTCATGTCTTCTTCTCCTTAATTAAGTGG
GATGATCTCATTAATAAGAAGATTACTCCCCCTTTTAACCCAAATGTGAGTGGGCCAAC
GAGCTACGGCACTTTGACCCCGAGTTTACCGAAGAGCCTGTCCCCAACTCCATTGGCAAG
TCCCCTGACAGCGTCCCTCGTCACAGCCAGCGTCAAGGAAGCTGCCGAGGCTTTCCTAGGC
TTTTCTATGCGCCTCCACGGACTCTTTCCTCTGA

SEQ ID NO: 19 AA107515_M

CGGGTCGACCCACGCGTCCGCCGGTTTCACTGCTCCCCTCAGTCTCTTTTGGGCTCTTTC
CGGGCATCGGGACGATGACCGTCAAAGCCGAGGCTGCTCGAAGCACCCCTTACCTACTCCA

FIGURE 2N

GAATGAGGGGAATGGTAGCGATTCTCATCGCTTTTATGAAACAGAGAAGGATGGGCCTGA
ACGATTTTATTTCAGAAGATTGCCAGCAACACCTATGCATGCAAACACGCTGAAGTTCAGT
CCATTTTGAAAATGTCCCATCCTCAGGAGCCGGAGCTTATGAACGCTAACCCCTCTCCTC
CGCCAAGTCCCTCTCAACAAATCAACCTGGGTCCGTCTCCAACCCTCACGCCAAACCCT
CCGACTTTCACCTTCTTGAAAGTGATCGGAAAGGGCAGTTTTTGAAAGGTTCTTCTGGCTA
GGCACAAGGCAGAAGAAGTATTCTATGCAGTCAAAGTTTTACAGAAGAAAGCCATCCTGA
AGAAGAAAGAGGAGAAGCATATTATGTCAGAGCGGAATGTTCTGTTGAAGAATGTGAAGC
ACCCTTTCCTGGTGGGCCTTCACTTCTCATTCCAGACCGCTGACAAGCTCTACTTTGTCC
TGGACTACATTAATGGTGGAGAGCTGTTCTACCATCTCCAGAGGGAGCGCTGCTTCCTGG
AACCACGGGCTCGATTCTACGCAGCTGAAATAGCCAGTGCCCTGGGCTATCTGCACTCCC
TAAACATCGTTTATAGAGACTTAAAACCTGAGAATATTCTCCTAGACTCCCAGGGGCACA
TCGTCTCTCACTGACNTATTTAGCTGCGTAGAATCGAGCATAACGGGACAACATCTACCT
TCTGTGGCAGCCTGAGTATCTGGCTCCTGAGGTCCTCCATAAGCAGCCGTATGACCGGA
CGGTGGACTGGTGGTGTCTTGGGGCTGTCTGTATGAGATGCTCTACGGCCTGCCCCCGT
TTTATAGCCGGAACACGGCTGAGATGTACGACAATATTCTGAACAAGCCTCTCCAGTTGA
AACCAATATTACAACTCGGCAAGGCACCTCCTGGAAGGCCTCCTGCAGAAGGACCGGA
CCAAGAGGCTGGGTGCCAAGGATGACTTTATGGAGATTAAGAGTCATATTTCTTCTCTT
TAATTAAGTGGGATGATCTCATCAATAAGAAGATTACACCCCATTTAACCCAAATGTGA
GTGGGCCCAGTGACCTTCGGCACTTCGATCCCGAGTTTACCGAGGAGCCGGTCCCCAGCT
CCATCGGCAGGTCCCCTGACAGCATCCTTGTACGGCCAGTGTGAAGGAAGCAGCAGAAG
CCTTCCTCGGCTTCTCCTATGCACCTCCTGTGGATTCTTCTCTCTGAGTGCTCCCGGGAT
GGTTCTGAAGGACTTCCTCAGCGTTTCTTAAAGTGTTTTCTGTTAGCCTTTGGTGGAGTTG
CCAGCTGACAGAACATTTTAAAAGAATTTGCACACCTGGAAGCTTGGCAGTCTCGCCTGC
CCGGCGTGGCGCGACGCAGCGCGCGCTGCTTGATGGGAGCTTTCGAAGAGCACACCCTC
CTCTCAATGAGCTTGTGAGGTCTTCTTTCTTCTCTTCTTCCAACGTGGTGCTAGCTCC
AGGCGAGCGAGCGTGAGAGTGCCGCCTGAGACAGACACCTTGGTCTCAGTTAGAAGGAAG
ATGCAGGTCTAAGAGGAATCCCCGCAGGTCTGTCTGAGCTGTGATCAAGAATATTCTGCA
ATGTGCCTTTTCTGAGATCGTGTTAGCTCCAAAGCTTTTCTCTATCGCAGAGTGTTCACT
TTGTGTTTGTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT
GTGGCGTGAGTGTGCTATGCCTGATCACAGACGGTGTGTTGTGAGCATCAATGTGACAC
TTGCAGGACACTACAATGTGGGACATTGTTTGTGTTTCTTCCACATTTGGAAGATAAATTTA
TGTGTAGACTGTTTTGTAAGATATAGTTAATAACTAAAACCTATTGAAACGGTCTTGCAA
TGACGAGCATTCAGATGCTTAAGGAAAGCATTGCTGCTACAAATATTTCTATTTTATAGAA
AGGGTTTTTATGGACCAATGCCCCAGTTGTGAGTCAAAGCCGTGGTGTGTTTCTATTGTTT
AAAATGTCACCTATAAAACGGGCATTATTTATGTTTTTTTTTCCCTTGTTCATATTCTTT
TGCATTCTGATTATTGTATGTATCGTGTAAGGAAGTCTGTACATTGGGTATAACACT
AGATATTTAACTTACAGGCTTATTTGTAAACCATCATTTTAATGTACTGTAATTAACAT
GGGTTATAATATGTACAATTCCTCCTCCTTACCACACAACCTTTTTTTGTGTGCGATAAAC
CAATTTTGGTTTGCAATAAAATCTTGAAAAC

SEQ ID NO: 20_AA109508_M

CCACCTGCAGCGGGAGCGCCGGTTCTTGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGT
GGCCAGCGCCATTGGCTACCTGCACTCCCTCAACATCATTTACAGGGATCTGAAACCAGA
GAACATTCTCTTGACTGCCAGGGACACGTGGTGTGACGGATTTTGGCCTCTGCAAGGA
AGGTGTAGAGCCTGAAGACACCACATCCACATTCTGTGGTACCCCTGAGTACTTGGCACC
TGAAGTGCTTCGGAAAGAGCCTTATGATCGAGCAGTGGACTGGTGGTGTGCTTGGGGGCAGT
CCTCTACGAGATGCTCCATGGCCTGCCGCCCTTCTACAGCCAAGATGTATCCAGATGTA
TGAGAACATTCTGCACCAGCCGCTACAGATCCCCGGAGGCCGACAGTGGCCGCCTGTGA
CCTCCTGCAAAGCCTTCTCCACAAGGACCAGAGGCAGCGCTGGGCTCCAAAGCAGACTT
TCTTGAGATTAAGAACCATGTATTCTTCAGCCCCATAAACTGGGATGACCTGTACCACAA

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FIGURE 20

GAGGCTAACTCCACCCTTCAACCCAAATGTGACAGGACCTGCTGACTTGAAGCATTGTTGA
CCCAGAGTTCACCCAGGAAGCTGTGTCCAAGTCCATTGGCTGTACCCCTGACACTGTGGC
CAGCAGCTCTGGGGCCTCAAGTGCATTCTCTGGGATTTTCTTATGCGCCAGAGGATGATGA
CATCTTGGATTGCTAGAAGAGAAGGACCTGTGAACTACTGAGGCCAGCTGGTATTAGTA
AGGAATTACCTTCAGCTGCTAGGAAGAGCGACTCAAACCTAACAATGGCTTCAACGAGAAG
CAGGTTTATTTTTTCCAGCACATAAAAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAG
GACAGGTCATCAGATACTCAGAGGCTGTATCTCTGCCCTGCCAACCTTGACAAATGGCTT
CCAATGTTAGGTTTGCTACAAGATGGTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAG
GGAAGGGAAAATGGAGGAAAGGGGAGAAGAGCAAAGGGCGCTTTTAAAGAGCTTTCCCAA
AAGCTCCACCCAATGACTTCTGCTTCCATCTCACTAACCACCCACCCCTACCTGGAATGG
AGGCTGGGAGATGTGGCTTATTTGCTGGGTACGTGACTATCCCTAATAACAAAGGGGTTT
TGACACTAAGACATTAGGGGAGAATGTTGGGTAGGCAGCCAGCACTCTTTTACCAGAGGG
CCTCCTGGTGTGTTGGATTTTGATCTCAATGTGTAAATGACAGAGATGTAACAAGCTCAT
AGGGTATCAATATCTCTTATTGTTCT

SEQ ID NO: 21_AA887783_H

CGGATGCATTTNTTGGTGTGCTCTTGAGGGATTAAATGCAAAGAGATCACACCATGGACT
ACAAGGAAAGCTGCCCAAGTGTAAGNATTCACAGCTCCGATGAACACAGAGAGAAAAAGA
AGAGGTTTACTGTTTATAAAGTTCTGGTTTTCAGTGGGAAGAAGTGAATGGTTTGTCTTCA
GGAGATATGCAGAGTTTGATAAACTTTATAACACTTTAAAAAACAGTTTCTCTGCTANGG
CCCTGAAGATTCTGCCAAGAGAATATTTGGTGATAATTTTGATCCAGATTTTATTAAC
AAAGACGAGCAGGACTAAACGAATTCATTTCAGAACCTAGTTAGGTATCCAGAACTTTATA
ACCATCCAGATGTCAGAGCATTCTTCAAATGGACAGTCCAAAACACCAGTCAGATCCAT
CTGAAGATGAGGATGAAAGAAGTTCTCAGAAGCTACACTCTACCTCACAGAACATCAACC
TGGGACCGTCTGGAAATCCTCATGCCAAACCAACTGACTTTGATTTCTTAAAGTTATTG
GAAAAGGCAGCTTTGGCAAGGTTCTTCTTGCAAACCGGAAACTGGATGGAAAATTTTATG
CTGTCAAAGTGTTACAGAAAAAATAGTTCTCAACAGAAAAAGAGCAAAAACATATTATGG
CTGAACGTAATGTGCTCTTGAAAAATGTGAAACATCCGTTTTTGGTTGGATTGCATTATT
CCTTCCAAACAACTGAAAAGCTTTATTTTGTCTGATTTTGTTAATGGAGGGGAGGGAC
ATGTTGTCTTAACAGATTTTGGGCTTTGTAAAGAAGGAATTGCTATTTCTGACACCACTA
CCACATTTTGTGGGACACCAGAGTATCTTGCACCTGAAGTAATTAGAAAACAGCCCTATG
ACAATACTGTAGATTGGTGGTGCCTTGGGGCTGTTCTGTATGAAATGCTGTATGGATTGC
CTCCTTTTTATTGCCGAGATGTTGCTGAAATGTATGACAATATCCTTCACAAACCCCTAA
GTTTGAGGCCAGGAGTGAGTCTTACAGCCTGGTCCATTCTGGAAGAAGTCTTAGAAAAAG
ACAGGCAAAATCGACTTGGTGCCAAGGAAGACTTTCTTGAAATTCAGAAATCATCCTTTTT
TTGAATCACTCAGCTGGGCTGACCTTGTACAAAAGAAGATTCCACCACCATTTAATCCTA
ATGTGGCTGGACCAGATGATATCAGAACTTTGACACAGCATTTACAGAAGAAACAGTTC
CATATTCTGTGTGTATCTTCTGACTATTCTATAGTGAATGCCAGTGTATTGGAGGCAG
ATGATGCATTTCGTTGGTTTCTCTTATGCACCTCCTTCAGAAGACTTATTTTTGTGAGCAG
TTTGCCATTCAGAAACCATTGAGCAAATAAGTCTATAGATGGGACTGAACTTCTATTT
GTGTGAATATATTCAAATATGTATACTAGTGCCTCATTTTTATATGTAATGATGAAAAC
TATGAAAAAATGTATTTTCTTCTATGTGCAAGAAAAATAGGGCATTTCAAAGAGCTGTTT
TGATTAAAAATTATATTCTTGTTTAAATAAGCTTATTTTAAACAATTTAAAGCTATTAT
TCTTAGCATTAACCTATTTTTAAAGAAACCTTTTTTGCTATTGACTGTTTTTCCCTCTA
AGTTTACACTAACATCTACCCAAGATAGACTGTTTTTTAAACAGTCAATTTTCAGTTCAGCT
AACATATATTAATACCTTTGTAACCTTTGCTATGGCTTTTGTTATCACACCAAACTAT
GCAATTGGTACATGTTTGTGTTAAAGAAGAAACCGTATTTTTCCATGATAAATCACTGTTTG
AAATATTTGGTTTCATGGTATGATCGAAATGTAAAAGCATAATTAACACATTGGCTGCTAG
TTAACAATTGGAATAACTTTATTCTGCAGATCATTTAAGAAGTAACAGGCCGGGCGCGGT
GGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGCGGGCAGATCACCTGAGGTCA

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FIGURE 2P

GGAGTTGGAGACCAGCCTGACCAACATGGACAAACCCCGTCTCTACTAAAAATACAAAAT
TGGCAGGGTGTGGTGGACATGCCTATAATCCCAGCTACTTGGGAGGCTAAGGCAGGAGA
ATCGCTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCCGAGATCGCACCATTGCACTCCTG
CCTGGGCAACAAGAGTGAAACTCCATCTCC

SEQ ID NO: 22_R47805_H

ATGGCGCACCAAACGGGCATCCACGCCACGGAAGAGCTGAAGGAATTCTTTGCCAAGGCA
CGGGCTGGCTCTGTGCGGCTCATCAAGGTTGTGATTGAGGACGAGCAGCTCGTGCTGGGT
GCCTCGCAGGAGCCAGTAGGCCGCTGGGATCAGGACTATGACAGGGCCGTGCTGCCACTG
CTGGACGCCCAGCAGCCCTGCTACCTGCTCTACCGCCTCGACTCACAGAATGCTCAGGGC
TTCGAATGGCTCTTCCTCGCCTGGTGCCTGATAACTCCCCCGTGCGGCTGAAGATGCTG
TACGCGGCCACGCGGGCCACAGTGAAAAAGGAGTTTGGAGGTGGCCACATCAAGGATGAG
CTCTTCGGGACTGTGAAGGATGACCTCTCTTTTGCTGGGTACCAGAAACACCTGTCGTCC
TGTGCGGCACCTGCCCGCTGACCTCGGCTGAGAGAGAGCTCCAGCAGATCCGCATTAAC
GAGGTGAAGACAGAGATCAGTGTGGAAGCAAGCACCAGACCCTGCAGGGCCTCGCCTTC
CCCCTGCAGCCTGAGGCCCAGCGGGCACTCCAGCAGCTCAAGCAGAAAATGGTCAACTAC
ATCCAGATGAAGCTGGACCTAGAGCGGGAAACCATTGAGCTGGTGCACACAGAGCCCACG
GATGTGGCCCAGCTGCCCTCCCGGTGCCCGAGATGCTGCCCGCTACCACTTCTTCCTC
TACAAGCACACCCATGAGGGCGACCCCTTGAGTCTGTAGTGTTTCATCTACTCCATGCCG
GGGTACAAGTGCAGCATCAAGGAGCGAATGCTCTACTCCAGCTGCAAGAGCCGCCTCCTC
GACTCCGTGGAGCAGGACTTCCATCTGGAGATCGCCAAGAAAATTGAGATTGGCGATGGG
GCAGAGCTGACGGCAGAGTTCCTCTACGACGAGGTGCACCCCAAGCAACACGCCTTCAAG
CAGGCCTTCGCCAAGCCCAAGGGCCAGGGGCAAGCGGGGCCATAAGCGCCTCATCCGC
GCCCCGGGTGAAAATGGGGATGACAGCTAG

SEQ ID NO: 23_H60215_H

CCACGCGTCCGGCGCCGCAGCCATGGAGGGAGGCGGCGGCGGCGGCGGCGGCTCGGG
TGGCTGCGCTGGGAGGCGGCGGTGAGAGGCTCGCACGCCTCCAGCCCGGCCCCGGCCCCC
CGGGAGGGAGAGCCGAGCAGCCCCGGCTCTGGGCTACGGACTATGGGCGAATAGCTCTGA
CCACCCGGCGAAGTGCACACACCCAGAAGCTATGTCCTTCGGCAGTAAAAGTTTTACAGC
ACAATATATGTGCTCTGCTCTCCTCCCGCAATCCTGCTCCAAGAGATCTTAAGCTGGAGG
CACCAGGTCTGAATTCCAGACTCCTCCCCACCACCCACACTTCACCTCCAAGTGGAGCAT
GACCACAGACCCATTGAGGGAGGCTGGCGGACTCTTCATCCTGGACAGTCCCTTACTGTA
TGTCAAAGCTGAGAATGAAGCGGAGAGCATCAGACAGAGGAGCTGGGGAAACGTCGGCCA
GGGCCAAGGCTCTAGGAAGTGGGATTTCTGGAATAATGCAAAGAGAGCTGGACCATTCA
TCCTTGGTCCCCGTCTGGGCAACTCACCGGTGCCAAGCATAAGTGCAGTGTGTTGGCGAGGA
AAGATGGCACGGATGACTTCTATCAGCTGAAGATCCTGACCCTGGAGGAGAGGGGGGACC
AAGGCATAGAGAGCCAGGAAGAGCGGCAGGGCAAGATGCTGCTGCACACCGAGTACTCAC
TGCTGTCTCTCCTGCACACGCAGGATGGCGTGGTGCACCACCACGGCCTCTTCCAGGACC
GCACCTGTGAAATCGTTGAGGACACAGAATCCAGCCGGATGGTTAAGAAGATGAAGAAGC
GCATCTGCCTCGTCTGGACTGCCTCTGTGCTCATGACTTCAGCGATAAGACCGCTGACC
TCATCAACCTGCAGCACTACGTCATCAAGGAGAAGAGGCTCAGCGAGAGGGAGACTGTGG
TAATCTTCTACGACGTGGTCCGCGTGGTGGAGGCCCTGCACCAGAAAAATATCGTGACAC
GAGACCTGAAGCTGGGGAACATGGTGTCTCAACAAGAGGACACATCGGATAACCATCACCA
ACTTCTGCCTCGGGAAGCATCTGGTGAGCGAGGGGGACCTGCTGAAGGACCAGAGAGGGA
GCCCTGCCTACATCAGTCCCGACGTGCTCAGCGGCCCGCCGTACCGTGGCAAGCCCAGTG
ACATGTGGGCCCTGGGCGTGGTGTCTTACCATGCTGTATGGCCAGTTCCCCTTCTACG
ACAGCATCCCGCAGGAGCTCTTCCGCAAGATCAAGGCTGCCGAGTATACCATTCCTGAGG
ATGGACGGGTTTCTGAGAACACCGTGTGTCTCATCCGGAAGCTGCTGGTCTTGAACCCCC
AGCAGCGCCTGGCCGCCCGCCGACGTCTTGAGGGCCCTCAGTGCCATCATTGCATCATGGC

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FIGURE 2Q

AGTCCCTGTCATCTCTGAGTGGGCCTTTTGCAAGTGGTTCCTGACATTGATGACCAAATGA
GCAATGCGGATAGCTCCCAGGAGGCGAAGGTGACGGAGGAGTGCTCCCAGTACGAGTTTG
AGAACTACATGCGTCAGCAGCTGCTGCTGGCCGAGGAGAAGAGCTCCATCCATGACACCC
GGAGCTGGGTACCCAAGCGGCAGTTCGGCAGCGCACCACCGGTGCGACGGCTGGGCCACG
ACGCACAGCCCATGACCTCCTTGGACACGGCCATCCTGGCGCAGCGCTACCTGCGGAAAT
AACAGCCTCAGCCGGGGGCCACCAGCACTGCTGCCACTTCTTCCAGCCCCAGCCAAAGGCG
TGGCTGTCAGGGCTGGGCCCTGTAGTGCTGGACTCTCCCGGGCCACAATAGGGACAGGGC
AGGGACAGGGACAGCCCAGGTACACAGTGGGGTCAGCAGAGGTACCACGAAGCTACCTTT
TGGGATGATTGCTCGATTGTTTGGTTTTTAAATCTGAGAAGCCTAGATAACTAATCTGCT
TTTAATCACGATGTTTTAATCTACCTCTGTCTCTTTAACCATGCTGTCTCTGGACTGAGC
AAGAGGGAGGAGGGAGCCTGCTACCCCCACTCCAGGGCCTTCCCCAGCGGCCACCAACTG
ACCTGGGGCGCTGCTCCCCACAGTCCAAATAAGCTGAAAGTGACGCTCGCTGCAGGCCCC
AGAGCGAGCTTCCCCTCCTCCCTGCTCTCCAGGCCCTGCCACAGCCTCTTTCCGTCCC
TCTCTTTCTGATCCAGGCCCTCAGTCCAAGCTTTGGAAACCTTCACCTCATCTTAAAC
CAAACCTCAAATATATTTATTTTTTTTACCAT

SEQ ID NO: 24 SGK324_H

GCCGCGATGGCCAGCACCAGGAGTATCGAGCTGGAGCACTTTGAGGAACGGGACAAAAGG
CCGCGGCCGGGGTCCGCGAGAGGGGCCCCAGCTCCTCCGGGGGCAGCAGCAGCTCGGGC
CCCAAGGGGAACGGGCTCATCCCCAGTCCGGCGCACAGTGCCCACTGCAGCTTCTACCGC
ACGCGGACCCTGCAGGCCCTCAGCTCGGAGAAGAAGGCCAAGAAGGCGCGCTTCTACCGG
AACGGGGACCGCTACTTCAAGGGCCTGGTGTGTGCCATCTCCAGCGACCGCTTCCGGTCC
TTCGATGCGCTCCTCATAGAGCTCACCCGCTCCCTGTCCGACAACGTGAACCTGCCCCAG
GGTGTCCGCACTATCTACACCATCGACGGCAGCCGGAAGGTACCAGCCTGGACGAGCTG
CTGGAAGGTGAGAGTTACGTGTGTGCATCCAATGAACCATTTTCGTAAAGTCGATTACACC
AAAAATATTAATCCAAACTGGTCTGTGAACATCAAGGGTGGGACATCCCGAGCGCTGGCT
GCTGCCTCCTCTGTGAAAAGTGAAGTAAAGAAAGTAAAGATTTTCATCAAACCCAAGTTA
GTGACTGTGATTGCAAGTGGAGTGAAGCCTAGAAAAGCCGTGCGGATCCTTCTGAATAAA
AAGACTGCTCATTCTTTGAACAAGTCTTAACAGATATCACCGAAGCCATTAAACNAGCC
TCAGGAGTCGTCAAGAGGCTCTGCACCCTGGATGGAAAGCAGGTGAGAGTTACGTGTGTG
CATCTGCCAGACTTTTTTGGTGATGACGATGTTTTTATTGTCATGTGGACCAGAAAAATTT
CGTTATGCCCAAGATGACTTTGTCTGGATCATAGTGAATGTCGTGTCTGAAGTCATCT
TATTCTCGATCCTCAGCTGTTAAGTATTCTGGATCCAAAAGCCCTGGGCCCTCTCGACGC
AGCCAGATTTCTGCTCATGGCAGATCTTCTTCCAATGTAAACGGTGGACCTGAGCTTGAC
CGTTGCATAAGTCTTGAAGGTGTGAATGGAAACAGATGCTCTGAATCATCAACTCTTCTT
GAGAAATACAAAATTGGAAAGGTCAATTGGTGATGGCAATTTTGCAGTAGTCAAAGAGTGT
ATAGACAGGTCCACTGGAAAGGAGTTTGCCCTAAAGATTATAGACAAAGCCAAATGTTGT
GGAAAGGAACACCTGATTGAGAATGAAGTGTCAATACTGCGCCGAGTGAAACATCCCAAT
ATCATTATGCTGGTCGAGGAGATGGAAACAGCAACTGAGCTCTTTCTGGTGATGGAATTG
GTCAAAGGTGGAGATCTCTTTGATGCAATTACTTCGTGACCAAGTACACTGAGAGAGAT
GGCAGTGCCATGGTGTACAACCTTAGCCAATGCCCTCAGGTATCTCCATGGCCTCAGCATC
GTGCACAGAGACATCAAACCAGAGAATCTCTTGGTGTGTGAATATCCTGATGGAACCAAG
TCTTTGAAACTGGGAGACTTTGGGCTTGCGACTGTGGTAGAAGGCCCTTTATACACAGTC
TGTGGCACACCCACTTATGTGGCTCCARAAATCATTGCTGAAACTGGCTATGGCCTGAAG
GTGGACATTTGGGCAGCTGGTGTGATCACATACATACTTCTCTGTGGATTCCCACCATTC
CGAAGTGAGAACAAATCTCCAGGAAGATCTCTTCGACCAGATCTTGGCTGGGAAGCTGGAG
TTTCCGGCCCCCTACTGGGATAACATCACGGACTCTGCCAAGGAATTAATCAGTCAAATG
CTTCAGGTAAATGTTGAAGCTCGGTGTACCGCGGGACAAATCCTGAGTCACCCCTGGGTG
TCAGATGATGCCTCCCAGGAGAATAACATGCAAGCTGAGGTGACAGGTAAACTAAAACAG
CACTTTAATAATGCGCTCCCCAAACAGAACAGCACTACCACCGGGGTCTCCGTTCATCATG

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FIGURE 2R

GTGAGTGGAAGGCGGCAGGTCTGGCCTGACTGCGGAGCCGGCCTTGAAGTTTTTGAATTA
GGTAGCCGGGAGCTGCCCTCACATGGAAGTTGGTGCCTTCCGTAGTCCTATTTTCATATGA
AGATTGGCTTGGCATGTGGAGGGCACTCATTTCGGCAACTCCCAGGCTTTGGGCAGTGTGT
GGAGGGGCTTGTGTAGGGACCAGCAGGCCTGGTGTGAGGGGTCCAGGCGTCAAGGAGCTC
CTGGCTGGGCCCTCTGGGCAGCTGCTTCCACTCTTGTCTCTGCCTTCTCATCTAGAGAGA
CTCCCAAGCCCTGGAGGGGTGTGTTGTGTGTAGGAATTAACCTCCCTGCCTACCCCAAGGCC
TCAGAAATAGATTATTAGAGATGTGAATTATTCTTTGAGACTTGGGATAAGAAACAGCCA
AAGCTAAACATATTTTCAGTTTTTAAAAAATCAGTGTTTTTATAAAACACAGTTTGGGGCTTT
TAAAGGTACATAATCAAGGAAAAAATATATATTTCATTTTTTCAGGGTTGGTAACATTTTA
TGAGATGTCAGTGACAACGATGGCCTTATTTTTTTTCAGCCTTTTCTTCTTCCAAAATGTT
TCTTAAGGCAACTCTCCTAAATACATAAACACAAATTAATAAGGAAAGTGACATGAG
AGTAAATGAATCAAAAGGAAAAAACATTGAACCAGAGGTGAGGGCAGCACACCCGCAGCA
GCTGTCCAGGCCTGAGCCAATGCAACCCTGGGCGGGAAGGCCAGCTCACCGTGAGCAGGT
AGAAGCCAGCCAGCCACCCAGGCAGGGACCTTGGTTCTCCCCACACACTCCAGGAGCAG
GGAACAGGGGTGGAGTGGCCTTTCCAGAGCTGGAGTTGGCTGCAGCAGCTTTTGAATCA
GACCTGCCAAGGTGATGGGCGTCTGAGTTTCACATCTGGGCCCCCGTGACCCCACTGAG
TCCTGACAGCTAAGGATGGGCCACCTCCACAGCTCCGTCACTCGTACTTGGGACAGGCCT
CTCATCCTCTGGGAAGGTCTCCTTGTTTTCTTACCCAAGTGAAGGGAAACAGTGGCATA
TTCTCATGGTACATGGTTGTCTGAAAGCCTTACCTAGGAAGACGCAGGGTCTAGATAGAA
GCTATAAGGAAGCCACACACATAACCCACATCCCCACACCCCAACATCCCCACACTCC
CCACACCCCCCACACCCCCACATCCCCACCATAATTACCCCCACCTCCAAATATCTCAT

SEQ ID NO: 25_W30246_M SGK324_M

ACCAAGTCCTCCAGCTCCTCTCCAACAGCCCGGAAGTTTCAGAGGATTGAAGATTTCT
GCTCAGGGCAGATCTTCTTCCAACGTAAACGGTGGGCCTGAACTTGACCGTTGCCTGAGC
CCTGAAGGTGTGAATGGAAACCGGTGCTCCGAGTCGTTCCCCCTTCTGGAGAAATACAGA
ATAGGGGAAGGTCATCGGGGACGGCAACTTCGCGGTAGTTAAGGAGTGCGTGGACAGGTAC
ACTGGAAAAGAGTTTGCATTAAAGATTATAGACAAAGCCAAATGCTGTGGAAAGGAGCAT
CTGATTGAGAACGAAGTGTCAATCCTGCGCCGAGTGAAGCACCCCAACATCATCATGTTG
GTTGAAGAGATGGAAACAGCAACTGACCTCTTTCTAGTGATGGAAGTGGTCAAAGGTGGA
GATCTCTTTGATGCGATTACCTCTTCAACCAAGTACACTGAGAGAGATGGAAGCGCCATG
GTGTACAACCTAGCCAATGCCCTCCGGTACCTGCACAGCCTCAGCATCGTCCACAGGGAC
ATCAAGCCTGAGAATCTGCTGGTGTGCGAATACCCAGATGGAACCAAGTCTTTGAAGCTG
GGAGACTTTGGGCTGGCGACGGTGGTTGAAGGCCCGTTGTACACGGTCTGTGGCACGCCA
ACTTATGTGGCACCAGAGATCATAGCTGAAACAGGTTATGGCCTGAAGGTGGATGTTTGG
GCAGCTGGTGTGATTACATACTTCTCTGTGGATTCCCACCATTCCGGAGTGAGAAC
AATCTCCAGGAAGATCTCTTTGACCAGATCTTGGCTGGAAAGCTGGAATTCCCAGCCCCC
TACTGGGACAACATTACAGACTCTCCTTGTGTGTGTTTTAGGAAATGCTTATGAAGCTGG
CCCGTGGGCTTCCCAGTGGGACGTGCAGCAGTTCTTGGCAGAGCAGGGCCAGCTCTGCTG
TGTCATCTCCAGGGTCTCCCATCACCTCTGCTCTTTGCCATGGCAGGTCTGCTGAGACCC
CGCGGGGACGGGGGCATGGTGTCTCCTGATTGGCCTGTGACCAACCTTCTGGAAGGCTGC
TGGCAGTTTTTCCCTGTTTTCCACCACCCCACTCTTTTAAATAATTGTATATACTGTACT
TGTTCTACTTGCTTGTCTTTAAACAGGGGGCCCCACAGTTCACCTCTCACTGTTAGATTT
TGCCTTTTCCAGGTATCCCCAACCTGCAATAAACTCTTCCCTCTTCAG

SEQ ID NO: 26_AA383293_H

CCAGCAGCCAAGAGGGTAGTGGTGTACCGGAATGGGGACCCATTCTTCCCAGGCTCCCAG
CTGGTGGTGAATCAACGCCGCTTCCCCACCATGGAGGCCTTCCCTCTGCGAGGTGACATCA
GCTGTGCAGGCCCCACTGGCTGTGCGTGCCCTCTACACACCTTGTTCATGGCCACCCCTGTC
ACCAACCTGGCAGACTTGAAGAACAGAGGGCAGTATGTGGCCGCTGGATTGTAACGATTC

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FIGURE 2S

CACAAGCTCCCCCTTACCAGGCTTTTTGTCTCAGTGTGTTTCAGGAATGGGGACCTGGTA
AGTCCCCCATTTAGTCTGAAGCTGTCCCAGGCTGCCAGCCAGGACTGGGAAACTGTGTTG
AAGCTCCTGACTGAGAAGGTCAAGTTGCAGAGTGGGGCTGTGAGACTCTGCACCCTAGAG
GGGCTCCCACTGTCAGCAGGGAAGGAGCTGGTAACTGGCCATTACTATGTGGCTGTGCGA
GAGGATGAGTTCAAGGACCTTCCCTATCCAGCTCTGTCCACAAGAGGGCTCCTGGCAGCA
GGCAATGAAGCCACCTGAGGAGTGGAGTGGGGACTGTGCTGGTTCCCCCAAGCCTCTT
GGAAGGAAGGCTAAGAAGGAGACATGCCTAATCGTGACCCTGACCCTGAAATACCAGCAG
TCAGAAACAAGCAGAGACGGGCAATCATTCCCATCAGGAGTTATAGGAGTATATGGAGCT
CCCCACCGAAGGAAGGAGACAGCGGGGCCCTGGAAGTAGCAGATGATGAAGACACTCAG
ACAGAGGAGCCCTTGATCAGAGGGCAGCACAGATAGTGGAACAGGTTACTTGTCTGCAA
GACTTTTTTGGTGATGACGATGTTTTTATTGCATGTGGACCAGAAAAATTTTCGTTATGCC
CAAGATGACTTTGTCCTGGATCATAGTCGTGACGGCTCCTGAGAGAGCACCAGGCGGGC
TTTGAGAAGCTCCGCAGGACCCGAGGAGAAGAGAAGGAGGCAGAGAAGGAGAAAAAGCCA
TGTATGTCTGGAGGCAGAAGGATGACTCTCAGAGATGACCAACCTGCAAAGCTAGAAAAG
GAGCCCAAGACGAGGCCAGAAGAGAACAAGCAGAGCGGCCAGCGGTGCGAAGCCACGG
CCCATGGGCATCATTGCCGCCAATGTGGAAGCATTATGAGACTGGCCGGGTGATTGGG
GATGGGAACTTTGTCTGTGTAAGGAGTGCAGACACCGCGAGACCAGGCAGGCCTATGCG
ATGAAGATCATTGACAAGTCCAGACTCAAGGGCAAGGAGGACATGGTGGACAGTGAGATC
TTGATCATCCAGAGCCTCTCTCACCCCAACATCGTGAAATTGCATGAAGTCTACGAAACA
GACATGGAAATCTACCTGATCCTGGAGTACGTGCAGGGAGGAGACCTTTTTGACGCCATC
ATAGAAAGTGTGAAGTTCCCGGAGCCCGATGCTGCCCTCATGATCATGGACTTATGCAAA
GCCCTCGTCCACATGCACGACAAGAGCATTGTCCACCGGGACCTCAAGCCGGAAAAACCTT
TTGGTTTCAGCGAAATGAGGACAAATCTACTACCTTGAAATTGGCTGATTTTGGACTTGCA
AAGCATGTGGTGAGACCTATATTTACTGTGTGTGGGACCCCAACTTACGTAGCTCCCGAA
ATTCTTTCTGAGAAAGGTTATGGACTGGAGGTGGACATGTGGGCTGCTGGCGTGATCCTC
TATATCCTGCTGTGTGGCTTTCCCCCATTCGCGAGCCCTGAXXGAGGGGACCAGGACGAG
CTCTTTAACATCATCCAGCTGGGCCACTTTGAGTTCTCTCCCCCTTACTGGGACAATATC
TCTGATGCTGCTAAAGATCTGGTGAGCCGGTTGCTGGTGGTAGACCCCAAAAAGCGCTAC
ACAGCTCATCAGGTTCTTCAGCACCCCTGGATCGAAACAGCTGGCAAGACCAATACAGTG
AAACGACAGAAGCAGGTGTCCCCAGCAGCGATGGTCACTTCCGGAGCCAGCACAAAGAGG
GTTGTGGAGCAGGTATCATAGTCACCACCTTGGGAATCTGTCCAGCCCCCAGTTCTGCTC
AAGGACAGAGAAAAGGATAGAAGTTTGAGAGAAAAACAATGAAAGAGGCTTCTTCACATA
ATTGGTGAATCAGAGGGAGAGACACTGAGTATATTTTAAAGCATATTAAAAAAATTAAGT
CAATGTAAATGTCACAACATATTTTTAGATTTGTATATTTAAAGCCTTTAATACATTTT
TGGGGGGTAAGCATTGTTCATCAGTGAGGAATTTTGGTAATAATGATGTGTTTTGCTTCCC
CTTTGTAACCAAGTTTATTCTGTACTACAGGAGTGGTGCTTACCAGGGTCTAAACTCCCC
CTGTGAGATTAATAAGGTGCATTG

SEQ ID NO: 28_AA197883_M

ATGCCAACCGCGCCGGTCTGCGCCCGCCGCGCCGCGCCAGCGACCCCCGCCCCGCGGCA
CCCAGTCGCCCTGCGCCTCCCATTCGGGGCCACCGAGGCCCATGTGACCATTCTCTGAAA
TGCTTAAGCTCGAAGATCTCTGAGAGAAAGCTGCCAGGCCCTGGTTACCTGCGGGACGA
GGACCTCTGGAGAAGCCAGTTCTGGGGCCACGTGGTGCCGTCATGCCGCTGTTTCAGCCCT
CAGAGCAGCCTCCACTCAGTCCGCGCAGAGCACAGCCCACTGAAGCCCAGGGTGGTGACG
GTGGTGAAGCTGGGTGGGCAGCCCCCTCCGTAAGGCCACCTGCTCCTCAACCGGCGCTCA
GTGCAGACCTTTGAGCAGCTCCTATCAGACATCTCCGAAGCCTTGGGCTTCCCACGCTGG
AAGAACGACCGTGTGCGGAAGCTGTTTACCCTCAAGGGCAGGGAGGTGAAGAGTGTGTCT
GACTTCTTCCGGGAGGGTGATGCTTTCATAGCTATGGGCAAAGAGCCGCTGACATTGAAG
AGTATCCAGTTGGCCATGGAGGAGCTGTATCCTAAGAACCAGGGCTCTTGCCCTGGCCCCCT
CACAGTAGAGTCCCCTCCCCAAGGCTGAGAAGCAGACTTCCCAGCAAGCTTCTGAAAGGA

FIGURE 2T

AGTCACCGCTGTGGGGAGGCAGGAAGCTATAGCGCGGAAATGGAGAGTAAGGCAGTCTCT
AGGCATCAGGGCAAGACTTCCACAGTGCTGGCCCCAGAAGACAAGGCGAGGGCCCAGAAG
TGGGTAAAGAGGGAAACAGGAGTCAGAACCTGGTGGCCCCGCTTCACCCGGGGCAGCCACT
CAGGAGGAGACTCATGCAAGTGGAGAGAAACATCTGGGGGTGGAGATCGAAAAGACCTCC
GGGGAGATTGTCAGATGTGAGAAGTGTAAAGAGAGAAAGAGAGCTGCAGTTGGGCCTGCAG
AGGGAGCCGTGCCCCGCTGGGAACCAGTGAGCTGGACCTGGGGAGAGCTCAGAAGAGGGGAT
TCCGAGAAGTTGGTGAGGACCAAGAGCTGCAGGAGGCCTTCTAAGGCAAAATTTACAGAT
GGAGAGGAAGGGTGGAAGGGTGACAGCCATCGGGGCAGTCCCAGGGACCCCCCTCAGGAA
ATGAGGAGGCCCAACAGCAACTCAGACAAGAAAGAGATCAGAGGCTCAGAAAGTCAGGAC
AGTTATCCTCAGGGGGCACCCAAGGCCCAGAAGGACTTCGTGGAAGGGCCACCAGCTGTA
GAGGAGGGGGCCGATAGACATGAGGAGAGAGGACCGGCACACATGCAGGAGCAAGCATGCC
GCCTGGCTCCGGAGAGAGCAGCAGGCCGAACCCCCACAGCTCCCCAGAACCCGAGGGGAG
GAGAAGCAAGCAGAGCACGAGAAGAAGCCAGGCGGCTTAGGAGAGAGGAGGGCGCCAGAG
AAGGAGTCTAAGAGGAAGCTAGAAGAGAAGAGGCCAGAACGACCCAGTGGCCGGAAGCCG
AGGCCCAAGGGCATCATCTCAGCGGATGTGGAGAAGCACTATGACATAGGTGGGGTCATT
GGGGATGGCAACTTTGCCACCGTGAAGGAATGCAGGCACCGAGAGACCAAGCAGGCTTAC
GCCATGAAGATGATTGACAAGTCCCAGCTGAAGGGTAAGGAGGACATTGTGCACAGTGAG
ATTTTAATCATCCAGAGTCTCTCTCATCCCAACATTGTGAAACTGCATGAGGTCTACGAA
ACGGAGGCGGAGATCTACCTGATCATGGAGTATGTGCAGGGAGGGGACCTTTTTTGATGCC
ATCGTTGAAAATGTGAAGTTTCCAGAGCCCCGAGGCTGCAGTTATGATCACAGACTTGTGT
AAGGCCTTCGTCCACATGCACGACAAGAATATCGTCCACCGGGACGTGAAACCAGAAAAC
CTCCTGGTTCAGCGAAATGAAGACAAGTCTATCACCTTGAAGCTGGCTGATTTTGGCTTG
GCCAAATATGTGGTGAGGCCTATATTTACTGTGTGTGGGACGCCAACATATGTAGCTCCT
GAAATTCTTTCTGAGAAAGGTTACGGCCTGGAGGTGGACATGTGGGCGGCAGGTGTGATC
CTATACATCCTCTTGTGTGGCTTCCCCCTTTCCGAAGTCTTGAGAGGGACCAAGACGAG
CTCTTCAACATCATCCAAGTGGGCCAGTTTGAGTTCTCTCTCTTACTGGGACAACATT
TCTGATGCTGCCAAAGATCTGGTGAGAAATTTGCTGGAGGTGGACCCTAAGAAGCGGTAC
ACGGCCGAACAGGTCCTACAGCATCCCTGGATTGAGATGGTTGGGCATACCAACACAGGG
AACTCACAGAAGGAGGAGTCCCCCAACAGTTTAGGTCACCTCCAGAGTCAGCACAGAAG
GTTGCAGAGCAGATGCCATAA

SEQ ID NO: 29_DRK2_H

CTCCGCTGCTGTGCGCCAGGAGTCACTTCACGAGAAGCCAGGTACACAACCGTCGGCCCTTG
TCTGGAAGAAAGTAAAAGTGGATCCTGCCACGTTCCGAGCTCCCTGGCGCCTCGCCCCGGCTG
GAGCTAGAGAACTCGTCCTGTGGCGGCCCCCGGCGTGGGGCGGGACAGCGGCCCCCTGGA
GGGGGCAGTCCCGGGAGAACCTGCGGCGGCGGAGCGGTAAAAATAAGTGACTAAAGAAG
CAGACCTGGGAATCACCTAACATGTGAGGAGGAGATTTGATTGCCGAAGTATTTCAGGC
CTACTAACTACAACCTCTCAAATTTCCAATAAAAAATGGAAAACTTTAATAATTTCTATATA
CTTACATCTAAAGAGCTAGGGAGAGGAAAATTTGCTGTGGTTAGACAATGTATATCAAAA
TCTACTGGCCAAGAATATGCTGCAAAAATTTCTAAAAAAGAGAAGAAGAGGACAGGATTGT
CGGGCAGAAATTTTACACGAGATTGCTGTGCTTGAATTGGCAAAGTCTTGTCCCCGTGTT
ATTAATCTTCATGAGGTCTATGAAAATACAAGTGAAATCATTTTGATATTGGAATATGCT
GCAGGTGGAGAAATTTTCAGCCTGTGTTTACCTGAGTTGGCTGAAATGGTTTCTGAAAAT
GATGTTATCAGACTCATTAAACAAATACTTGAAGGAGTTTATTATCTACATCAGAATAAC
ATTGTACACCTTGATTTAAAGCCACAGAATATATTACTGAGCAGCATATACCTCTCGGG
GACATTAAAATAGTAGATTTTGGAAATGTCTCGAAAAATAGGGCATGCGTGTGAACTTCGG
GAAATCATGGGAACACCAGAATATTTAGCTCCAGAAATCCTGAACTATGATCCCATTACC
ACAGCAACAGATATGTGGAATATTGGTATAATAGCATATATGTTGTTAACTCACACATCA
CCATTTGTGGGAGAAGATAATCAAGAAACATACCTCAATATTTCTCAAGTTAATGTAGAT
TATTCGGAAGAACTTTTTTCATCAGTTTCACAGCTGGCCACAGACTTTATTCAGAGCCTT

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FIGURE 2U

TTAGTAAAAAATCCAGAGAAAAGACCAACAGCAGAGATATGCCTTTCTCATTCTTGGCTA
CAGCAGTGGGACTTTGAAAACCTTGTTTCACCCTGAAGAACTTCCAGTTCCTCTCAAACCT
CAGGATCATTCTGTAAGGTCCTCTGAAGACAAGACTTCTAAATCCTCCTGTAATGGAACC
TGTGGTGATAGAGAAGACAAAGAGAATATCCAGAGGATAGCAGCATGGTTTCCAAAAGA
TTTCGTTTTCGATGACTCATTACCCAATCCCCATGAACTTGTTTCAGATTTGCTCTGTTAG
CACTTTTTTCTTTGACTCATTTGGACTGAATTTGAAATTTTATATCCACTCCAGTGAGAT
TATGATTTGTAGCTTCATATATGACATGTTTATATTGTAAATGCACTTTTCCATGGAATA
ATTTAGGGAAGTGTTTTAATGTAAATTACTAGTTGCTAGCATGTTATGATTTTCATATCC
TGAGATAGCTCTGCAGATAAGAAAATATTTAAATATATGACAAAAGTAAAATTGTACAT
GTGAAAG

SEQ ID NO: 30_W44160_M DRAK2_M

CCAGACGCGGCTGCACTTTTCAAACCTCAACTGTAAGAAGCGTCGGTCAGCGTCTGTGCG
GTCGCCGCCGGGAGTCGCCTCACAGGGGCCTGGCTGACGGCGACCAGCCGTTGTGGGGAA
GAGTGCGAGGTAAAAGTCTGCCTAGAGAAGCAGGTCTGGCAGTCATCAACATGTCTCGGA
GGAGATTCGATTGCCGAAGTGTCTCAGGCTTGCTAACTACAACCCCTCAAACGCCGATTA
AAACAGAGAATTTTAATAATTTCTATACTCTTACCCCAAAGAACTTGGGAGAGGAAAAT
TTGCTGTGGTTAGACAATGTATATCAAAATCAACTGGACAAGAGTATGCTGCCAAATCCC
TGAAAAGAGGAGAAGAGGGCAGGATTGCCGGGCGGAAATTTCTGCATGAGATAGCTGTGC
TGGAGCTGGCCAGGTCTTGTCACCGTGATTAATCTGCATGAGGTCTACGAAAATGCAA
CGGAAATCATTGTTGTTAGAAATATGCTGCGGGTGGAGAAATTTTCAACCTGTGTTTAC
CTGAGTTAGCCGAAATGGTATCTGAAAATGATGTTATCAGACTCATTAAACAAATCCTTG
AAGGAGTTCATTATCTACATCAGAATAACATTGTTTACCTTGATTTAAAGCCACAGAATA
TACTTTTGAGCAGTATATACCCACTCGGGGACATAAAAATTTGTAGATTTTGGAAATGTCTC
GAAAAATTGGGAATGCAAGTGAGCTTCGGGAAATCATGGGAACACCTGAATACTTAGCTC
CAGAAATCCTCAACTATGATCCCATACCACAGCAACAGATATGTGGAATATTGGCATAA
TAGCGTATATGTTGTTAACTCATACATCACCATTGTTAGGAGAAGATAATCAAGAAACAT
ATCTGAATATTTCTCAAGTGAATGTAGATTATTCAGAAGAAATGTTTTTCATCAGTTTCAC
AGCTGGCCACAGACTTCATCCAGAGCCTTCTAGTAAAGAACCAGAGAAAAGACCAACAG
CAGAATCCTGCCTATCCCACTCATGGCTGCAGCAGTGGGACTTTGGAAGCTTGTTTCATC
CTGAGGAAACTTCAGGCTCCTCTCAAATTCAGGATCTGACTCTCAGGTCCTCTGAAGAGA
AGACCTCCAAGTCTCCTGTAATGGGAGCTGTGGAGCCCGGGAGGACAAGGAGAACATCC
CTGAAGATGGCAGCTTAGTTTCTAAAAGATTTTCGATTTCGATGACTCCTTGCCCAGCCCC
ATGAACTTGTTCCAGATTGTTCTGTTAGCATTTTTCTCTGTGACTCATCTGGACTGACT
CGGAAATTTGAAATCTCTGGTGTGAGATTGTGTTTGTAGCTTCATATATTATGTTTATAT
TATAAATGCACTTCTGCTTAGAAGAAGCTTAAGGAACAGTTTAAATGCTAGGCTTCTGTTG
GCTAGCATATCATTCTGTCTGAAATTTGTTTTGCAGAGGAAAATATTTAAGTATATGA
CAAAAAATGTAAATTTGTGTTTAAAGAGAACACATGCAACTGAAAGAAGCTCAAGTTCAGTCA
GACTTATAAAATGGGTTATATTATGGTTAGTAAAGTTGAAAAAAATGAAAACAGGAAT
TTAGTAGGTTCTAAGGTAAGCCCTATACCATAACTCTATTACAGAGAATCTGTTTGGGGA
AATGCTGTCAAGGGTAAACCACAACATATACTGCTTTATAAATACTCCAGAGAGAGTTTA
TAGTTGAAAGTATTTCCAGTTACCAATAATAGCTTGAAACTGTAAGATTTTCTTTGTGT
GCCATGTGCTCGGTGAGAGGACACAGTCAACCAGAGCAGGGTTGATCCAGGCTGTTTCTC
TGCAAACCGAGTCAAAACTCGACATCATTTCAGCTCATGTATTTGTACGTGCATCATA
TATCAGATCTAATAAGATCTGGAAGATGGATATGCAAATAAGAGGCCTTTGTCTTCTAGA
ATGATTAGAGTAGAGGAGAATTGGATAGTACAGAATATGCTCTAGTTTCAGTCAGACATA
TTCATAAAGGGAAATGTTAAGTTCTGGCAGCTGACTTAGTGTTGGATGTCTCCTAAGTCT
CAGGATAGAAGCCCATCATTAGAGCATAGGCACTTCAGGAATTCTTGTTGTGAAATTTCTAG
TGAGTGAGGAGGTGTGACATGCAGCTATCTTTGGGCTCCTTTTGTGTGTGTTCTGCTGGA
CACAAACATGGGAGTGTTTCAAGTGTGTCGTTGTTCAATATCTATGTTTCAAGTCTGATGG

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FIGURE 2V

GAGGGGCCTAGGGACTGCTTTGGAGATTTCCCACTGGTGTCCATTTTAAGGTCTGTAATA
ATGTCATGTTAAGATAACAGATCTCATAAATATGCTACTCTATCAGACTCCGTTGCCAAA
ACAAATTAAAAGCCTGTGTATTGAAGTGGGTGTTAGTCTAACAACCTGTAAATTCTTGAA
ATTGTTACTAAAATTCCAAATTCTTTAGATAACTTTAAACTATTTAAATTGAGCATTGCT
GTCTTTGTTTGATTAAAGGTTGAGTTCCTTTATATCTGTTATTTTTAAAGGAAAAGTTGT
TTGCCTTTTGTATATGTGTGTGCATATGTGTATGTGTACAGGTATATGTATATATGTATT
GATAGATAAAATACAGCCTTTAAACAACCTC

SEQ ID NO: 31_H01248_H, DRK1_H

ATGATCCCTTTGGAGAAGCCAGGCAGCGGGCGGCTCCTCCCCAGGCGCCACCTCAGGCTCG
GGCCGGGCAGGCCGGGGTCTGAGCGGGCCGTGCCGGCCGCCGCCGCCGCCGCCGCCGCCGCC
GGGCTGCTGACAGAGATACGCGCCGTGGTGCACACCGAGCCCTTCCAGGACGGCTACAGC
CTGTGCCCCGGGCCGGGAGCTGGGCAGGGGGAAATTTGCAGTGGTGAGAAAATGTATAAAG
AAAGATTCTGGGAAAGAATTTGCTGCAAAGTTCATGAGAAAAGAAGAAAAGGCCAAGAT
TGTCGGATGGAAATAATTCATGAGATTGCTGTACTTGAAGTAGCACAAGACAATCCTTGG
GTCATTAATTTACATGAAGTTTATGAGACTGCATCAGAAATGATCTTAGTTCTGGAATAT
GCTGCTGGGGGTGAAATCTTTGACCAGTGTGTTGCAGACAGAGAAGAAGCCTTTAAAGAA
AAAGATGTTCAAAGACTTATGCGACAGATTTTAGAAGGTGTTCACTTTTACACACTCGT
GATGTAGTTCATCTTGATTTGAAGCCTCAGAATATTCTGTTGACAAGTGAATCTCCATTG
GGTGACATTAAGATTGTTGATTTTGGCCTTTCAAGAATATTGAAGAACAGTGAAGAGCTC
CGAGAAATTATGGGTACCCCTGAATATGTGGCTCCTGAAATTCTTAGTTATGATCCTATA
AGCATGGCAACAGATATGTGGAGCATTGGAGTGTTAACATATGTCATGCTTACAGGAATA
TCACCTTTCTTAGGCAATGATAAACAAGAAACATTCTTAAACATCTCACAGATGAATTTA
AGTTATTCTGAGGAAGAATTTGATGTTTTGTCTGAGTCGGCTGTTGATTTTCATCAGGACA
CTTTTAGTTAAGAAACCTGAAGATCGAGCCACTGCTGAAGAATGTCTAAAGCACCCCTGG
TTGACACAGAGCAGTATTCAAGAGCCTTCTTTCAGGATGGAAAAGGCACTAGAAGAAGCA
AATGCCCTCCAAGAAGGTCATTCTGTGCCTGAAATTAATTCGGATACCGACAAATCAGAA
ACCGAGGAATCCATTGTAACCGAAGAGTTAATTGTAGTTACTTCATATACTCTAGGACAA
TGCAGACAGTCTGAAAAGAGAAAATGGAGCAAAAGGCCATTTCCAAACGATTTAAATTT
GAGGAACCTTTGCTACAAGAAATTCAGGAGAATTTATCTACTGA

SEQ ID NO: 32_AA021445_H

CGGGGCTGCCGGGGCCGGGACTGGGGGAGCCGGGGCCCCGCGGGCCGCCTGCTGCCTCCGCC
CGCGCCGGGGTCCCCAGCCGCCCCCGCTGCCGTGTCCCCTGCGGCCGGCCAGCCGCGTCC
CCCAGCCCCGGCCTCCCGCGGACCCATGCCCGCCCGTATCGGCTACTACGAGATCGACCG
CACCATCGGCAAGGGCAACTTCGCGGTGGTCAAGCGGGCCACGCACCTCGTCACCAAGGC
CAAGGTTGCTATCAAGATCATAGATAAGACCCAGCTGGATGAAGAAAACCTGAAGAAGAT
TTTCCGGGAAGTTCAAATTATGAAGATGCTTTGCCACCCCCATATCATCAGGCTCTACCA
GGTTATGGAGACAGAACGGATGATTTATCTGGTGACAGAATATGCTAGTGGAGGGGAAAT
ATTTGACCACCTGGTGGCCCATGGTAGAATGGCAGAAAAGGAGGCACGTCGGAAGTTCAA
ACAGATCGTCACAGCTGTCTATTTTTGTCACTGTGCGGAACATTGTTTCATCGTGATTTAAA
AGCTGAAAATTTACTTCTGGATGCCAATCTGAATATCAAAATAGCAGATTTTGGTTTTCAG
TAACCTCTTCACTCCTGGGCAGCTGCTGAAGACCTGGTGTGGCAGCCCTCCCTATGCTGC
ACCTGAACTCTTTGAAGGAAAAGAATATGATGGGCCCAAAGTGACATCTGGAGCCTTGG
AGTTGTCTCTACGTGCTTGTGTGCGGTGCCCTGCCATTTGATGGAAGCACACTGCAGAA
TCTGCGGGCCCCGCGTGTGAGTGGAAAGTTCCGCATCCCATTTTTTATGTCCACAGAATG
TGAGCATTGATCCGCCATATGTTGGTGTAGATCCCAATAAGCGCCTCTCCATGGAGCA
GATCTGCAAGCACAAAGTGGATGAAGCTAGGGGACGCCGATCCCAACTTTGACAGGTTAAT
AGCTGAATGCCAACAACTAAAGGAAGAAAGACAGGTGGACCCCTGAATGAGGATGTCCT
CTTGGCCATGGAGGACATGGGACTGGACAAAGAACAGACACTGCAGTCATTAAGATCAGA

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FIGURE 2W

TGCCTATGATCACTATAGTGCAATCTACAGCCTGCTGTGTGATCGACATAAGAGACATAA
AACCTGCGTCTCGGAGCACTTCCTAGCATGCCCGAGCCCTGGCCTTTCAAGCACCAGT
CAATATCCAGGCGGAGCAGGCAGGTACTGCTATGAACATCAGCGTTCCCCAGGTGCAGCT
GATCAACCCAGAGAACCAAATTGTGGAGCCGGATGGGACACTGAATTTGGACAGTGATGA
GGGTGAAGAGCCTTCCCCTGAAGCATTGGTGGCTATTTGTCAATGAGGAGGCACACAGT
GGGTGTGGCTGACCCACGCACGGAAGTTATGGAAGATCTGCAGAAGCTCCTACCTGGCTT
TCCTGGAGTCAACCCCCAGGCTCCATTCCCTGCAGGTGGCCCCCTAATGTGAACCTCATGCA
CAACCTGTTGCCTATGCAAACTTGCAACCAACCGGGCAACTTGAGTACAAGGAGCAGTC
TCTCCTACAGCCGCCACGCTACAGCTGTTGAATGGAATGGGCCCTTGGCCGGAGGGC
ATCAGATGGAGGAGCCAACATCCAACCTGCATGCCAGCAGCTGCTGAAGCGCCACGGGG
ACCCTCTCCGCTTGTCAACATGACACCAGCAGTGCCAGCAGTTACCCCTGTGGACGAGGA
GAGCTCAGACGGGGAGCCAGACCAGGAAGCTGTGCAGAGGTACTTGGCAAATAGGTCCAA
AAGACATACTGGCCATGACCAACCCTACAGCTGAGATCCCACCGGACCTACAACGGCA
GCTAGGACAGCAGCCTTTCCGTTCCCGGGTCTGGCCTCCTCACCTGGTACCTGATCAGCA
TCGCTCTACCTACAAGGACTCCAACACTCTGCACCTCCCTACGGAGCGTTTCTCCCCTGT
GCGCCGGTTCTCAGATGGGGCTGCGAGCATCCAGGCCTTCAAAGCTCACCTGGAAAAAT
GGGCAACAACAGCAGCATCAAACAGCTGCAGCAGGAGTGTGAGCAGCTGCAGAAGATGTA
CGGGGGGCGAGATTGATGAAAGAACCTGGAGAAGACCCAGCAGCAGCATATGTTATACCA
GCAGGAGCAGCACCATCAAATTCTCCAGCAACAAATTCAAGACTCTATCTGTCTCTCTCA
GCCATCTCCACCTCTTCAGGCTGCATGTGAAAATCAGCCAGCCCTCCTTACCCATCAGCT
CCAGAGGTTAAGGATTACGCCTTCAAGCCCCCCCCCAACCAACCAACATCTCTT
CAGGCAGCCAGTAATAGTCCTCCCCCATGAGCAGTGCCATGATCCAGCCTCACGGGGC
TGCATCTTCTTCCCAGTTTCAAGGCTTACCTTCCCGCAGTGCAATCTTTCAGCAGCAACC
TGAGAACTGTTCTCTCTCTCCCAACGTGGCACTAACCTGCTTGGGTATGCAGCAGCCTGC
TCAGTCACAGCAGGTCAACATCCAAGTCCAAGAGCCTGTTGACATGCTCAGCAACATGCC
AGGCACAGCTGCAGGCTCCAGTGGGCGCGGCATCTCCATCAGCCCCAGTGCTGGTCAGAT
GCAGATGCAGCACCGTACCAACCTGATGGCCACCCTCAGCTATGGGCACCGTCCCTTGTC
CAAGCAGCTGAGTGCTGACAGTGACAGGCTCACAGCTTGAACGTGAATCGGTTCTCCCC
TGCTAACTACGACCAGGCGCATTTACACCCCCATCTGTTTTCGGACCAGTCCCGGGGTTC
CCCCAGCAGCTACAGCCCTTCAACAGGAGTGGGGTTCTCTCCAACCCAAGCCCTGAAAGT
CCCTCCACTTGACCAATTCACCACTTCCCTCCCAGTGACATCAGCAGCCGCCACACTA
TACCACGTCGGCACTACAGCAGGCCCTGCTGTCTCCACGCGCCAGACTATAACAAGACA
CCAGCAGGTACCCACATCCTTCAAGGACTGCTTTCTCCCCGGCATTCGCTCACCGGCCA
CTCGGACATCCGGCTGCCCCCAACAGAGTTTGCACAGCTCATTAAAAGGCAGCAGCAACA
ACGGCAGCAGCAGCAGCAACAGCAGCAACAGCAAGAATACCAGGAAGTGTTCAGGCACAT
GAACCAAGGGGATGCGGGGAGTCTGGCTCCAGCCTTGGGGGACAGAGCATGACAGAGCG
CCAGGCTTTATCTTATCAAATGCTGACTCTTATCACCATCACACCAGCCCCCAGCATCT
GCTACAAATCAGGGCACAAGAATGTGTCTCACAGGCTTCCTCACCCACCCGCCCCACGG
GTATGCTCACCAGCCGGCACTGATGCATTACAGAGCATGGAGGAGGACTGCTCGTGTGA
GGGGGCCAAGGATGGCTTCCAAGACAGTAAGAGTTCAAGTACATTGACCAAGGTTGCCA
TGACAGCCCTCTGCTCTTGAGTACCGGTGGACCTGGGGACCCTGAATCTTTGCTAGGAAC
TGTGAGTCATGCCAAGAATTGGGGATACATCCCTATGGTCATCAGCCAACCTGCTGCATT
CAGTAAAAATAAGGTGCCCAGCAGAGAGCCTGTATAGGGAAGTGCATGGATAGAAGTTC
TCCAGGACAAGCAGTGGAGCTGCCGGATCACAATGGGCTCGGGTACCCAGCACGCCCTC
CGTCCATGAGCACCAAGGCCCGGGCCCTCCAGAGACACCACAGATCCAGAACAGCGA
CGATGCTTATGTACAGCTGGATAACTTGCCAGGAATGAGTCTCGTGGCTGGGAAAGCACT
TAGCTCTGCCCCGATGTCCGATGCAGTTCTCAGTCAGTCTTCGCTCATGGGCAGCCAGCA
GTTTCAGGATGGGGAAAATGAGGAATGTGGGGCAAGCCTGGGAGGTCATGAGCACCCAGA
CCTGAGTGATGGCAGCCAGCATTTAAACTCCTCTTGCTATCCATCTACGTGTATTACAGA
CATTCTGCTCAGCTACAAGCACCCCGAAGTCTCCTTCAGCATGGAGCAGGCAGGCGTGTA

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FIGURE 2X

ACAAGAAACAGAGAGTTTTGTGTACAGCTTGGGAATGAAAAGGTTGATTGTAAACCCACA
GTATCTAGCAGCGTTGTGCCAAATTGCCCTTGTGTTTCTCTCCACCCAAAATATCACAGC
TGCTTTTCTCACATTTGGTTCATCCGTGTGCTGTTCTTTTGGGTTCTGAGAGGGTTTTGC
CATGTTTGCTTGTATGACCAAGTCACCAAGGAAATAAACAGGAAGGAAATCCATGTTCTC
C

SEQ ID NO: 33_2R22-5-11_H

CTGGGCCGCTGCCGGTCAGGTCGGCCGCCCTGACAGCTCCGGGAGCCTCAAGCGCGACA
GGGCGCCCTCACCTCGGGACATCCACACACCGACCGCTCCTGCTCCAGAGGCAACAACCC
AGCGCGCCTAGCCTGGCGCCGTGCAGCGAAGCCCAAGAGCTGGCCTCGCCACGAAGGTTG
AACCAGCCAAATTTTCGAGACAGCTCACGGCTTAGAGGAAGGTTTCATCTAAATAAAGGCC
GGCTAAAGTGACATTGCAGGGATTAAATCCTTCTTTGGCTGCCTGTGTGACCAGAAGGCT
TATTTGCAAGTTTCTTCTTCTTCTGGGGTCCAGATTATTAGGTCTCCAGCGCCCTGCAGCT
TGACAGAAAGAGAAGCATGAAATGAAGGTGAGAGATGAGATCCCGCAGCAGGGACGTGGG
GGCCTCCAGGGGCATTTACGCACCAGAGTGCAAGATTCTCTGGCCATCAAGGGAAATAG
CAAACAGAAGCCTTTGTCTGGGGCACAGCCACCTACCACAAAGCATCAGACTCCACGTC
TGGCCAGAAAGTTCTGAGTCCCATCAGGCCAGTGGGTATGTAACATGTGCCTAATTGT
ACAGCTAGAGCCTGCAAGTTCAACGTGAGGGAAGGTGGGAAATGTCTTGAGTGAGGCGAG
CAGCTCCTGGCTGGGCTGGGCAGACTCAGCTACCACGTTCACTGCCTTCTCTCACTAAA
GCCGAGAGGGAGGCTGCTCAGCTCTCAGGAAAACCTCTTTTGAACCCTGGGCACCTGCTGT
CCTCAGTTGGCATCTCCACCCCTCTGAGCCTCTTCTGCTCCTGCACAACCTGCCTCTTCG
CTGAGATGGAGACGTGAGCCCCCGTGGACGATGACTGCAGTGTATATGAATGGAGGTGGC
CTGGTGAACCCCCACTATGCCCGGTGGGATCGGCGCGACAGTGTAGAAAGTGGCTGTGAG
ACCGAGAGTAGCAAGGAGGGTGAGGAGGGACAGCCCCGCCAGCTGACGCCCTTCGAGAAA
CTGACACAGGACATGTCCCAGGATGAGAAGGTGGTGAGGGAGATCACGCTGGGGAAACGG
ATAGGCTTCTACCGAATTCGAGGGGAAATCGGAAGTGGAACCTTCTCCCAAGTGAAGCTT
GGGATTCACTCCCTAACCAAGAAAAGGTGGCCATTAAGATCCTGGACAAGACCAAGTTA
GACCAGAAAACCCAGAGGCTACTATCCCGAGAAATCTCCAGCATGGAAAAGCTGCACCAT
CCCAACATCATCCGCCTTTACGAAGTGGTGGAGACCCTATCCAAGCTGCACTTGGTGATG
GAGTATGCAGGGGGTGGGGAGCTCTTCGGAAAAAATTAGCACTGAGGGGAAGCTCTCTGAA
CCAGAAAGCAAGCTCATCTTCTCCAGATTGTGTCTGCCGTGAAGCACATGCATGAAAAC
CAAATTATTTCATAGAGATCTGAAAGCAGAAAATGTATTCTATACCAGTAATACTTGTGTG
AAGGTGGGCGATTTTGGATTTCAGCACAGTAAGCAAAAAAGGTGAAATGCTGAACACTTTC
TGTGGGTCTCCTCCCTACGCTGCGCCTGAACTCTTCCGGGACGAGCACTACATCGGCATT
TACGTGGATATCTGGGCCTTGGGGGTGCTTTTGTACTTCATGGTGACTGGCACCATGCCA
TTTCGGGCAGAAACCGTGGCCAAACTAAAAAAGAGCATCCTCGAGGGCACATACAGTGTA
CCGCCGCACGTGTCAGAGCCCTGCCACCGACTCATCCGAGGAGTCCTTCAGCAGATCCCC
ACGGAGAGGTACGGAATCGACTGCATCATGAATGATGAATGGATGCAAGGGGTGCCATAC
CCTACACCTTTGGAACCTTTCCAACCTGGATCCCAACATTTGTTCGGAAACCAGCACTCTC
AAGGAAGAAGAAAATGAGGTCAAAGCACTTTAGAACATTTGGGCATTACAGAAGAGCAT
ATTTCGAAATAACCAAGGGAGAGATGCTCGCAGCTCAATCACAGGGGTCTATAGAATTATT
TTACATAGAGTCCAAAGGAAGAAGGCTTTGGAAAGTGTCCAGTCATGATGCTACCAGAC
CCTAAAGAAAGAGACCTCAAAAAAGGGTCCCGTGTCTACAGAGGGATAAGACACACATCC
AAATTTTGCTCGATTTTATAAATTGCACTAGACTGCTTGTAACCTAACCAAGATGATTGTT
GCTGCTTCTAAATTTTTTTTCAAGGACAACCTTGAGTGGAGACATTTTTTGTAATTTTTAAAT
AAACTTAAATTTGAGATATGCAAAAAAAA

SEQ ID NO: 34_R31237_1_H, AAC33487

ATGTCCACTAGGACCCCATTTGCCAACGGTGAATGAACGAGACACTGAAAACACACGTCA
CATGGAGATGGGCGTCAAGAAGTTACCTCTCGTACCAGCCGCTCAGGAGCTCGGTGTAGA

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FIGURE 2Y

AACTCTATAGCCTCCTGTGCAGATGAACAACCTCACATCGGAACTACAGACTGTTGAAA
ACAATCGGCAAGGGGAATTTTGCAAAAGTAAAATTGGCAAGACATATCCTTACAGGCAGA
GAGGTTGCAATAAAAATAATTGACAAAACCTCAGTTGAATCCAACAAGTCTACAAAAGCTC
TTCAGAGAAGTAAGAATAATGAAGATTTTAAATCATCCCAATATAGTGAAGTTATTGAA
GTCATTGAAACTGAAAAACACTCTACCTAATCATGGAATATGCAAGTGGAGGTGAAGTA
TTTGACTATTTGGTTGCACATGGCAGGATGAAGGAAAAAGAAGCAAGATCTAAATTTAGA
CAGATTGTGTCTGCAGTTCAATACTGCCATCAGAAACGGATCGTACATCGAGACCTCAAG
GCTGAAAATCTATTGTTAGATGCCGATATGAACATTAAATAGCAGATTTCCGTTTTAGC
AATGAATTTACTGTTGGCGGTAAACTCGACACGTTTTGTGGCAGTCCTCCATACGCAGCA
CCTGAGCTCTTCCAGGGCAAGAAATATGACGGGCCAGAAGTGGATGTGTGGAGTCTGGGG
GTCATTTTATACACACTAGTCAGTGGCTCACTTCCCTTTGATGGGCAAAACCTAAAGGAA
CTGAGAGAGAGAGTATTAAGAGGGAAATACAGAATTCCTTCTACATGTCTACAGACTGT
GAAAACCTTCTCAAACGTTTTCTGGTGCTAAATCCAATTAACGCGGCACTCTAGAGCAA
ATCATGAAGGACAGGTGGATCAATGCAGGGCATGAAGAAGATGAACTCAAACCATTTGTT
GAACCAGAGCTAGACATCTCAGACCAAAAAAGAATAGATATTATGGTGGGAATGGGATAT
TCACAAGAAGAAATTCAAGAATCTCTTAGTAAGATGAAATACGATGAAATCACAGCTACA
TATTTGTTATTGGGGAGAAAATCTTCAGAGCTGGATGCTAGTGATTCCAGTTCTAGCAGC
AATCTTTCACTTGCTAAGGTTAGGCCGAGCAGTGATCTCAACAACAGTACTGGCCAGTCT
CCTCACCAAAAGTGCAGAGAAGTGTTTTCTTCAAGCCAAAAGCAAAGACGCTACAGTGAC
CATGCTGGACCAGCTATTCCTTCTGTTGTGGCGTATCCGAAAAGGAGTCAGACAAGCACT
GCAGATGGTGACCTCAAAGAAGATGGAATTTCTCCCGGAAATCAAGTGGCAGTGCTGTT
GGAGGAAAGGGAATTGCTCCAGCCAGTCCCATGCTTGGGAATGCAAGTAATCCTAATAAG
GCGGATATTCCTGAACGCAAGAAAAGCTCCACTGTCCCTAGTAGTAACACAGCATCTGGT
GGAATGACACGACGAAATACTTATGTTTTGCAGTGAGAGAAGTACAGCTGATAGACACTCA
GTGATTGAGAATGGCAAAGAAAACAGCACTATTCCTGATCAGAGAAGTCCAGTTGCTTCA
ACACACAGTATCAGTAGTGCAGCCACCCAGATCGAATCCGCTTCCCAAGAGGCACTGCC
AGTCGTAGCACTTTCCACGGCCAGCCCCGGGAACGGCGAACCAGCAACATATAATGGCCCT
CCTGCCCTCTCCAGCCTGTCCCATGAAGCCACACCATTGTCCAGACTCGAAGCCGAGGC
TCCACTAATCTCTTTAGTAAATTAACCTTCAAACTCACAAAGGAGTCGCAATGTATCTGCT
GAGCAAAAAGATGAAAACAAAGAAGCAAAGCCTCGATCCCTACGCTTACCTGGAGCATG
AAAACCACTAGTTCAATGGATCCCGGGGACATGATGCGGGAAATCCGCAAAGTGTGAGC
GCCAATAACTGCGACTATGAGCAGAGGGAGCGCTTCTTGCTCTTCTGCGTCCACGGAGAT
GGGCACGCGGAGAACCTCGTGCAGTGGGAAATGGAAGTGTGCAAGCTGCCAAGACTGTCT
CTGAACGGGGTCCGGTTTAAGCGGATATCGGGGACATCCATAGCCTTCAAAAATATTGCT
TCCAAAATTGCCAATGAGCTAAAGCTGTAA

SEQ ID NO: 35_W90839_M

AAAGGGCCGTCCTGGTCCAGCCGTTCCCTGGGTGCCCCGTTGCCGGAACCTCTATCGCTTCC
TGCCCTGAGGAACAACCCCATGTGGGCAACTATAGGCTGCTAAGGACCATCGGGAAGGGC
AACTTCGCCAAAGTCAAGCTGGCTCGGCATATCCTCACGGGCCGGGAGGTGCTATTAAAG
ATCATTGATAAGACCCAGCTGAACCCAGTAGCTTGCAAGAGCTGTTTACAGAGAAGTCCGA
ATTATGAAGGGACTCAACCACCCCAACATCGTGAAGCTTTTTGAGGTGATAGAGACGGAG
AAGACGCTATACCTGGTGATGGAATACGCTAGCGCAGGAGAAGTGTGTTGACTACCTCGTG
TCGCACGGCCGCATGAAGGAGAAGGAGGCTCGAGCCAAGTTCCGGCAGATCGTGTACGCC
GTGCACTACTGTCATCAGAAGAACATTGTACACAGGGATCTAAAGGCTGAAAACCTGTTG
CTGGATGCCGAGGCCAACATCAAAATCGCCGACTTCGGCTTCAGCAATGAGTTCACGCTG
GGCTCCAAGCTGGACACCTTCTGTGGGAGCCCCCATACGCCGCCCCAGAGCTGTTCCAG
GGCAAGAAGTATGATGGGCCAGAGGTGGACATCTGGAGCCTGGGTGTCATCCTGTACACG
CTGGTCAGCGGCTCCCTGCCCTTCGATGGGCACAACCTCAAGGAGCTGCGGGAGCGAGTC
CTCAGAGGAAAGTACCGGGTCCCCTTCTACATGTCTACAGACTGCGAGAGCATTCTGCGG

FIGURE 2Z

AGATTTCTGGTGCTGAACCCCGCAAAACGCTGTACTCTGGAGCAAATCATGAAAGACAAA
TGGATCAACATCGGCTATGAGGGTGAGGAGCTGAAGCCAGACACGGAGCTCAAAGAAGAG
CGGATGCCGGGTTCGGAAGCGAGCTGCAGTGCAGTGGGCAGTGGGAAGTCGAGGCTTGCCC
CCCTCCAGCCCCATGGTCAGCAGTGCCACAACCCCAATAAGGCAGAGATCCCTGAGCGG
CGGAAGGACAGCACTAGCACCCCTAACCACTCCCCCCCAGCATGATGACCCGAAGAAAC
ACCTATGTGTGCACAGAGCGACCAGGATCTGAACGCCCGTCTTTGTTGCCAAATGGCAAA
GAAAATAGCTCCGGTACCTCGCGGGTGCCCCCTGCCTCGCCTTCCAGTCATAGCCTGGCT
CCCCCGTCAGGCGAGCGGAGCCGCCTGGCTCGGGGCTCCACCATCCGCAGCACCTTCCAT
GGGGGCCAGGTCCGAGACCGGCGGGCAGGGAGCGGGAGTGGCGGGGGTGTGCAGAATGGA
CCCCCAGCCTCACCCACGCTTGCCACGAGGCCGCACCCCTGCCCTCCGGGCGGCCTCGC
CCCACCACCAACCTCTTCACCAAGCTGACCTCCAACTGACCCGAAGGGTCACAGACGAA
CCTGAGAGAATCGGGGACCTGAGGTCACAAGTTGCCATCTACCTTGGGATAAAACGGAA
ACCGCCCCCAGGCTGCTCCGATTCCCCTGGAGTGTGAAGCTGACCAGCTCGCGACCTTCC
TGAGGCCCTGATGGCTGCCCTGCGACAGGCCACA

SEQ ID NO: 36_406786.5_H

GTAGCCGGCTTGCGGTGACCGTCGCCTGATCCAGTTGTTAGAGGTGGAAGCTTGGCAGTT
GGCCTCCCTTCTTCCCATGGAGGTTCGGGGGCTTAACAGTCTTTGAAGAGGACCAGAGATG
CCTTTCCAGAGCCTCCCCTTGCCAGTGTGAGCAGAGGGCCAGCTGCACAGACCACTGC
TGAGCCCAGCAGGTCTTTTCTCAGCCACAGACACCTGAGCAGAAGGAATGGGCTTTC
CAGACTCTGCCAGAGCAGGACGGCGCTCTCTGAAGACAGATGGAGCTCCTATTGTCTATC
ATCACTGGCTGCCCAGAATATTTGTACAAGTAACTGCACTGCCCTGCTGCCCTGAGCA
CACGGACCCGTCCGAACCGCGGGGCAGTGTGTCTGCTGCTCCCTGCTGCGGGGACTGTC
CTCAGGGTGGTCTCACCTCTGCTTCCGGCCCCCTGTGTGCAACCCTAACAAAGGCCATCTT
CACGGTGGATGCCAAGACCACAGAGATCCTCGTTGCTAACGACAAAGCTTGCGGGCTCCT
GGGGTACAGCAGCCAGGACCTGATTGGCCAGAAGCTCACGCAGTCTTTCTGAGGTCAGA
TTCTGATGTGGTGGAGGCCCTCAGCGAGGAGCACATGGAGGCCGACGGCCACGCTGCGGT
GGTGTGTTGGCACGGTGGTGGACATCATACCCGTAGTGGGGAGAAGATTCCAGTGTCTGT
GTGGATGAAGAGGATGCGGCAGGAGCGCCGCTATGCTGCGTGGTGGTCTTGAGCCCGT
GGAGAGGGTCTCGACCTGGGTGCTTTCCAGAGCGATGGCACCATCACGTATGTGACAG
TCTCTTTGCTCATCTTCACGGGTACGTGTCTGGGGAGGACGTGGCTGGGCAGCATATCAC
AGACCTGATCCCTTCTGTGCAGCTCCCTCCTTCTGGCCAGCACATCCCAAAGAATCTCAA
GATTACAGAGGTCTGTTGGAAGAGCCAGGGACGGTACCACCTTCCCTCTGAGCTTAAAGCT
GAAATCCCAACCCAGCAGCGAGGAGGCGACCACCGGTGAGGCGGCCCCCTGTGAGCGGCTA
CCGGGCATCTGTCTGGGTGTTCTGCACCATCAGTGGCCTCATCACCTCCTGCCGGATGG
GACCATCCACGGCATCAACCACAGCTTCGCGCTGACACTGTTTGGTTACGGAAAGACGGA
GCTCCTGGGCAAGAATATCACTTTCTGATTCTGTTTCTACAGCTACATGGACCTTGC
GTACAACAGCTCATTACAGCTCCAGACCTGGCCAGCTGCCTGGACGTGCGCAATGAGAG
TGGGTGTGGGGAGAGAACCTTGGACCCGTGGCAGGGCCAGGACCCAGCTGAGGGGGGCCA
GGATCCAAGGATTAATGTCGTGCTTGCTGGTGGCCACGTTGTGCCCCGAGATGAGATCCG
GAAGCTGATGGAAAGCCAAGACATCTTCACCGGGACTCAGACTGAGCTGATTGCTGGAGG
CCAGCTCCTTTCCTGCCTCTCACCTCAGCTGCTCCAGGGGTGGACAATGTCCCAGAAGG
AAGCCTGCCAGTGCACGGTGAACAGGCGCTGCCCAAGGACCAGCAAATCACTGCCTTGGG
GAGAGAGGAACCTGTGGCAATAGAGAGCCCCGGACAGGATCTTCTGGGAGAAAGCAGGTC
TGAACCAGTGGATGTGAAGCCATTTGCTTCTGCGAAGATTCTGAAGCTCCAGTCCCAGC
TGAGGATGGGGGCAGTGATGCTGGCATGTGTGGCCTGTGTGAGAAGGCCAGCTAGAGCG
GATGGGAGTCAGTGGTCCCAGCGGTTAGACCTTTGGGCTGGGGCTGCCGTGGCCAAGCC
CCAGGCCAAGGGTCAGCTGGCGGGGGGACGCTCCTGATGCACTGCCCTTGCTATGGGAG
TGAATGGGGCTTGTGGTGGCGAAGCCAGGACTTGGCCCCCAGCCCCCTCTGGGATGGCAGG
CCTCTCGTTTGGGACACCTACTCTAGATGAGCCGTGGCTGGGAGTGGAAAACGACCGAGA

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FIGURE 2AA

AGAGCTGCAGACCTGCTTGATTAAGGAGCAGCTGTCCCAGTTGAGCCTTGACGAGCCCT
GGATGTCCCCACGCCGAACCTCGTTCCGACAGAGTGCCAGGCTGTCACCGCTCCTGTGTC
GTCCTGCGATCTGGGAGGCAGAGACCTGTGCGGTGGCTGCACGGGCAGCTCCTCAGCCTG
CTATGCCTTGGCCACGGACCTCCCTGGGGGCCTGGAAGCAGTGGAGGGCCAGGAGGTGTA
TGTGAATTCGTTTTCTTGGAACCTCAAGGAACCTCTTTTTCAGTGACCAGACAGACCAAAC
GTCATCAAATTGTTCTGTGCTACGTCTGAACTCAGAGAGACACCCTCTTCCTTGGCAGT
GGGCTCCGATCCAGATGTAGGCAGTCTCCAGGAACAGGGGTCTGTGTGTCCTGGATGACAG
GGAGCTGTTACTACTGACCGGCACCTGTGTTGACCTTGGCCAAGGCCGACGGTTCGCGGA
GAGCTGTGTGGGACATGATCCAACAGAACCCTTGAGGTTTGTGTGGTGTCTCTGAGCA
TTATGCAGCAAGCGACAGAGAAAGCCCAGGACACGTTTCTTCCACGTTGGATGCTGGCCC
TGAGGACACGTGCCCATCAGCAGAGGAGCCAAGGCTGAACGTCCAGGTACCTCCACGCC
CGTGATCGTGATGCGCGGGGCTGCTGGCCTGCAGCGGGAGATCCAGGAGGGTGCCTACTC
CGGGAGCTGCTACCATCGAGATGGCTTACGGCTGAGTATACAGTTTGAGGTGAGGCGGGT
GGAGCTCCAGGGCCCCACACCTCTGTTCTGCTGCTGGCTGGTGAAAGACCTCCTCCACAG
CCAACGCGACTCAGCCGCCAGGACCCGCCTGTTCTTGCCAGCCTGCCCGGCTCCACCCA
CTCTACCGCTGCTGAGCTCACCGACCCAGCCTGGTGGAAAGTGCTCAGAGCCAGACCCTG
GTTTGAGGAGCCCCCAAGGCTGTGGAACCTGGAGGGGTGGCGGCCTGTGAGGGCGAGTA
CTCCCAAAGTACAGTACCATGAGCCCGCTGGGCAGTGGGGCCTTCGGCTTCGTGTGGAC
TGCTGTGGACAAGGGAAAAACAAGGAGGTGGTGGTGAAGTTTATTAAGAAGGAGAAGGT
CTTGAGGATTGTTGGATTGAGGATCCCAAACCTGGGAAAGTTACTTTAGAGATCGCAAT
TCTATCCAGGGTGGAGCACGCCAATATCATCAAGGTATTGGATATATTTGAAAACCAAGG
GTTCTTCCAGCTTGTGATGGAGAAGCACGGCTCCGGCCTAGACCTCTTCGCTTTCATCGA
CCGCCACCCAGGCTGGATGAGCCCCTGGCGAGCTACATCTTCCGACAAGTGAGAGCAGG
CCAGAGCCGTCTAGTGTGAGCAGTGGGATACCTGCGCTGAAGGACATCATCCACCGTGA
CATCAAGGATGAGAACATCGTGATCGCTGAGGACTTCACAATCAAGCTGATAGACTTTGG
CTCGGCCCGCTACTTGGAAGGGGAAAATATTTTATACTTTTGTGGGACCATCGAGTA
CTGTGCACCGGAAGTTCTCATGGGGAATCCCTACAGAGGGCCGGAGCTGGAGATGTGGTC
TCTGGGAGTCACTCTGTACACGCTGGTCTTTGAGGAGAACCCCTTCTGTGAGCTGGAGGA
GACCGTGGAGGCTGCCATACACCCGCCATACCTGGTGTCCAAAGAACTCATGAGCCTTGT
GTCTGGGCTGCTGCAGCCAGTCCCTGAGAGACGCACCACCTTGGAGAAGCTGGTGACAGA
CCCGTGGGTAAACACAGCCTGTGAATCTTGCTGACTATACATGGGAAGAGGTGTTTCGAGT
AAACAAGCCAGAAAGTGGAGTTCTGTCCGCTGCGAGCCTGGAGATGGGGAACAGGAGCCT
GAGTGATGTGGCCAGGCTCAGGAGCTTTGTGGGGGCCCCGTTCCAGGCGAGGCTCCTAA
TGGCCAAGGCTGTTTGCATCCCGGGGATCCCCGTCTGCTGACCAGCTAAACACCAATTTT
TTCTGCTTTTCTCCTACTTGGTTTGGAAAATCACACAGTTTTTCAGGCTCCATCTGTTTG

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CCACGCGTCCGCATCCCTGCTTGATGAGCCCTGGCGAGTTTCATCTTTCGACAACTAG
TGTCTGCTGTAGGATACCTGCACTCCCAAGGCATCATCCATAGAGACATCAAGGATGAGA
ACATTGTGATTGCTGAGGACTTCACAATTAAGCTGATAGATTTTGGCTCAGCTGCCTACT
TAGAGAGGGGCAAACCTATTTTATACCTTTTGTGGAACAATCGAATACTGTGCACCTGAGG
TTCTCATTTGGAATCCCTACAGAGGGCCAGAGCTGGAGATGTGGTCTCTGGGGGTACCCC
TGTACACGCTCATCTTCGAGGAGAATCCCTTCTGTGAGGTGGAGGAGACCATGGAGGCAG
TTATTCATCCCCATTCTGGTTTCCCAAGAACTTATGAGTCTTCTGTCTGGACTGCTGC
AGCCTTGCCCTGAGCAGCGGACCCTTTGGAGAAGCTGATCAGGGACCCCTGGGTGACAC
AGCCTGTGAACCTTGCTAGCTATACTTGGGAAGAGGTGTGTAGGACCAACCAGCCAGAAA
GTGGCCTGCTGTGAGCTGCAAGTCTGGAGATTGGGAGTAGGAGTCCAAGTGAAATGGCTC
AGAGAGAGGGTCTCTGTGGGCCTCCTGCTCCAGGGAGACTCGTGGTGACCAGCACTGCT
TGCATCTTAAGGACCCCTCTTTGCCAGTCAGCTGAGCAAGCTCTCCTGCTCTTTGGTTTG
GGCAGTTGTATGGATTTTCAGGGCTTTCTACCTGGAGAAAGGAAGTTGTGAAGGATTGGGA

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FIGURE 2BB

TGACTTCTGCTTCTAGATTCCCTATGCAAATGCTACAAGAGCCTGCGATGCTAGTTTTCTT
AGGTTTATGATATAGACTTGTAATTCATGTTTTTTTTATAACCTTGAAAATCATTCTAATG
TTCAGTTATACTGTACTATTAAAGGGCTTTAAGTTGTAAGCCTCAGAAAGACACAAGGAG
TGTTTAAGTTCTCTATTTTTGTGTTTGTGTTTTGCTTGTAAGTTTTTGAGACAGGATCTC
ACCATGTAACTTTGGCTGGCCTGGAACCACTATGTAGACCAGGTAGACCTTAAACTGA
CAGATCTGCCTGCGCTTGCCTCCCAAGCATTAGGACTGATGGTGTGTGTCACCATGCCCA
GTTCTTCCTGGTTTTGTGTGTAGGTTTTCTTCCCCTGACTTGGTACATGTGACATGTGA
CAGATGTATGGAGTCTATAGAAGTGGCCAGACAAAATGGCCAGAAATTTTATTTATTTT
CTTAAAAATTTTCCAAATTAAAGCTACTTAGTTAACAGTTAAACTGGCCAGGACTATATG
AGATAAACTTGGTTTTCTATTTCTTTTTGT

SEQ ID NO: 38_AA785735_H

GGCAGCAGGCGCGCCTGGCTGGGCCCTGCGGAGGANGGGAAGGAGCGAAGGAGCGAAGGA
GCAAGCGGAGCGCAGTTCGCCCAAGCCAAGCCGCGCTGCCAACCCCTCCCGCCCCGCGCG
CTCCTGTCCGCGTGTCTAGCAGCGGGGCCAGCATGGTTCATGGCGGATGGCCCGAGGCA
CTTGACGCGCGGCGGCTCCGGGTGGGGTTCTACGACATCGAGGGCACGCTGGGCAAGGG
CAACTTCGCTGTGGTGAAGCTGGGGCGGCACCGGATCACCAAGACGGAGGTGGCAATAAA
AATAATCGATAAGTCTCAGCTGGATGCAGTGAACCTTGAGAAAATCTACCGAGAAGTACA
AATAATGAAAATGTTAGACCACCCTCACATAATCAAACCTTTATCAGGTAATGGAGACCAA
AAGTATGTTGTACCTTGTGACAGAATATGCCAAAAATGGAGAAATTTTTGACTATCTTGC
TAATCATGGCCGGTTAAATGAGTCTGAAGCCAGGCGAAAATTCTGGCAAATCCTGTCTGC
TGTTGATTATTGTCATGGTTCGGAAGATTGTGCACCGTGACCTCAAAGCTGAAAATCTCCT
GCTGGATAACAACATGAATATCAAAATAGCAGATTTTCGGTTTTGGAAATTTCTTTAAAAG
TGGTGAACCTGCTGGCAACATGGTGTGGCAGCCCCCTTATGCAGCCCCAGAAGTCTTTGA
AGGGCAGCAGTATGAAGGACCACAGCTGGACATCTGGAGTATGGGAGTTGTTCTTTATGT
CCTTGTCTGTGGAGCTCTGCCCTTTGATGGACCGACTCTTCCAATTTTGAGGCAGAGGGT
TCTGGAAGGAAGATTCCGGATTCCGTATTTTCATGTGAGAAGATTGCGAGCACCTTATCCG
AAGGATGTTGGTTCCTAGACCCATCCAAACGGCTAACCATAGCCCAAATCAAGGAGCATAA
ATGGATGCTCATAGAAGTTCCTGTCCAGAGACCTGTTCTCTATCCACAAGAGCAAGAAAA
TGAGCCATCCATCGGGGAGTTTAATGAGCAGGTTCTGCGACTGATGCACAGCCTTGGAAAT
AGATCAGCAGAAARCCATTGAGTCTTTGCAGAACAAAGAGCTATAACCACTTTGCTGCCAT
TTATTTCTTGTGTTGGTGGAGCGCCTGAAATCACATCGGAGCAGTTTCCCAGTGGAGCAGAG
ACTTGATGGCCGCCAGCGTCGGCCTAGCACCATTGCTGAGCAAACAGTTGCCAAGGCACA
GACTGTGGGGCTCCCAGTGACCATGCATTCACCGAACATGAGGCTGCTGCGATCTGCCCT
CCTCCCCCAGGCATCCAACGTGGAGGCCTTTTCATTTCCAGCATCTGGCTGTCAGGCGGA
AGCTGCATTCATGGAAGAAGAGTGTGTGGACACTCCAAAGGTCAATGGCTGTCTGCTTGA
CCCTGTGCCTCCTGTCTGGTGCGAAGGGATGCCAGTCACTGCCAGCAACATGATGGA
GACCTCCATTGACGAAGGGCTGGAGACAGAAGGAGAGGCCGAGGAAGACCCCGCTCATGC
CTTTGAGGCATTTTCAGTCCACACGCAGCGGGCAGAGACGGCACACTCTGTCAGAAGTGAC
CAATCAACTGGTCGTGATGCCTGGGGCAGGGAAAAATTTCTCCATGAATGACAGCCCTC
CCTTGACAGTGTGGACTCTGAGTATGATATGGGGTCTGTTTCAGAGGGACCTGAACTTTCT
GGAAGACAACCCCTTCCCTTAAGGACATCATGTTAGCCAATCAGCCTTCACCCCGCATGAC
ATCTCCCTTCATAAGCCTGAGACCTACCAACCCAGCCATGCAGGCTCTGAGCTCCCAGAA
ACGAGAGGTCCACAACAGGTCTCCAGTGAGCTTCAGAGAGGGCCGAGAGCATCAGATAC
CTCCCTCACCCAGGGAATTGTAGCATTAGACAACATCTTCAGAATCTGGCTAGAACCAA
AGGAATTCTAGAGTTGAACAAAGTGCAGTTGTTGTATGAACAAATAGGACCGGAGGCAGA
CCCTAACCTGGCGCCGGCGGCTCCTCAGCTCCAGGACCTTGCTAGCAGCTGCCCTCAGGA
AGAAGTTTCTCAGCAGCAGGAAAGCGTCTCCACTCTCCCTGCCAGCGTGCATCCCCAGCT
GTCCCCACGGCAGAGCCTGGAGACCCAGTACCTGCAGCACAGACTCCAGAAGCCAGCCT
TCTGTCAAAGGCCCAGAACACCTGTGAGCTTTATTGCAAAGAACCACCGCGGAGCCTTGA

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FIGURE 2CC

GCAGCAGCTGCAGGAACATAGGCTCCAGCAGAAGCGACTCTTTCTTCAGAAGCAGTCTCA
ACTGCAGGCCTATTTTAATCAGATGCAGATAGCAGAGAGCTCCTACCCACAGCCAAGTCA
GCAGCTGCCCCCTTCCCCGCCAGGAGACTCCACCGCCTTCTCAGCAGGCCCCACCGTTCAG
CCTGACCCAGCCCCCTGAGCCCCGTCTGGAGCCTTCCTCCGAGCAGATGCAATACAGCCC
TTTCTCAGCCAGTACCAAGAGATGCAGCTTCAGCCCCCTGCCCTCCACTTCCGGTCCCCG
GGCTGCTCCTCCTCTGCCCACGCAGCTACAGCAGCAGCAGCCGCCACCGCCACCACCCCC
TCCACCACCACGACAGCCAGGAGCTGCCCCAGCCCCCTTACAGTTCTCCTATCAGACTTG
TGAGCTGCCAAGCGCTGCTTCCCCTGCGCCAGACTATCCCACTCCCTGTCAGTATCCTGT
GGATGGAGCCCAGCAGAGCGACCTAACGGGGCCAGACTGTCCCAGAAGCCCAGGACTGCA
AGAGGCCCCCTCCAGCTACGACCCACTAGCCCTCTCTGAGCTACCTGGACTCTTTGATTG
TGAAATGCTAGACGCTGTGGATCCACAACACAACGGGTATGTCCTGGTGAATTAGTCTCA
GCACAGGAATTGAGGTGGGTGAGGTGAAGGAAGAGTGTATGTTCTTATTTTTATTCCAGC
CTTTTAAATTTAAAGCTTATTTTCTTGCCCTCTCCCTAACGGGGAGAAATCGAGCCACCC
AACTGGAATCAGAGGGTCTGGCTGGGGTGGATGTTGCTTCCTCCTGGTTCTGCCCCACCA
CAAAGTTTTCTGTGGCAAGTGCTGGAACATAGTTGTAGGCTGAGGCAGGAGAATGGCGTG
AACCCGGGAGGCGGAGCTTGCACTGAGCCAAGATCGTGCCACTGCACTCCAGCCTGGGCG
ACTGAGCAAGACTCCACCTCAAAAAAAAAAAAAAAAAAGGACAAGAGCAGTATCATCTGCCTC
TGTTTCTAAACTGGACAAAGAGATTTTCTTAAAGTTTCTATCATCTCCCTTCTGACAGGT
TCTACAGTGTGGTCTGAAGCACCTGTAATGTCAGAGCCCTTGTCTGGCCCTTGGTGGCAG
GTGAACGAAAGCAGTGGAGCCTCTCACCTTCCAGTAGCCTCTCACATTCTTATTTTACCA
TTTTTGTCTAATTAAGGTAGCCTAGCTGATTCTAGAAGACAGCCATCCTACGTGCACCC
CCACCTTGTGTCCACATCTTCTCCAGGCAGGTTTCAACCTATCAGCAGACTCAGGCACAC
ACTGGGGCACAGATAGAGAACCAGGCGGCAGCAGTGCTCGCAGACCCACCCAGGGAGAGC
TGTGATGGGTTCTGCCCAGATACTCTGCTCGCCACCCACAAGGGAGCAATAGCTTATAT
TTGTACATTAGTTTTTACCAAGCACTTTCTCTTCTAACCTCACAACAATTCTATGAAATT
AGCTGGGGAGATACTGTCCTTATTTTTTACAGCTGAAGAAACCAAAGCTTTGGGAAGTTT
GTGACTTCTCTGAGATCACAGCTGGTGATAGAAGGAGCTGGGACACGCGCTTGGGTGAC
TGGCTTCTGGTTTTTGGTTCTCTGGCTTCTAGTGCTGGAAGAAGCCCTCTCTTTCCCTTCT
CTTTCCTCAGTAGCATCTGACTCTTTTTCATAAGCAAACAGCTGTATAAAACAAAGCCCCCA
TTTTTGGTCAAGCACAGGGTGAATGTGATATTGTTCCCAACCTTATTCTCCACTCAACA
GCCGCTGGCTTTGGGGAAGAGGCCGCTTTCAGGTGACAGTGCAGCTGTCCAGGTGGCCG
TGCCTGAACCAGGCTGAGGGAGACAAAAACCCCGCAGACCCGCTGCCTTTTCAGCGTCC
AGTTAACTGCAGAAGTTTAGGCTCACCTCAAAGATGTCTAGTTTTTCCAAGTTACAATAC
AGCAGTTTCTTACAGAACACCCCTTCTCTCAATTGCCAAGGGGCGCATCGCACGGCATC
AGGCCACCACTGCAGGCCAGCAGATTCCACCCAGGAACGGTCATGAACTCAGCCTTTGT
CTCAACGAGGGGCGTAACATTTCTTACAGTCAAGCCCCATCACTAGAAGTGCTTATTA
CTTTTAGGATTAAAAAAGTAATAACAGACTTTGACTTAATACTCTGTCTTTTCAGAGGCA
AAGTGGGTGGGTAGAGGGGAGCTTTAAAAATAGAAGTACAAAACAACATCCTGGAAACAT
ATGACCCCAAGATGGAATAATGTCACATTCCCCAGTGCAGATAATGGGCTGCTGCTGGCTC
TGTGGTGTCTGTCTGCAGAAGATTTGCTCAGTCAAGGAAATTCAAGTGGTGAGACCTTTC
CACCATGGGTGGTAAGAGAAACCTGCCTTCACCAAAATCTCTGAAGGGGAAAGAAGTGGA
GAGAAAGGTTTGCTTCACTTCGGGGACTGCAGTTTGAGAAATAAAAGGGATACAGAGATA
TCTGCCTTTGTAGAAAGGGCAAGATTATTTGCTTATATCTGAAGGGAGGTGGGTGGTTT
TGCTGGATGTTTGGTCTGAAAGAGTTACTTTTGATAAAGTTAATCTAATTGTAGTTATAT
TTTCTGTGTGCTTTTTTTTAAATTACTAAGAAAAAAATTTGGTGAGTTCAGTAGCTTTGGTA
TTATGAGTGCAAATCATAATAGCTCCAATGTGAAAAAAATAATCTCTGTACCAAATAGT
ACTTAATGTTAGAAAAATTGCCTAAAATGCAGTGTAATAAATAATCTCTGTACCAAATAGT
AATTTAAATGGGGTAATTTTCTGCAAGGAAAATGTACTGTTTTTATGTTTCCAACCCTCT
TGA

FIGURE 2DD

SEQ ID NO: 39_AA207220_H

GCTGTGGCTCCCCGTCCTGGTGCGGGACCTGTGCCCCGCGCTTCAGCCCTCCCCGCAAGC
CTATTGATTCCCCTGCCGCCCTTGCTCCACCTCCTGCTCGCCATGGAGTCGCTGGTTTTTC
GCGCGGCGCTCCGGCCCCACTCCCTCGGCCGAGAGCTAGCCCCGGCCGCTGGCGGAAGGG
CTGATCAAGTCGCCCCAAGCCCCCTAATGAAGAAGCAGGCGGTGAAGCGGCACCACCACAAG
CACAACTGCGGCACCGCTACGAGTTCCTGGAGACCCTGGGCAAAGGCACCTACGGGAAG
GTGAAGAAGGCGCGGGAGAGCTCGGGGCGCCTGGTGGCCATCAAGTCAATCCGGAAGGAC
AAAATCAAAGATGAGCAAGATCTGATGCACATACGGAGGGAGATTGAGATCATGTCATCA
CTCAACCACCCTCACATCATTGCCATCCATGAAGTGTTTGAGAACAGCAGCAAGATCGTG
ATCGTCATGGAGTATGCCAGCCGGGGCGACCTTTATGACTACATCAGCGAGCGGCAGCAG
CTCAGTGAGCGCGAAGCTAGGCATTTCTTCCGGCAGATCGTCTCTGCCGTGCACTATTGC
CATCAGAACAGAGTTGTCCACCGAGATCTCAAGCTGGAGAACATCCTCTTGATGCCAAT
GGGAATATCAAGATTGCTGACTTCGGCCTCTCCAACCTCTACCATCAAGGCAAGTTCCTG
CAGACATTCTGTGGGAGCCCCCTCTATGCCTCGCCAGAGATTGTCAATGGGAAGCCCTAC
ACAGGCCCCAGAGGTGGACAGCTGGTCCCTGGGTGTTCTCCTCTACATCCTGGTGCATGGC
ACCATGCCCTTTGATGGGCATGACCATAAGATCCTAGTGAAACAGATCAGCAACGGGGCC
TACCGGGAGCCACCTAAACCCTCTGATTGCCTGNNTGGCCTGATCCGGTGGCTGTTGATG
GTGAACCCACCCGCGGGGCCACCCTGGAGGATGTGGCCAGTCACTGGTGGGTCAACTGG
GGCTACGCCACCCGAGTGGGAGAGCAGGAGGCTCCGCATGAGGGTGGGCACCCTGGCAGT
GACTCTGCCCGCGCCTCCATGGCTGACTGGCTCCGGCGTTCCTCCCGCCCCCTCCTGGAG
AATGGGGCCAAGGTGTGCAGCTTCTTCAAGCAGCATGCACCTGGTGGGGGAAGCACCACC
CCTGGCCTGGAGCGCCAGCATTGCTCAAGAAGTCCCGCAAGGAGAATGACATGGCCCCAG
TCTCTCCACAGTGACACGGCTGATGACACTGCCCATCGCCCTGGCAAGAGCAACCTCAAG
CTGCCAAAGGGCATTCTCAAGAAGAAGGTGTGAGCCTCTGCAGAAGGGGTACAGGAGGAC
CCTCCGGAGCTCAGCCCAATCCCTGCGAGCCAGGGCAGGCTGCCCCCTGCTCCCCAAG
AAGGGCATTCTCAAGAAGCCCCGACAGCGCGAGTCTGGCTACTACTCCTCTCCCGAGCCC
AGTGAATCTGGGGAGCTCTTGAGCGCAGGCGACGTGTTTGTGAGTGGGGATCCCAAGGAG
CAGAAGCCTCCGCAAGCTTCAGGGCTGCTCCTCCATCGCAAAGGCATCCTCAAACCTCAAT
GGCAAGTTCTCCCAGACAGCCTTGAGCTCGCGGCCCCCACCACCTTCGGCTCCCTGGAT
GAACTCGCCCCACCTCGCCCCCTGGCCCCGGGCCAGCCGACCCTCAGGGGCTGTGAGCGAG
GACAGCATCCTGTCTCTGAGTCCTTTGACCAGCTGGACTTGCCCTGAACGGCTCCCAGAG
CCCCCACTGCGGGGCTGTGTGTCTGTGGACAACCTCACGGGGCTTGAGGAGCCCCCTCA
GAGGGCCCTGGAAGCTGCCTGAGGCGCTGGCGGCAGGATCCTTTGGGGGACAGCTGCTTT
TCCCTGACAGACTGCCAGGAGGTGACAGCGACCTACCGACAGGCACTGAGGGTCTGCTCA
AAGCTCACCTGAGTGGAGTAGGCATTGCCCCAGCCCGGTGAGGCTCTCAGATGCAGCTGG
TTGCACCCCGAGGGGAGATGCCTTCTCCCCACCTCCAGGACCTGCATCCAGCTCAGA
AGGCTGAGAGGGTTTGCAGTGGAGCCCTGAGCAGGGCTGGATATGGGAAGTAGGCAAATG
AAATGCGCCAAGGGTTCAAGTGTCTGTCTTCAGCCCTGCTGAACGAAGAGGATACTAAAGA
GAGGGGAACGGGAATGCCCGCGACAGAGTCCACATTGCCTGTTTCTTGTGTACATGGAGG
GGCCACAGAGA

SEQ ID NO: 40_AA426580_H, MAK_V_H

ATGCCGGCGGCGGGCGGGGACGGGCTCCTGGGGGAGCCGGCGGCGCCTGGGGGCGGCGGC
GGCGCGGAGGACGCGGCCAGGCCCGCGGCGGCCTGCGAGGGAAGTTTCTGCCTGCCTGG
GTGAGCGGCGTGCCCCGCGAGCGGCTCCGCGACTTCCAGCACCAACAAGCGCGTGGGCAAC
TACCTCATCGGCAGCAGGAAGCTGGGCGAGGGCTCCTTTGCCAAGGTGCGCGAGGGGCTG
CACGTGCTGACCGGGGAGAAGGTGGCCATAAAAGTCATTGATAAGAAGAGAGCCAAAAAG
GACACCTATGTACCAAAAACCTGCGGCGAGAGGGTCAGATCCAGCAGATGATCCGCCAC
CCCAATATCACTCAGCTCCTTGATATTTAGAAACGGAAAACAGCTACTACCTGGTTCATG
GAGCTGTGCCCTGGGGGCAACCTGATGCACAAGATCTATGAGAAGAAGCGGCTGGAGGAG

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FIGURE 2EE

TCCGAAGCCCGCAGATACATCCGACAGCTCATCTCTGCCGTAGAGCACCTGCACCGGGGCC
GGGGTGGTCCACAGAGACTTGAAGATAGAGAATTTGCTACTAGATGAAGACAATAATATC
AAGCTGATTGACTTTGGTTTGAGCAACTGCGCAGGGATCCTGGGTTACTCGGATCCGTTC
AGCACACAGTGTGGCAGCCCTGCCTACGCTGCACCTGAACTGCTCGCCAGGAAGAAATAC
GGCCCCAAAATCGATGTCTGGTCCATAGGTGTGAACATGTATGCCATGTTGACCGGGACG
CTGCCTTTTCACGGTGGAGCCTTTTCAGCCTGAGGGCTTTGTACCAGAAGATGGTAGACAAA
GAAATGAACCCCCCTCCCCACTCAGCTCTCCACAGGTGCCATCAGTTTCTGCGCTCTCTC
CTGGAACCGGATCCTGTGAAGAGGCCAAATATTTCAGCAGGCACTGGCGAATCGCTGGCTT
AATGAGAATTACACGGGCAAAGTGCCTGTAAATGTACCTATCCCAACAGGATTTCTCTG
GAAGATCTGAGCCCGAGCGTCGTGCTGCACATGACCGAGAAGCTGGGTTACAAGAACAGC
GACGTGATCAACACTGTGCTCTCCAACCGCGCTGCCACATCCTGGCCATCTACTTCCTC
TTAAACAAGAACTGGAGCGCTATTTGTGAGGGAAATCTGACATCCAGGACAGCCTCTGC
TACAAGACCCGGCTCTACCAGATAGAAAAGTACAGGGCCCCCAAGGAGTCTATGAGGCC
TCTCTGGACACCTGGACACGAGATCTTGAATTCCATGCCGTGCAGGATAAAAAGCCCCAA
GAACAAGAAAAAAGAGGGGATTTTCTTCATCGACCATTTCTCCAAGAAGTTGGACAAGAAC
CTGCCCTCGCACAAACAGCCCTCAGGCTCGCTTATGACACAGATTCAGAACACCAAAGCC
CTCCTGAAGGACCGGAAGGCCTCCAAGTCCAGCTTCCCCGACAAAGATTCTTTGGCTGC
CGCAATATTTTCCGCAAAACCTCAGATTCCAATTGTGTGGCTTCTTCTCCATGGAGTTC
ATCCCCGTGCCACCGCCAGGACCCCGAGGATTGTGAAGAAACCGGAGCCCCATCAGCCA
GGGCCCGGAAGCACTGGCATCCCCACAAGGAAGACCCCTGATGCTGGACATGGTGC GC
TCCTTCGAGTCTGTGGATCGCGACGACACGTAGAAGTGCTGTCTCCCTCTCATCACTAC
AGGATTCTGAACTCCCCGGTCAGCTTGGCTCGCAGAAATTCCAGCGAGAGGACGCTGTCC
CCGGGTCTGCCATCCGGAAGCATGTGCGCTCTCCATACTCCTTTGCATCCAACTCTGGTC
TCTTTTGCTCACGAAGATAAGAACAGCCCCCAAAAGAGGAGGGCCTGTGTTGCCACCT
CCGGTTCCAGCAATGGCCCCATGCAGCCTCTGGGGAGCCCCAATTGTGTGAAAAGCCGA
GGCCGGTTCCCTATGATGGGCATCGGACAGATGTTAAGGAAGCGCCATCAGAGTCTGCAG
CCATCTGCAGATAGGCCCTGGAGGCCAGCCTGCCCCCACTGCAGCCCCTAGCCCCTGTG
AACCTTGCCCTTTGACATGGCCGATGGGGTCAAGACCCAGTGCTAA

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ATGGACACAAAGCTGAACATGCTGAACGAGAAGGTGGACCAGCTCCTGCACTTCCAAGAA
GATGTACAGAGAAGTTGCAGAGCATGTGCCGAGACATGGGCCACCTGGAGCGGGGCCTG
CACAGGCTGGAGGCCTCCCGGGCACCGGGCCCGGGCGGGGCTGATGGGGTTCCCCACATT
GACACCCAGGCTGGGTGGCCCGAGGTCTGGAGCTGGTGAGGGCCATGCAGCAGGATGCG
GCCAGCACGGTGGCAGGCTGGAGGCCCTCTTCAGGATGGTGGCTGCGGTGGACAGGGCC
ATCGCTTTGGTGGGGGCCACGTTCCAGAAATCAAAGGTGGCGGATTTCTTCATGCAGGGG
CGTGTGCCCTGGAGGAGAGGCAGCCAGGTGACAGCCCTGAGGAGTGGGTAAAAGAGGAG
GAGGTCTGTTTCATGCCTCCAGTTCCCCCAGCTCCGGGGGCAGCAGGACAGAGCCTGCAG
AAGGATAAGGGGGAGCTGTCTGCCGAGCAGGGGATCTGGGCCACATTGATGACGCTGGTG
ATCATGGTGACAGCGGCAAATAAAGAGCGAGTGGAAGAAGAGGGAGGAAAACCAAAGCAT
GTGCTGAGCACCAGTGGGGTGCAGTCTGATGCCAGGGAGCCTGGGGAAGAGAGCCAGAAG
GCGGACGTGCTGGAGGGGACAGCGGAGAGGCTGCCCCCATCAGAGCGTCAGGGCTGGGA
GCTGACCCCGCCAGGCAGTGGTCTCACCGGGCCAGGGAGATGGTGTTCCTGGCCCAGCC
CAGGCATTCCCTGGCCACCTGCCCCCTGCCACAAAGGTGGAAGCCAAGGCTCCTGAGACA
CCCAGCGAGAACCTCAGGACTGGCCTGGAATTGGCTCCAGCACCCGGCAGGGTCAATGTG
GTCTCCCCGAGCCTGGAGGTTGCACAGGTGCAGGACAAGGAGCATCGTCCAGCAGGCCT
GACCTGAGCCCTTAGAGGAAGGCACGAGGCTGACTCCAGGGCCTGGCCCTCAGTGCCCA
GGGCTCCAGGGCTGCCAGCCCAGGCCAGGGCAACCCACAGTGGTGGAGAAACACCTCCA
AGGGCAGCCCTGCTGAAGGGCGCTGTGGCCCCGGGCTTCTCTCGGAGGGACCTGGTGTTC
CCTAGCATCTTCTGCGCCTGCCTAGGGATCTCCATCCACATAAAGAGATGGATACTCCT

FIGURE 2FF

GGGGAGATGCTGATGACAGGCAGGGGAGCCTTGGACCCACCCTCACCACAGAGGCTCCA
GCAGCTGCCAGCCAGGCAAGCAGGGCCACCTGGGACCGGGCGCTGCCTCCAAGCCCCT
GGGACTGAGCCCGGAGAACAGACCCCTGAAGGAGCCAGAGAGCTCTCCCCGCTGCAGGAG
AGCAGCAGCCCCGGGGGAGTGAAGGCAGAGGAGGAGCAAAGGGCTGGGGCCGAGCCTGGC
ACGAGACCAAGCTTGGCCAGGAGTGACGACAATGACCACGAGGTTGGGGCCCTGGGCCTG
CAGCAGGGCAAAGCCCAGGGGCGGGAAACCTTGAGCCTGAGCAGGACTGTGCAGCCAGG
GCTCCGGTGAGAGCTGAAGCAGTAAGGAGGATGCCCCAGGCGCCGAGGCTGGCAGCGTG
GTTCTGGATGACAGTCCGGCCCCACCAGCTCCTTTTGAACACCGGGTAGTGAGCGTCAAG
GAGACCTCCATCTCTGCGGGTTACGAGGTGTGCCAGCACGAAGTCTTGGGAGGGGGTTCGG
TTTGGCCAGGTCCACAGGTGCACAGAGAAGTCCACAGGCCTCCCACTGGCTGCCAAGATC
ATCAAAGTGAAGAGCGCCAAGGACCGGGAGGACGTGAAGAACGAGATCAACATCATGAAC
CAGCTCAGCCACGTGAACCTGATCCAGCTCTATGACGCCTTCGAGAGCAAGCACAGCTGC
ACCCTTGTCTATGGAGTACGTGGACGGGGGTGAGCTCTTCGACCGGATCACAGATGAGAAG
TACCACCTGACTGAGCTGGATGTGGTCCTGTTTACCAGGCAGATCTGTGAGGGTGTGCAT
TACCTGCACCAGCACTACATCCTGCACCTGGACCTCAAGCCGGAGAACATATTGTGCGTC
AATCAGACAGGACATCAAATTAAGATCATTGACTTTGGGCTGGCCAGAAGGTACAAGCCT
CGAGAGAAGCTGAAGGTGAACCTTCGGCACTCCTGAGTTCCTGGCCCCAGAAGTCGTCAAT
TATGAGTTTGTCTCATTCCTCCACAGACATGTGGAGTGTGGGAGTCATCACCTACATGCTA
CTCAGTGGCTTGTCCCCATTTCTAGGGGAAACAGATGCAGAGACCATGAATTTTATTGTA
AACTGTAGCTGGGATTTTGATGCTGACACCTTTGAAGGGCTCTCGGAGGAGGCCAAGGAC
TTTGTTCCTCGGTTGCTGGTCAAAGAGAAGAGCTGCAGAATGAGTGCCACACAGTGCCTG
AAACACGAGTGGCTGAATAATTTGCCTGCCAAAGCTTCAAGATCCAAAACCTCGTCTCAA
TCCCAACTACTGCTGCAGAAATACATAGCTCAAAGAAAATGGAAGAAACATTTCTATGTG
GTGACTGCTGCCAACAGGTAAAGGAAATTTCCAACTTCTCCCTAA

SEQ ID NO: 42_SGK088_H

GGGGAGATGGCGCTGTTTGAAGTGCCTGGTGGCGGGGCCCACTGACGTGGAGGTGGATTGG
CTGTGCCGTGGCCGCCTGCTGCAGCCTGCACTGCTCAAATGCAAGATGCATTTTCGATGGC
CGCAAATGCAAGCTGCTACTTACATCTGTACATGAGGACGACAGTGGCGTCTACACCTGC
AAGCTCAGCACGGCCAAAGATGAGCTGACCTGCAGTGCCCGGCTGACCGTGCGGCCCTCG
TTGGCACCCCTGTTTACACGGCTGCTGGAAGATGTGGAGGTGTTGGAGGGCCGAGCTGCC
CGTTTCGACTGCAAGATCAGTGGCACCCCGCCCCCTGTTGTTACCTGGACTCATTTTGGC
TGCCCCATGGAGGAGAGTGAGAACTTGC GGCTGCGGCAGGACGGGGGTCTGCACTCACTG
CACATTGCCCATGTGGGCAGCGAGGACGAGGGGCTCTATGCGGTGAGTGTGTTAACACC
CATGGCCAGGCCCACTGCTCAGCCCAGCTGTATGTAGAAGAGCCCCGGACAGCCGCCTCA
GGCCCCAGCTCGAAGCTGGAGAAGATGCCATCCATTCCTCGAGGAGCCAGAGCAGGGTGA
CTGGAGCGGTGTCCATTCCCGACTTCTGCGGCCACTGCAGGACCTGGAGGTGGGACTG
GCCAAGGAGGCCATGCTAGAGTGCCAGGTGACCGGCCTGCCCTACCCCAACATCAGCTGG
TTCCACAATGGCCACCGCATCCAGAGCAGCGACGACCGGCGCATGACACAGTACAGGGAT
GTCCATCGCTTGGTGTTCCTGCCGTGGGGCCTCAGCACGCCGGTGTCTACAAGAGCGTC
ATTGCCAACAAGCTGGGCAAAGCTGCCTGCTATGCCACCTGTATGTACAGATGTGGTC
CCAGGCCCTCCAGATGGCGCCCCGAGGTGGTGGCTGTGACGGGGAGGATGGTCACTC
ACATGGAACCCCCCAGGAGTCTGGACATGGCCATCGACCCGGACTCCCTGACGTACACA
GTGCAGCACCAGGTGCTGGGCTCGGACCAGTGGACGGCACTGGTCAAGGCCTGCGGGAG
CCAGGTGGGCAGCCACAGGGCTGCGTAAGGGGGTCCAGCACATCTTCGGGTCTCAGC
ACCACTGTCAAGAGCAGCAGCAAGCCCTCACCCCTTCTGAGCCTGTGCAGCTGCTGGAG
CACGGCCCAACCCTGGAGGAGGCCCTGCCATGCTGGACAAACCAGACATCGTGTATGTG
GTGGAGGGACAGCCTGCCAGCGTCACCGTCACATTCAACCATGTGGAGGCCAGGTGCTC
TGGAGGAGCTGCCGAGGGGCCCTCCTAGAGGCACGGGCCGGTGTGTACGAGCTGAGCCAG
CCAGATGATGACCAGTACTGTCTTCGGATCTGCCGGGTGAGCCGCCGGACATGGGGGCC

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FIGURE 2GG

CTCACCTGCACCGCCCCGAAACCGTCACGGCACACAGACCTGCTCGGTACATTGGAGCTG
GCAGAGGCCCTCGGTTTGAGTCCATCATGGAGGACGTGGAGGTGGGGGCTGGGGAACT
GCTCGCTTTGCGGTGGTGGTCGAGGGAAAACCACTGCCGGACATCATGTGGTACAAGGAC
GAGGTGCTGCTGACCGAGAGCAGCCATGTGAGCTTCGTGTACGAGGAGAATGAGTGCTCC
CTGGTGGTGCTCAGCACGGGGGCCAGGATGGAGGCGTCTACACCTGCACCGCCCAGAAC
CTGGCGGGTGAGGTCTCCTGCAAAGCAGAGTTGGCTGTGCATTTCAGCTCAGACAGCTATG
GAGGTCGAGGGGGTTCGGGGAGGATGAGGACCATCGAGGAAGGAGACTCAGCGACTTTTAT
GACATCCACCAGGAGATCGGCAGGGGTGCTTTCTCCTACTTGCGGCGCATAGTGGAGCGT
AGCTCCGGCCTGGAGTTTGCGGCCAAGTTCATCCCCAGCCAGGCCAAGCCAAAGGCATCA
GCGCGTCGGGAGGCCCGGCTGCTGGCCAGGCTCCAGCACGACTGTGTCTCTACTTCCAT
GAGGCCTTCGAGAGGCGCCGGGGACTGGTCATTGTACCGAGCTCTGCACAGAGGAGCTG
CTGGAGCGAATCGCCAGGAAACCCACCGTGTGTGAGTCTGAGATCCGGGCCTATATGCGG
CAGGTGCTAGAGGGAATACACTACCTGCACCAGAGCCACGTGCTGCACCTCGATGTCAAG
CCTGAGAACCTGCTGGTGTGGGATGGTGTGCTGCGGGCGAGCAGCAGGTGCGGATCTGTGAC
TTTGGGAATGCCCAGGAGCTGACTCCAGGAGAGCCCCAGTACTGCCAGTATGGCACACCT
GAGTTTGTAGCACCCGAGATTGTCAATCAGAGCCCCGTGTCTGGAGTCACTGACATCTGG
CCTGTGGGTGTTGTTGCCTTCCTCTGTCTGACAGGAATCTCCCCGTTTGTGGGGAAAAT
GACCGGACAACATTGATGAACATCCGAAACTACAACGTGGCCTTCGAGGAGACCACATTC
CTGAGCCTGAGCAGGGAGGCCCGGGGCTTCCTCATCAAAGTGTTGGTGCAGGACCGGCTG
AGACCTACCGCAGAAGAGACCCTAGAACATCCTTGGTTCAAACTCAGGCAAAGGGCGCA
GAGGTGAGCACGGATCACCTGAAGCTATTCTCTCCCCGCGAGGTGGCAGCGCTCCCAG
ATCAGCTACAAATGCCACCTGGTGCTGCGCCCCATCCCCGAGCTGCTGCGGGCCCCCCCCA
GAGCGGGTGTGGGTGACCATGCCCAGAAGGCCACCCCCAGTGGGGGGCTCTCATCCTCC
TCGATTCTGAAGAGGAAGAGCTGGAAGAGCTGCCCTCAGTGCCCCGCCCCACTGCAGCCC
GAGTTCTCTGGCTCCCCGGGTGTCCCTCACAGACATTCCTACTGAGGATGAGGCCCTGGGG
ACCCAGAGACTGGGGCTGCCACCCCCATGGACTGGCAGGAGCAGGGAAGGGCTCCCTCT
CAGGACCAGGAGGCTCCCAGCCCAGAGGCCCTCCCCCTCCCCAGGCCAGGAGCCCCGAGCT
GGGGCTAGCCCCAGGCGGGGAGAGCTCCGCAGGGGCAGCTCGGCTGAGAGCGCCCTGCCC
CGGGCCGGGCGCGGGAGCTGGGCCGGGGCCTGCACAAGGCGGCGTCTGTGGAGCTGCCG
CAGCGCCGGAGCCCCGGCCGGGAGCCACCCGCCTGGCCCCGGGGAGGCTGGGTGAGGGC
GAGTATGCCCAGAGGCTGCAGGCCCTGCGCCAGCGGCTGCTGCGGGGAGGCCCCGAGGAT
GGCAAGGTGAGCGGCCTCAGGGGTCCCCTGCTGGAGAGCCTGGGGGGCGGTGCTCGGGAC
CCCCGGATGGCACGAGCTGCCTCCAGCGAGGCAGCGCCCCACCACCAGCCCCCACTCGAG
AACCGGGGCTGCAAAAGAGCAGCAGCTTCTCCAGGGTGAGGCGGAGCCCCGGGGCCGG
CACCGCCGAGCGGGGGCGCCCCCTGAGATCCCCGTGGCCAGGCTTGGGGCCCCGTAGGCTA
CAGGAGTCTCCTTCCCTGTCTGCCCTCAGCGAGGCCAGCCATCCAGCCCTGCACGGCCC
AGCGCCCCCAAACCCAGTACCCCTAAGTCTGCAGAACCTTCTGCCACCACACCTAGTGAT
GCTCCGCAGCCCCCGCACCCAGCCTGCCAAGACAAGGCTCCAGAGCCCAGGCCAGAA
CCAGTCCGAGCCTCCAAGCCTGCACCACCCCCCAGGCCCTGCAAACCTAGCGCTGCC
CTCACACCCTATGCTCAGATCATTCAGTCCCTCCAGCTGTCAGGCCACGCCCAGGGCCCC
TCGCAGGGCCCTGCCGCGCCGCTTCAGAGCCCAAGCCCCACGCTGCTGTCTTTGCCAGG
GTGGCCTCCCCACCTCCGGGAGCCCCCGAGAAGCGCGTGCCTCAGCCGGGGGTCCCCCG
GTGCTAGCCGAGAAAGCCCGAGTTCCACAGGTGCCCCCCAGGCCAGGCAGCAGTCTCAGT
AGCAGCATCGAAACTTGAGTTCGGAGGCCGTGTTTCGAGGCCAAGTTCAAGCGCAGCCGC
GAGTCGCCCCGTGCTGGGGCTGCGGCTGCTGAGCCGTTTCGCGCTCGGAGGAGCGCGGC
CCCTTCCGTGGGGCCGAGGAGGAGGATGGCATATACCGGCCAGCCGGCGGGGACCCCCG
CTGGAGCTGGTGCGACGGCCTGAGCGCTCACGCTCGGTGCAGGACCTCAGGGCTGTGCGA
GAGCCTGGCCTCGTCCGCCGCTCTCGCTGTCACTGTCCCAGCGGCTGCGGCGGACCCCT
CCCCGCGAGCGCCACCCGGCCTGGGAGGCCCGCGGCGGGGACGGAGAGAGCTCGGAGGGC
GGGAGCTCGGCGCGGGGCTCCCCGGTGCTGGCGATGCGCAGGCGGCTGAGCTTCACCCTG

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FIGURE 2HH

GAGCGGCTGTCCAGCCGATTGCAGCGCAGTGGCAGCAGCGAGGACTCGGGGGGCGCGTCC
GGCCGCAGCACGCCGCTGTTTCGGACGGCTTCGCAGGGCCACGTCCGAGGGCGAGAGTCTG
CGGCGCCTTGGCCTTCCGCACAACCAGTTGGCCGCCAGGCCGGCGCCACCACGCCTTCC
GCCGAGTCCCTGGGCTCCGAGGCCAGCGCCACGTCTGGGCTCCTCAGCCCCAGGGGAAAGC
CGAAGCCGGCTCCGCTGGGGCTTCTCTCGGCCGCGGAAGGACAAGGGGTTATCGCCACCA
AACCTCTCTGCCAGCGTCCAGGAGGAGTTGGGTACCCAGTACGTGCGCAGTGAAGTACAGC
TTCCCCCAGTCTTCCACATCAAACCTCAAGGACCAGGTGCTGCTGGAGGGGGAGGCAGCC
ACCCTGCTCTGCCTGCCAGCGGCCTGCCCTGCACCGCACATCTCCTGGATGAAAGACAAG
AAGTCCTTGAGGTCAGAGCCCTCAGTGATCATCGTGTCTTGCAAAGATGGGCGGCAGCTG
CTCAGCATCCCCCGGGCGGGCAAGCGGCACGCCGCTCTCTATGAGTGTCTGGCCACCAAC
GTACTGGGCAGCATCACCAGCTCCTGTACCGTGGCTGTGGCCCGAGTCCAGGAAAGCTA
GCTCCTCCAGAGGTAACCCAGACCTACCAGGACACGGCGCTGGTGTGTGGAAGCCGGGA
GACAGCCGGGCACCTTGCACGTATACGCTGGAGCGGCGAGTGGATGGGGAGTCTGTGTGG
CACCCTGTGAGCTCAGGCATCCCCGACTGTTACTACAACGTGACCCACCTGCCAGTTGGC
GTGACTGTGAGGTTCCGTGTGGCCTGTGCCAACCCTGCTGGGCAGGGGGCCCTTCAGCAAC
TCTTCTGAGAAGGTCTTTGTGAGGGGTACTCAAGATTCTTCAGCTGTGCCATCTGCTGCC
CACCAAGAGGGCCCTGTACCTCAAGGCCAGCCAGGGCCCCGGCCTCCTGACTCTCCTACC
TCACTGGCCCCACCCCTAGCTCCTGCTGCCCCCACACCCCGTCAGTCACTGTACGCCCC
TCATCTCCCCCACACCTCCTAGCCAGGCCTTGTCTCGCTCAAGGCTGTGGGTCCACCA
CCCCAAACCCCTCCACGAAGACACAGGGGCCTGCAGGCTGCCCGGCCAGCGGAGCCACC
CTACCCAGTACCCACGTACCCCAAGTGAGCCCAAGCCTTTCGTCTCTTGACACTGGGACC
CCGATCCCAGCCTCCACTCCTCAAGGGGTAAACCAGTGTCTTCTCTACTCCTGTGTAT
GTGGTGACTTCCTTTGTGTCTGCACCACCAGCCCCCTGAGCCCCAGCCCCCTGAGCCCCCT
CCTGAGCCTACCAAGGTGACTGTGCAGAGCCTCAGCCCCGGCCAAGGAGGTGGTCAGCTCC
CCTGGGAGCAGTCCCCGAAGCTCTCCAGGCCTGAGGGTACCACTCTTCGACAGGGTCCC
CCTCAGAAACCCCTACACCTTCTTGAGGAGAAAGCCAGGGGGCCGCTTTGGTGTGTGCGA
GCGTGCCGGGAGAATGCCACGGGGCGAAGCTTCGTGGCCAAGATCGTGCCCTATGCTGCC
GAGGGCAAGCCGCGGGTCTGCAGGAGTACGAGGTGCTGCGGACCCTGCACCACGAGCGG
ATCATGTCCCTGCACGAGGCCTACATCACCCCTCGGTACCTCGTGCTCATTGCTGAGAGC
TGTGGCAACCGGGAACCTCTGTGGGCTCAGTGACAGGTTCCGGTATTCTGAGGATGAC
GTGGCCACTTACATGGTGCAGCTGCTACAAGGCCTGGACTACCTCCACGGCCACCACGTG
CTCCACCTAGACATCAAGCCAGACAACCTGCTGCTGGCCCCCTGACAATGCCCTCAAGATT
GTGGACTTTGGCAGTGCCAGCCCTACAACCCCCAGGCCCTTAGGCCCTTGGCCACCGC
ACGGGCACGCTGGAGTTCATGGCTCCGAGATGGTGAAGGGAGAACCCATCGGCTCTGCC
ACGGACATCTGGGGAGCGGGTGTGCTCACTTACATTATGCTCAGTGGACGCTCCCCGTTT
TATGAGCCAGACCCCCAGGAAACGGAGGCTCGGATTGTGGGGGGCCGCTTTGATGCCTTC
CAGCTGTACCCCAATACATCCCAGAGCGCCACCCTCTTCTTGCGAAAGGTTCTCTCTGTA
CATCCCTGGAGCCGGCCCTCCCTGCAGGACTGCCTGGCCCCACCCATGGTTGCAGGACGCC
TACCTGATGAAGCTGCGCCGCCAGACGCTCACCTTACACCACCAACCGGCTCAAGGAGTTC
CTGGGCGAGCAGCGGCGGCGCCGGGCTGAGGCTGCCACCCGCCACAAGGTGCTGCTGCGC
TCCTACCCTGGCGGCCCTTAGAGGCACGGACCACAGCCAGGCCTCGGGCTTCAACTGGGG
TTCCACCAATGCCACGGGACATTCCAGGGCCCACGCTGAGCCAGGCGGGCCTGGGGCTT
CGGTTACCACCAGCAGCAACATCTGGCTGGGCTCTTACCTCATAGACCTTCAAGGACAGA
GACCCAGGGCCTGGACCTGATGCCACCCAGGCCAAAGCCAGAGTGGGAGACCCATTGG
TCAGGCTCAGCAGGGTGGGAACAGGCAGAGGGACAAGAGGGGAATGGAGAAGTGGAGAGG
AAAAGGAATCGAGGGACAGGAAGGGGGAGGCTCTAGGAAGGTTCTGGGTTGGGGGTGAGT
GCATCTCAGGGAGAACCAAGGAAGGTGGGCATGGCTGGAGAGGAGGAAAAGGAAGGAGCC
CCAGGTGTGAGGGCAGTAGGCTGGGAGTCAAGTGTGGCAAAGCGGGGGCAGGACACAGATA
CAGTGGCAGGGGGCCAGGGCTGGGACATGAGAGAAGGCAGCGAGGCGGCAGAGGGAGAAG
AGAGGACTCAGGTGGAGGTGGGGTGGGTGAGTGTGAGCATCCCTCAGAGGAGAAATGTG

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FIGURE 2II

GAGAGCTGGAGGCCAGCAGTCACTCACACTCGCTCTGTCTCCTGTCCAGTGGATACAGC
CCTGGGCGCTCTGCTGGCCCAAGGATGTCCCCACTGCCCCCTCCATGGCCTTTGGCCTTCT
TCCCATTCATATTTATTTATTTATTGACTTTTATGAAGTTTCCCCCTCCATCCGATCCCT
ACTGCCCATGTTGTCTGACCATCCCTCCCAGCCATCCAGCTGTCTGTCTGTCTGCCACA
AGGAAATAAAAATGGCAAGCAGCAAAAAA

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GCCACGGACATCTGGGGAGCGGGTGTGCTCACCTACATCATGCTTAGTGGGTACTCCCCA
TTCTATGAGCCAGACCCCCAGGAAACAGAGGCTCGGATTGTTGGGGGTGCTTTGATGCC
TTCCAGTTGTATCCTAACACATCCCAGAGTGCCACCCTCTTCTTGAGAAAGGTCCTCTCA
GTACATCCCTGGAGCCGGCCCTCTCTGCAGGACTGCTTGGCCACCCATGGCTGCAAGAT
GCCTACCTGATGAAGCTGCGCCGCCAGACACTCACCTTCACCACCAACCGGCTCAAGGAA
TTCTTGGGCGAGCAGCGGCGACGTGCGGGCTGAGGCTGCTACCCGTCACAAGGTGCTGCTC
CGCTCCTACCCTGGCAGCCCCCTAGGTGGCACAGACCGCAGCCCCGGCCACGGGCTTCAACT
TGGGTTCTCACTCGCGCTGCCAAGGGACATTCCAGAGCCCATGCTGAGCTGGACAGGCAG
GGGCTTCAGATACCAGCAGCAGCAGCAGCAGCAGCAGCAACATCTGGCTGGGCTATT
ACCTCATGGACCTAAGAGGACAAGGCCCTGGGGCTTCAGCCGAATGTCACCCCGGCCATA
ACCAGAGCAGGAGACCCACTGGCCAGGCTGGGCAAGGGTGAGAGCAGAAAGAGGCAAGA
GGGAGTTGGGAAGTGAAGAATGAGACGGAGGATAGAGAGGGAGGAGTTTGAGGAAGGTTT
TAGGCTGGAGTGGAATGCTATATCTCAGGGAGAAGCCAGAAGGGGACATGGCTGAAGAGG
AAGAAGGACCCTGTGATGTGGGAATGTGGTGGAGAGGAGGACTGGACATAGAGAGTGTGC
CAGGAGCCAGAGCAGAGACATAAGGGAGGGCAGAAGGGTAGAAGGCAACAGGAGTGGGCT
CAGGGGTGGCAGGGCAGGCCAGCAGCTGCATCTTCAGAAAGAGAGAGGAGAAAGGCAAAG
AGACGAAAGGCCGCTCCAGCTGGTCTCCTGTCCAGCCGATGCAGTTCTGGGCGTTCTCC
ACTGGCCCAGGGATGTCTCACTGCTCCTCCATGGCCTTTGCCCTCCTTCCCATTTGTAT
TTATTTATTTATTGCCTTTTGTGGAGTTTCTTTCTATCCAGTCCCTAGTGCCTATGTTG
TCCCGACCATCCCCCTCAGTCACCCAGCTGTCTGTGCAGCTGTCTGTCTGTCTGTCTCACA
AGGAAAATAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAAAACAGC

SEQ ID NO: 44_R19772_H

ATGAAGGGCGGCGACAGGGCTTACACCCGAGGTCCCTCTTTGGGGTGGCTCTTTGCTAAG
TGCTGCTGTTGCTTCCCGTGTAGAGATGCATACTCTCATTCTCAAGCGAGAATGGAGGC
AAGTCCGAGTCCGTAGCCAACCTGCAGGCCAGCCCTCCCTGAACTTCATCCACAGTTCC
CCGGGTCCCAAGCGCTCCACCAACACTCTTAAGAAGTGGCTGACGAGTCCTGTGCGTCGG
CTCAACAGCGGGAAGGCAGATGGAAACATCAAAAAGCAGAAGAAAGTTGCGGATGGTTCGG
AAGAGCTTTGACCTGGGATCTCCCAAGCCTGGGGATGAAACAACCCCTCAGGGAGACAGC
GCTGATGAGAGCAAGAAAGGTTGGGGTGAAGATGAGCCGGATGAAGAGTCACACACACCC
CTCCCACCACCTATGAAGATTTTGTACAACGACCCTACACAGGATGAAATGTCTCTCTCT
TTGCTAGCAGCCCGGCAGGCTTCCACTGAAGTACCTACTGCTGCAGACCTTGTCAATGCA
ATAGAAAAGTTGGTCAAAAACAAGCTGAGTCTAGAAGGAAGCTCATACCGGGGGAGCTTG
AAAGACCTGCAGGCTGCCTGAATGAGGGGATGGCCCCACCCACACCTCCTAAAAATCCA
GAAGAAGAACAGAAAGCCAAGGCCCTGAGAGGCAGGATGTTTGTCTGAATGAGCTGGTA
CAGACAGAGAAAGACTATGTCAAGGATCTGGGCATTGTGGTGGAGGGCTTCATGAAGAGA
ATAGAAGAAAAGGGTGTCCCTGAGGATATGCGAGGAAAGGACAAAATCGTGTTTGGAAAT
ATTCATCAGATTTTATGACTGGCATAAGGATTTTTTCTTGGCGGAAGCTGGAAAAGTGATC
CAGGAGCAAGACAGATTGGCACAGCTCTTTATTAAGCACGAGCGGAAGCTGCACATCTAC
GTGTGGTATTGTGAGAATAAGCCGCGCTCAGAGTACATCGTTGCTGAGTATGACGCCTAC
TTTGAGGAGGTAAAACAGGAGATAAATCAGAGGCTGACACTGAGTGACTTCTCATCAAG
CCCATTTCAGAGAATAACAAAATACCAGTTGCTCCTCAAGGACTTCCTGAGATACAGTGAG
AAGGCTGGTTTGGAGTGTTTCAGATATCGAGAAAGCAGTGGAGTTAATGTGCCTTGTTC

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FIGURE 2JJ

AAACGCTGCAATGACATGATGAATCTAGGACGTCTGCAGGGCTTTGAGGGCACTCTGACT
GCTCAGGGGAAGCTACTGCAGCAGGACACATTCTATGTGATCGAGCTGGATGCAGGCATG
CAGTCCCGGACCAAAGAGAGGGCGCGTGTTCCTCTTCGAGCAGATTGTTCATCTTCAGTGAA
CTGCTCAGGAAGGGATCCCTCACCCCTGGCTACATGTTCAAAGAGGAGCATCAAGATGAAT
TACTTGGTCTTGAGAGGGAATGTGGACAATGATCCCTGCAAGTTTGCACCTCATGAACAGA
GAGACTTCTGAGAGGGTGTTCCTGCAAGCCGCCAACGCTGACATCCAGCAGGCCTGGGTG
CAGGACATCAATCAAGTCTTAGAAACACAGCGAGACTTTTTGAATGCACTGCAATCGCCC
ATTGAGTATCAACGGAAAGAAAGGAGCACAGCTGTGATGAGGTCTCAACCTGCCAGGCTT
CCCCAAGCCAGCCCCAGGCCCTACTCCTCTGTTCTGCGGGCTCAGAGAAGCCCCCAAAG
GGCTCCAGCTATAACCCACCTCTGCCTCCCCTGAAGATATCTACCTCCAATGGCAGTCCA
GGGTTTGAATACCACCAGCCTGGGGACAAGTTCGAAGCCAGCAAGAACGACCTGGGAGGC
TGCAATGGGACCTCGTCCATGGCCGTGATCAAAGATTACTATGCACTGAAGGAGAATGAA
ATCTGTGTGAGCCAAGGTGAGGTGGTCCAGGTCTCGCCGTCAACCAGCAGAACATGTGT
CTGGTGTACCAGCCTGCCAGCGACCATTCCTCCCGCCGAGGGCTGGGTCCCAGGCAGC
ATCCTGGCGCCCCCTCACCAAAGCCACAGCAGCAGAAAGTAGTGACGGGAGCATCAAGAAG
TCATGTTTCATGGCATACTCTACGCATGAGAAAGCGGGCGGAAGTGGAGAACACGGGTAAA
AATGAAGCCACAGGGCCTCGTAAACCCAAGGATATTCTGGGCAACAAAGTCTCTGTTAAA
GAGACGAACAGTTCCGAGGAATCAGAGTGTGATGATCTTGACCCTAATACTAGCATGGAG
ATCTTAAATCCAAATTTTCATCCAAGAAGTGGCCCCAGAATTCTTGTGCCCTTGGTGGAT
GTGACCTGCTTGCTTGGGGACACAGTGATACTGCAGTGCAAAGTCTGTGGGCGGCCAAAG
CCCACCATCACTTGGAAGGGTCCAGACCAGAACATCCTTGACACTGATAACAGCTCAGCC
ACATACACGGTCTCCTCTTGTGATTCTGGAGAAATCACCTGAAGATCTGTAATCTGATG
CCCCAAGACAGTGGGATTTATACCTGCATAGCAACAAATGACCACGGGACCACATCAACG
TCTGCAACAGTCAAAGTGCAAGGTGTTCCAGCAGCCCCCTAACCGCCCCATTGCCCAGGAG
AGAAGCTGCACCTCCGTGATTCTCCGCTGGCTGCCCCCTCCAGCACAGGAACTGCACT
ATTTCTGGTTACACTGTGGAGTACAGAGAGGAAGTTCTCAGATCTGGCAGCAGTCAGTG
GCTTCGACCTTGGACACTTACCTCGTCATCGAAGACCTTAGTCCCGGGTGTCTTATCAG
TTCAGAGTCAGTGCCAGTAACCCCTGGGGAATCAGCCTTCCAGCGAGCCCTCGGAGTTT
GTGCGACTTCCAGAATACGATGCTGCTGCTGATGGTGCCACCATTTCTTGAAGGAAAAT
TTTGACTCAGCTTACACTGAGCTGAATGAAATTGGAAGAGGCCGTTTCTCTATAGTAAAG
AAATGCATTACAAAGCTACCCGCAAAGATGTGGCTGTGAAATTTGTTAACAAAAAATG
AAGAAGAAAGAACAGGCTGCCCCAGAGGCTGCCCTGCTTCAGCACCTACAGCACCCCCAG
TACATCACTCTCCATGACACCTATGAGTCCCCCACATCCTACATCCTGATCTTGGAACTG
ATGGATGATGGCCGGCTCTTAGACTACCTTATGAATCATGATGAACTGATGGAGGAAAAA
GTAGCTTTCTATATCCGAGACATCATGGAGGCTCTGCAGTACCTTCACAACTGCAGGGTT
GCACATTTGGACATAAAGCCTGAAAACCTGCTCATTGACCTACGGATTCCAGTGCCTCGA
GTGAAGCTCATTGACTTGGAGGATGCTGTCCAGATCTCGGGTCACTTCCACATTCACCAC
CTGCTGGGGAACCCCTGAGTTTGCTGCCCCAGAAGTCATTCAAGGCATCCCCGTCTCCCTG
GGGACAGACATCTGGAGCATCGGGGTTCTGACATATGTCATGCTGAGTGGGGTCTCCCCC
TTCTTGGATGAGAGCAAAGAGGAGACATGTATCAACGTATGCAGGGTGGATTTAGCTTC
CCCCATGAATACTTCTGTGGTGTGAGCAATGCTGCCAGAGATTTTCATCAATGTGATCTTA
CAGGAAGATTTTTCGGAGGCGGCCACAGCAGCCACATGCTTGCAGCATCCATGGCTGCAG
CCCCATAATGGCAGCTACTCTAAGATCCCCCTGGACACCTCCCGCCTAGCATGCTTCATA
GAACGTGCAAGCACCAGAATGATGTGCGGCCTATCCCCAATGTCAAGAGCTACATTGTC
AACCGGGTGAACCAAGGGACGTAG

SEQ ID NO: 45_5R72_8_2_H

CGCCGCTGTTTGTCTCGCGCGGCCCCGTCCACTGCCCTGCGGTTGCTCTGCGGGCTGAA
AAGTTTCTCCCGGTGCAGAATTCCGGGGCTCAGCGACAGCCTGCGCCGAGTGTGCGCACCT
GTCGGAGACCCGCCAGTCCGCCGGCCCCGGCTTTGTTCTGTCGGAACTGTAGTGGTGAGA

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FIGURE 2KK

AAAACCTCCATGTCTGGGCACGCCTGGCTGATCTTCACCTCTTTCTTCTAGGACCTTCCTC
TGGGCTGTACGTGTGAATATGTGTCTAGTGCATCCTTAACCTGAGGACTTCACCAGTTC
GAAATTACAGTTTTTACCATCAACTACCTTATCCTTTTTTGGCCTGGTTTTCTTCCTCAA
CAGTGGAACATTTTTAAAGTTGCTTTTGTGTCAGAGTTAAACAAATGGCTGATAGTGGC
TTAGATAAAAAATCCACAAAATGCCCCGACTGTTTCATCTGCTTCTCAGAAAGATGTACTT
TGTGTATGTTCCAGCAAAACAAGGGTTCTCCAGTTTTTGGTGGTGGAAATGTACAGACA
TCAAGCATTGGTAGTGCAGAATCTTTAATTTCACTGGAGAGAAAAAAGAAAAAATATC
AACAGAGATATAACCTCCAGGAAAGATTTGCCCTCAAGAACCTCAAATGTAGAGAGAAAA
GCATCTCAGCAACAATGGGGTTCGGGGCAACTTTACAGAAGGAAAAGTTCCTCACATAAGG
ATTGAGAATGGAGCTGCTATTGAGGAAATCTATACCTTTGGAAGAATATTGGGAAAAGGG
AGCTTTGGAATAGTCATTGAAGCGACAGACAAGGAAACAGAAACGAAGTGGGCAATTAAA
AAAGTGAACAAAGAAAAGGCTGGAAGCTCTGCTGTGAAGTTACTTGAACGAGAGGTGAAC
ATTCTGAAAAGTGTAAACATGAACACATCATACATCTGGAACAAGTATTTGAAACGCCA
AAGAAAATGTACCTTGTGATGGAGCTTTGTGAGGATGGAGAAGTCAAAGAAATTCTGGAT
AGGAAAGGGCATTCTCAGAGAATGAGACAAGGTGGATCATTCAAAGTCTCGCATCAGCT
ATAGCATATCTTCACAATAATGATATTGTACATAGAGATCTGAAACTGGAAAATATAATG
GTTAAAGCAGTCTTATTGATGATAACAATGAAATAAACTTAAACATAAAGGTGACTGAT
TTTGGCTTAGCGGTGAAGAAGCAAAGTAGGAGTGAAGCCATGCTGCAGGCCACATGTGGG
ACTCCTATCTATATGGCCCCCTGAAGTTATCAGTGCCACGACTATAGCCAGCAGTGTGAC
ATTTGGAGCATAGGAGTCGTAATGTACATGTTATTACGTGGAGAACCACCCTTTTTGGCA
AGCTCAGAAGCGAAGCTTTTTGAGTTAATAAGAAAAGGAGAACTACATTTTGAAAATGCA
GTCTGGAATTCCATAAGTGAAGTGTGCTAAAAGTGTGTTTGAAACAACTTATGAAAGTAGAT
CCTGCTCACAGAATCACAGCTAAGGAACTACTAGATAACCAGTGGTTAACAGGCAATAAA
CTTTCTTCGGTGAGACCAACCAATGTATTAGAGATGATGAAGGAATGGAAAAATAACCCA
GAAAGTGTTGAGGAAAACACAACAGAAGAGAAGAATAAGCCGTCCACTGAAGAAAAGTTG
AAAAGTTACCAACCCTGGGGAAATGTCCTTGAGACCAATTACACTTCAGATGAAGAGGAG
GAAAAACAGTCTACTGCTTATGAAAAGCAATTTCTTGCAACCAGTAAGGACAACCTTTGAT
ATGTGCAGTTCAAGTTTCACATCTAGCAAACTCCTTCCAGCTGAAATCAAGGGAGAAATG
GAGAAAACCCCTGTGACTCCAAGCCAAGGAACAGCAACCAAGTACCCTGCTAAATCCGGC
GCCCTGTCCAGAACCACAAAAGAACTCTAAGGTTCCCTCCAGTGTGAGACAGTACAAAA
CAAAGCTGCTCTTGTAGCACTTTGATGAGGGGGTAGGAGGGGAAGAAGACAGCCCTATG
CTGAGCTTGCTAGCCTTTTAGCTCCACAGAGCCCCGCCATGTGTTTGACACAGCTTAAAT
TGAAGCTGCTTATCTCAAAGCAGCATAAGCTGCACATGGCATTAAAGGACAGCCACCAG
TAGGCTTGGCAGTGGGCTGCAGTGGAAATCAACTCAAGATGTACACGAAGGTTTTTTAGG
GGGGCAGATACCTTCAATTTAAGGCTGTGGGCACACTTGCTCATTTTTTACTTCAAATTTCT
TATGTTTtaggcacagctattttataggggaaaacaagaggccaaatatagtaatggagggtg
ccaaataattatgtgcaactttgcaactagaagactttgttagaaaattactaataaaacttg
ccatacgtattacagcagaagtgcttcagtcattcacatgtgttcgtgagatTTTtaggtt
gctatagattgtTTAAGACAGCTTATTTTAAATGTAGAAAAATAGGAGATTTTGTAACTG
CTTGCCATTAACTTGCTGCTAAATTCCCAATGTATTGATTAAATCAATAAAAAACAGATG
TTACTC

SEQ ID NO: 46_SGK309_H

GGGTCCGCAGCCCCGCCCTCACAGGCCCTCCTCACTCCCCCTAGGTAGATGGCCCCCTCAGG
GCAGGCCCCGGCGGACACCCCTCCCTCTGGCTGGCGGATGCAGTGCCTAGCGGCCGCCCTT
AAGGACGAAACCAACATGAGTGGGGGAGGGGAGCAGGCCGACATCCTGCCGGCCAACTAC
GTGGTCAAGGATCGCTGGAAGGTGCTGAAAAAGATCGGGGGCGGGGGCTTTGGTGAATC
TACGAGGCCATGGACCTGCTGACCAGGGAGAATGTGGCCCTCAAGGTGGAGTCAGCCAG
CAGCCCAAGCAGGTCTCAAGATGGAGGTGGCCGTGCTCAAGAAGTTGCAAGGTTTCGGGC
CTCGGGCAGGGGGATGGGAAGGAAGAGATGATGAAGCCAGGGGGCTAAGAGAGGGGAAGGAC

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FIGURE 2LL

CATGTGTGCAGGTTTCATTGGCTGTGGCAGGAACGAGAAGTTTAACTATGTAGTGATGCAG
CTCCAGGGCCGGAACCTGGCCGACCTGCGCCGTAGCCAGCCGCGAGGCACCTTCACGCTG
AGCACCACATTGCGGCTGGGCAAGCAGATCTTGAGTCCATCGAGGCCATCCACTCTGTG
GGCTTCCTGCACCGTGACATCAAGCCTTCAAACCTTGCCATGGGCAGGCTGCCCTCCACC
TACAGGAAGTGCTATATGCTGGACTTCGGGCTGGCCCGGCAGTACACCAACACCACGGGG
GATGTGCGGCCCCCTCGGAATGTGGCCGGGTTTCGAGGAACGGTTCGCTATGCCTCAGTC
AATGCCCACAAGAACCGGGAGATGGGCCGCCACGACGACCTGTGGTCCCTCTTCTACATG
CTGGTGGAGTTTGAGTGGGCCAGCTGCCCTGGAGGAAGATCAAGGACAAGGAACAGGTA
GGGATGATCAAGGAGAAGTATGAGCACCGGATGCTGCTGAAGCACATGCCGTCAGAGTTC
CACCTCTTCTGGACCACATTGCCAGCCTCGACTACTTCACCAAGCCCGACTACCAGTTG
ATCATGTGAGTGTTTGAGAACAGCATGAAGGAGAGGGGCATTGCCGAGAATGAGGCCTTT
GACTGGGAGAAGGCAGGCACCGATGCCCTCCTGTCCACGAGCACCTCTACCCCGCCCCCA
GCAGAACACCCGGCAGACGGCAGCCATGTTTGGGGTGGTCAATGTGACGCCAGTGCCTGG
GGACCTGCTCCGGGAGAACACCGCGGATGTGCTACAGGGAGAGCACCTGAGTGACCAGGA
GAATGCACCCCCAATTCTGCCCCGGGAGGCCCTCTGAGGGGCTGGGCCACAGTCCCCACCT
TGTCCCCACCCCGGGGGTCTGAGGCTGAAGTCTGGGAGGAGACAGATGTCAACCGGAA
CAAACCTCCGGATCAACATCGGCAAAGTAACTGCCGCCAGGGCGAAGGGCGTGGGTGGCCT
TTTCTCTACCCCCGATTCCAGCCTTGTGCCCTGCCCTGTTCTCTAAGCACCCCTGT
CCCCCGCAATCTCCCTGCTTGCCCCGGCCTCTGTTTCCGGTCCCTCTCCCGGCACTAGCC
TCGCTGTGTCTTCCATCATCATCATCTCTGTCTCCTTCACACTGAGGAGACCATCCGCC

SEQ ID NO: 47_AA234451_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCGGCGGCGGCGGCAGGAGGGG
GAGCAGGTGCTGGCACAAGAGCAGCGGCTTGGGGGAGCCGGCAGCAGCAGTAACAGCAGC
AGCAGCCGCCCGCCGCCGCCAGTAAACGCGGACCGTACCCAGGGGACTACCCAGCCG
GCCGGCCCTGGAAGCCGCGCTCGGGTCCCGCCGCGAGTCGGCGGTGGGGGATGGGCAGGCA
GTGGCGGTCCCGCCTGCCGAGGGTTAACCCCGCCGGTCCCGGTCTCTGAGCTGGACCAGA
GCCCTCCTCCAGAAACCCCTGCGTCCGCCACGGCCCAGGTAAATGGAAACACCCCTTG
GAACTGGATGCCTGTGTAGCTGTTCTACCATATCAGTGTATTGCAATGAGTGGGGGAGGA
GAGCAGCTGGATATCCTGAGTGTTGGAATCCTAGTGAAAGAAAGATGGAAAGTGTGAGA
AAGATTGGGGGTGGGGGCTTTGGAGAAATTTACGATGCCTTGGACATGCTCACCAGGGAA
AATGTTGCACTGAAGGTGGAATCAGCTCAACAACCAAAACAAGTTCTGAAAATGGAAGTT
GCTGTTTTGAAAAAGCTGCAAGGGAAAGACCATGTTTGTAGATTTATTGGCTGTGGGAGG
AATGATCGATTCAACTATGTGGTCATGCAGTTGCAGGGTCGGAATCTGGCAGATCTTCGC
CGTAGCCAGTCCCGAGGCACATTCACCATTAGTACCACTCTCCGGCTGGGTAGACAGATT
TTGGAGTCTATTGAAAGCATTCAATTCTGTGGGATCTTGNCATCGAGACATCAAACCGTCG
AACTTCGCTATGGGTCGCTTTCCTAGTACATGTAGGAAATGTTACATGCTTGATTTTGGC
TTGGCTCGACAATTTACCAATTCCTGTGGTGACGTCAGACCACCTCGAGCTGTGGCAGGT
TTTCGAGGGACAGTTCGTTATGCATCAATCAACGCACATCGGAACAGGGAAATGGGAAGA
CATGATGACCTTTGGTCCTTATTCTACATGTTGGTGGAGTTTGTGGTTGGTCAGCTGCCC
TGGAGAAAAATAAAGGACAAGGAGCAAGTAGGCTCTATTAAGGAGAGATATGACCACAGG
CTCATGTTGAAACATCTCCCTCCAGAATTCAGCATCTTTCTAGACCATATCTCTTCTTTG
GATTATTTTACAAAACCAAGACTACCAGCTTCTTACATCCGTGTTTGACAATAGCATCAAG
ACTTTTGGAGTAATTGAGAGTGACCCTTTTGAAGTGGGAGAAGACTGGAAATGATGGCTCC
CTAACAACCACCACTACTTCTACCACCCCTCAGTTGCACACTCGCTTGACCCCTGCTGCA
ATTGGAATTGCCAATGCTACTCCCATCCCTGGAGACTTGCTTCGAGAAAATACAGATGAG
GTATTTCCAGATGAACAGCTTAGCGATGGAGAAAATGGCATCCCTGTTGGTGTGTACCA
GATAAATTGCCTGGATCTCTGGGACACCCCGTCCCCAGGAGAAGGATGTTTGGGAAGAG
ATGGATGCCAACAAAAACAAGATAAAGCTTGGAATTTGTAAGGCTGCTACTGAAGAGGAG
AACAGCCATGGCCAGGCAAATGGTCTTCTCAATGCTCCAAGCCTTGGGTACCAATTCGT

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FIGURE 2MM

GTCCGCTCAGAGATTACTCAGCCAGACAGAGATATTCCACTGGTGCGAAAGTTACGTTCC
ATTCACAGCTTTGAGCTGGAAAAACGTCTGACCCTGGAGCCAAAGCCAGACACTGACAAG
TTCCTTGAGACCTGGTATAAAATAGTGTATTTTTCTTTTAAAGCTTCTAAGGTACCATT
ATTATTGTTGTCATTGTTGTTATTATTATTGTATATTTCTGTACATAAAGTCTTTCAA
TAAGAAATCCTTGCATTTTTGTAACACTGAGTCTATTTCAGCTCCAATTTTCATCCATGTT
TTTAATTATTATTATCCTGATTCTTAATTATTATAAATTCTATAGCATATCCTTTGGCTT
TGGAAGCTGAGCAGTAAGAGCTGATGACTTCCTAACACTAGGTACAAGTTAAATGAACAT
TTTTACAGTAACTTTGTTTAGAAAGTAATCTCTTCCACACAACAGTGTAGTGCTGGAGAG
GGCATGATAAAGATGGCATTAGGCAGAGATGAGGGGAATACATAAAGGAGGGGAAAAAGT
AATTCATACACAAGGGACGGTGAGTTCAATTCACTTTAGTGAAGACCCTCTAGGAGTAAG
ATACTGTGGGAAAACAGATACCAATAAGTATATCATGCTTGCCCTAGAGAGTTTGCAATC
TACCTAGAGAGAAAGGAAGGTGAACTTGAGAGATCTATATACATAGGTAAAGATTGTAG
TGCATGTTTTTGAGGCACATTATCCCTACAACAAATTTTGATAACAGAAGAC

SEQ ID NO: 48_AA435956_H

ACTTTTACTATATTCTTTGAGATGACTGTTTTTGATTAGAGGCGAAATCAGCACGTGGT
GGCTCAAATCTCCTTATGGATAGTGTCTTCTCCTTCCAGCTTTTCATGTTTCAACTTTTG
CGGGGCCTGGCGTACATCCACCACCAACACGTTCTTCACAGGGACCTGAAACCTCAGAAC
TTACTCATCAGTCACCTGGGAGAGCTCAAACCTGGCTGATTTTGGTCTTGCCCGGGCCAAG
TCCATTCCCAGCCAGACATACTCTTCAGAAGTCGTGACCCTCTGGTACCGGCCCCCTGAT
GCTTTGCTGGGAGCCACTGAATATTCCTCTGAGCTGGACATATGGGGTGCAGGCTGCATC
TTTATTGAAATGTTCCAGGGTCAACCTTTGTTTCTGTTTCCACATCCTTGAACAG
CTGGAGAAAATCTGGGAGGTGCTGGGAGTCCCTACAGAGGATACTTGGCCGGGAGTCTCC
AAGCTACCTAACTACAATCCAGAATGGTTCCCACTGCCTACGCCTCGAAGCCTTCATGTT
GTCTGGAACAGGCTGGGCAGGGTTCTGAAGCTGAAGACCTGGCCTCCAGATGCTAAAA
GGCTTTCCCAGAGACCGCGTCTCCGCCAGGAAGCACTTGTTTCATGATTATTTTCAGCGCC
CTGCCATCTCAGCTGTACCAGCTTCCTGATGAGGAGTCTTTGTTTACAGTTTCAGGAGTG
AGGCTAAAGCCAGAAATGTGTGACCTTTTGGCCTCCTACCAGAAAGGTCAACCCAGCC
CAGTTTAGCAAATGCTGGTGAAAAGAAAGGGCGAGATCACCAAGGTTCTTCCAGGGCTGT
ATTTCTGCAGTTTCGGTTTTTCATTTGCTTCAGCTTACTAAGAAGCTTCAAATCTAACTCC
ATACTGAACAAGGGGCTTTATGTCTCACCTATGACCTGGAATAGTTTAAATATGGTGT
CAAGGCAATAGTACATAATAGTGGAAGAAAATTCAGTGGAAGGTTATTGCTATTGTGCTATT
TGCATAGAATTTAAGTGATTGATTTAAAAAACTGGACATAAACTAAGTCTAAGAAG

SEQ ID NO: 49_AA626859_H

AAATGGAGTTGCTGATGGAGTGATCAAAGCGTATTATGGCAAACACTTCAAGCTCTTAA
TTTCTGTACATACATAACTGTATTACAGAGATATAAAACCTGAAAATATTCTAATAAC
TAAGCAAGGAATAATCAAGATTTGTGACTTCGGGTTTGACAAATTCTGATTCCAGGAGA
TGCTTACACCGATTATGTAGCTACGAGATGGTACCGAGCTCCTGAACCTTCTTGTGGGAGA
TACTCAGTATGGTTCTTCAGTCGATATATGGGCTATTGGTTGTGTTTTTGAGAGCTCCT
GACAGGCCAGCCACTGTGGCCTGGAAAATCAGATGTGGACCAACTTTATCTGATAATCAG
AACACTAGGAAAATTAATCCCAAGACATCAATCAATCTTTAAAAGTAACGGGTTTTTCCA
TGGCATCAGTATACCTGAGCCAGAAGACATGGAACTCTTGAGGAAAAGTTCTCAGATGT
TCATCCTGTGGCTCTGAACCTTCATGAAGGGGTGTCTGAAGATGAATCCAGATGACAGATT
AACCTGTTCCCAACTCCTGGAGAGCTCCTACTTTGATTCTTTTCAAGAGGCCCAAATTAA
AAGAAAAGCACGTAATGAAGGAAGAAACAGAAGACGCCAACAGAATCAACTGTTGCCTCT
CATACCAGGAAGCCACATCTCCCCACACCTGATGGAAGAAAACAAGTCTCCAGTTAAA
ATTTGATCACCTTCCAAACATTTAGGAAAATGTTCTTTCAAGTGCAAAGTAATTTAATAT
GTACACATTTTGTACAAGTGAGATAGGAATTCTCAGTGTTTCAAATGCAAATGAGCCATA

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FIGURE 2NN

TGAAAATTAAGATGCCTTCTAGAATTGGTTTGCTCTGATCATTGCTGATTCCCTTTCCCCA
TGCTTTTACAT

SEQ ID NO: 50_AA061797_M

GAAAATAGCCCTGCGGAAATCCGTATGCTGAAGTTGAAACACCCAAACCTCGTGAACCT
CATCGAGGTGTTTCAGAAGAAAGAGAAAGATGCATCTAGTTTTTGAGTACTGTGATCACAC
ACTGTTAAACGAGCTGGAGAGAAACCCAAACGGAGTTTCTGATGGAGTGATTAAAAGTGT
GCTATGGCAAACCTTCAAGCCCTTAACCTTCTGTCAACAAGCACAATTGTATTCATCGGGA
TGTA AACCTGAAAACATCCTAATAACCAAGCAAGGGATGATAAAGATTTGTGACTTTGG
ATTTGCACGAATTCTAATTCCAGGAGACGCTACACAGACTATGTTGCCACCAGGTGGTA
CCGAGCCCCCGAACTTCTCGTGGGAGACACGAAGTACGGTTCCTCTGTAGACGTGTGGGC
CGTCGGCTGTGTTTTTGCAGAGCTCCTGACGGGTGAGCCACTCTGGCCGGGAAAATCCGA
CGTGGACCAGCTTTACCTGATCATCAGGACGTTGGGGGAAGCTGATTCCAAGACACCAGTC
TATCTTTAGGAGTAACCAGTTTTTCCGCGGCATCAGCATACCTGAACCAGAGGACATGGA
GACTCTTGAAGAAAAATTCTCAAATGTTTACGCTGTGGCTTTAAGTTTTCATGAAGGGATG
CCTGAAGATGAATCCTGATGAGAGGCTGACCTGTGCCCAGCTGCTGGACAGTGCCTACTT
TGAGTCTTTTCAAGAGGATCAAATGAAAAGAAAAGCCCCGAGTGAGGGGAGAAGCCGAAG
GCGCCAGCAGAATCAACTGCTGCCTCTTATTCCTGGAAGCCACATCTCCCCACACCTGA
TGGAAGGAAACAAGTCGTCCAGTTAAAGTTCGATCATCTTCAAACATTTAGGGGACTCA
TCCTTCCCAGCACATCCTTTTAATATTGTCTACATAGGAATAAGACGGGAATCCTCAGCA
TCTCAAATACAGTGAGCGACGTGAACACCAGGGCACCTCTAATCACCACGGGCTCCTCCC
CTGTGCTTTTTTCCACGCCAGCTCCATCTCCTAAAACATTCTCTTTAAATGTTGCAGTATC
AAAATGGCACATCCGAAAGAGATGCTTCCAGTTTCACCAGAGCCGGGCTTCTCAGGCAA
TCGGTACTGTGCATCTGTGGACTTATGCTCCGACCTAGGGAAAGATTTCCACGTAGCCGT
CTCACTTCAGCCGACCAGTGGTGTCTGAAGCAGACCCAGATCTGCTGGCTGCTGTTTGT
GGAGGGGATGGCCCTGAGCCCTCTCACTGGAGTTTCTTCTCCGTGCAGCCAGGTCTTACT
TTAGACTACATTTGTGTTATTGTGGCATGGCAATCGTGAAAGGTGGTCTAGGTTTACCCT
TGACTCCACAGCAGATGCTAGTCTCCTTCTCGTGAGGAGCTGACAAGTCTGCTTCTAAAA
CGAACTAGAGAAAATTCCAAACGTGACCAGTTAGTGGACAGACTACAAGGAATCGACCAC
CATACCACAGTAACGCCCTTGGATCCCTGGCTGCCACCCACTCTAAGGCTATCCTGGTT
CACCATGGTTTCTCTTTCTTTTCTTTTCTTTTAAATCTATTTGTACATATGAGAAAGAGGC
AGAGGGGCGAGAGAAACCTCGTGTGTGAAAATCAAAAGACAAGCAGGAGGCCAGCCTAAG
CTACATAGCAAGGCCTTTTCTCTACACCCATTCTCTAAGGTTGCTTAAACCCAAGTCCCT
GCTGCTGATTGTATAAACTATGAATAAGTTCTACATATGTAGGACATATTGTTGTCATTG
TTGAAATATCTAAGGATCTTGGTAGAAGCAGAAGTGTCTAAATATTCTCCACACTGGTG
AGTATCTTGGCATTTCATTTCTGACCTCATCACAGATGAACACATCAAAGGATGAGTATG
TATCACTTTGCATCTTAGAATTCTACCTGTTTTAGCTGCGTTAAACCTTGTGAAAGGGCG
GGGCCATAACTGAACCTGTGGAGTTCTTGCCTGTGTGCAGGAAACCTCTGGTTTTGTCT
CCAGCATGGAAGAAAACAGCTATAGTCACACCTACCTGAAAGTAGAAATTCAAAGTCACT
GTCCTTGACTACATATGCAGTCCAAGGCCACGCTGGGCTACACTTCTCCAGGCATGAAGG
TCCGTGTTTGTATCAAGGGGCAGGAAAGGAGAGTCCAAGGTCAAGGCCAGCCGAGGCTGC
ATAGTGAGTTGAGGCTCTTCAGCAAAAGAAAAGCAAACCTAATAGGAGTCGTTGAAGGTAG
CCACCGGCCATTTCTCTAAATATCATTCTGCTGAAAAGGGGGCTTAGTTTTAGTTTAGAAT
GCATTAATGTATGTAGAAGCTGGGCTATTTTCAATTATTTGAAATTGTAGCTATTGTTAA
TTAGCACTTAATAACTAAGTATGTTAGTCTAAACTATTAGAGTTTACTACAAAG
AGGTTTTGATTGAATTATATTAACATATAATATGGATTTTAAAAATTTAAGATGTTTAA
GAAAGCTATATAAAGATTAAACATTTTTTGTGGCTGTATATTTGTGTATATACCTTGTTG
TTCTTTAAATTATTTTAATAAAAGCCAGAAACATT

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FIGURE 200

SEQ ID NO: 51_AA397553_H

ATGCCCAATTTCAGAGAGACATGGGGGCAAGAAGGACGGGAGTGGAGGAGCTTCTGGA
TTGCAGCCGTCATCGGGAGGCGGCAGCTCTAACAGCAGAGAGCGTCACCGCTTGGTATCG
AAGCACAAGCGGCATAAGTCCAAACACTCCAAAGACATGGGGTTGGTGACCCCGAAGCA
GCATCCCTTGGGCACAGTTATCAAACCTTTGGTGGAGTATGATGATATCAGCTCTGATTCC
GACACCTTCTCCGATGACATGGCCTTCAAACCTAGACCGAAGGGAGAACGACGAACGTCGT
GGATCAGATCGGAGCGACCGCCTGCACAAACATCGTCACCACCAGCACAGGCGTTCCCGG
GACTTACTAAAAGCTAAACAGACCGAAAAAGAAAAAGCCAAGAAGTCTCCAGCAAGTCG
GGATCGATGAAGGACCGGATATCGGGAAGTTCAAAGCGTTCGAATGAGGAGACTGATGAC
TATGGGAAGGCGCAGGTAGCCAAAAGCAGCAGCAAGGAATCCAGGTCTCCAAGCTCCAC
AAGGAGAAGACCAGGAAAGAACGGGAGCTGAAGTCTGGGCACAAAGACCGGAGTAAAAGT
CATCGAAAAAGGGAAACACCCAAAAGTTACAAAACAGTGGACAGCCCAAACGGAGATCC
AGGAGCCCCCACAGGAAGTGGTCTGACAGCTCCAAACAAGATGATAGCCCCTCGGGAGCT
TCTTATGGCCAAGATTATGACCTTAGTCCCTCACGATCTCATACCTCGAGCAATTATGAC
TCCTACAAGAAAAGTCTTGGAAGTACCTCGAGAAGGCAGTCGGTCAGTCCCCCTTACAAG
GAGCCTTCGGCCTACCAGTCCAGCACCCCGGTACCGAGCCCCTACAGTAGGCGACAGAGA
TCTGTCAAGTCCCTATAGCAGGAGACGGTCTGTCAGCTACGAAAGAAGTGGCTCTTACAGC
GGGCGATCGCCAGTCCCTATGGTGAAGGCGGTCCAGCAGCCCTTTCTTGAGCAAGCGG
TCTCTGAGTCGGAGTCCACTCCCCAGTAGGAAATCCATGAAGTCCAGAAGTAGAAGTCT
GCATATTCAAGACATTCTCTCTCATAGTAAAAAGAAGAGATCCAGTTCACGCAGTCGT
CATTCCAGTATCTCACCTGTCAGGCTTCCACTTAATTCCAGTCTGGGAGCTGAACTCAGT
AGGAAAAAGAAGGAAAGAGCAGCTGCTGCTGCTGCAGCAAAGATGGATGGAAAGGAGTCC
AAGGGTTCACCTGTATTTTGCCTAGAAAAGAGAACAGTTCAGTAGAGGCTAAGGATTCA
GGTTTGGAGTCTAAAAAGTTACCCAGAAGTGTAATAATTGAAAAATCTGCCCCAGATACT
GAACTGGTGAATGTAACACATCTAAACACAGAGGTAAAAAATTCTTCAGATACAGGGAAA
GTAAGTTGGATGAGAACTCCGAGAAGCATCTTGTTAAAGATTTGAAAGCACAGGGAACA
AGAGACTCTAAACCCATAGCACTGAAAGAGGAGATTGTTACTCCAAAGGAGACAGAAACA
TCAGAAAAGGAGACCCCTCCACCTCTTCCCACAATTGCTTCTCCCCACCCCTCTACCA
ACTACTACCCCTCCACCTCAGACACCCCTTTGCCACCTTTGCCTCCAATACCAGCTCTT
CCACAGCAACCACCTCTGCCTCCTTCTCAGCCAGCATTAGTCAGGTTCTGCTTCCAGT
ACTTCAACTTTGCCCCCTTCTACTCACTCAAAGACATCTGCTGTGCTCTCAGGCAAT
TCTCAGCCCCCTGTACAGGTTTCTGTGAAGACTCAAGTATCTGTAACAGCTGCTATTCCA
CACCTGAAAACCTTCAACGTTGCCTCCTTTGCCCTCCCACCTTATTACCTGGAGGTGAT
GACATGGATAGTCCAAAAGAACTCTTCCTTCAAACCTGTGAAGAAAGAGAAGGAACAG
AGGACACGTCACTTACTCACAGACCTTCTCCTCCCTCCAGAGCTCCCTGGTGGAGATCTG
TCTCCCCCAGACTCTCCAGAACCAAGGCAATCACACCACCTCAGCAACCATATAAAAAG
AGACCAAAAATTTGTTGTCCTCGTTATGGAGAAAGAAGACAAACAGAAAGCGACTGGGGG
AAACGCTGTGTGGACAAGTTTGACATTATTGGGATTATTGGAGAAGGAACCTATGGCCAA
GTATATAAAGCCAGGGACAAAGACACAGGAGAACTAGTGGCTCTGAAGAAGGTGAGACTA
GACAATGAGAAAGAGGGCTTCCCAATCACAGCCATTCTGTAATCAAATCCTTCGTCTAG
TTAATCCACCGAAGTGTTGTTAACATGAAGGAAATTGTACAGATAAACAAGATGCACTG
GATTTCAAGAAGGACAAAGGTGCCTTTTACCTTGTATTTGAGTATATGGACCATGACTTA
ATGGGACTGCTAGAATCTGGTTTGGTGCACCTTTTCTGAGGACCATATCAAGTCGTTCTAG
AAACAGCTAATGGAAGGATTGGAATACTGTCAAAAAAGAATTTCTGCATCGGGATATT
AAGTGTTCTAACATTTTGTCTGAATAACAGTGGGCAAATCAAACCTAGCAGATTTTGGACTT
GCTCGGCTCTATACTCTGAAGAGAGTCGCCCTTACACAAACAAAGTCATTACTTTGTGG
TACCGACCTCCAGAACTACTGCTAGGAGAGGAACGTTACACACCAGCCATAGATGTTTGG
AGCTGTGGATGTATTCTTGGGGAACATTTACAAAGAAGCCTATTTTTCAAGCCAATCTG
GAACTGGCTCAGCTAGAAGTATGATCAGCCGACTTTGTGGTAGCCCTTGTCCAGCTGTGTGG
CCTGATGTTATCAAACCTGCCCTACTTCAACACCATGAAACCGAAGAAGCAATATCGAAGG

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FIGURE 2PP

CGTCTACGAGAAGAATTCTCTTTTCATTCTCTTCTGCAGCACTTGATTTATTGGACCACATG
CTGACACTAGATCCTAGTAAGCGGTGCACAGCTGAACAGACCCTACAGAGCGACTTCCTT
AAAGATGTGGAAGTAAAGAAACGGCGACGTCAGCGACAAAGTGGTGTGTAGTCGAAGAGCCA
CCTCCATCCAAAACCTCTCGAAAAGAACTACCTCAGGGACAAGTACTGAGCCTGTGAAG
AACAGCAGCCCAGCACACCCTCAGCCTGCTCCTGGCAAGGTGGAGTCTGGGGCTGGGGAT
GCAATAGGCCTTGCTGACATCACACAACAGCTGAATCAAAGTGAATTGGCAGTGTATTATTA
AACCTGCTGCAGAGCCAAACCGACCTGAGCATCCCTCAAATGGCACAGCTGCTTAACATC
CACTCCAACCCAGAGATGCAGCAGCAGCTGGAAGCCCTGAACCAATCCATCAGTGCCCTG
ACGGAAGCTACTTCCCAGCAGCAGGACTCAGAGACCATGGCCCCAGAGGAGTCTTTGAAG
GAAGCACCTCTGCCCCAGTGATCCTGCCTTCAGCAGAACAGATGACCCCTTGAAGCTTCA
AGCACACCAGCTGACATGCAGAATATATTGGCAGTTCTCTTGAGTCAGCTGATGAAAACC
CAAGAGCCAGCAGGCAGTCTGGAGGAAAACAACAGTGACAAGAACAGTGGGCCACAGGGG
CCCCGAAGAACTCCCACAATGCCACAGGAGGAGGCAGCAGCATGTCTCTCTCACATTCTT
CCACCAGAGAAGAGGGCCCCCTGAGCCCCCCCCGACCTCCACCGCCGCCACCTCCACCCCCCT
CTGGTTGAAGGCGATCTTTCCAGCGCCCCCAGGAGTTGAACCCAGCCGTGACAGCCGCC
TTGCTGCAACTTTTATCCCAGCCTGAAGCAGAGCCTCCTGGCCACCTGCCACATGAGCAC
CAGGCCTTGAGACCAATGGAGTACTCCACCCGACCCCGTCCAAACAGGACTTATGGAAAC
ACTGATGGGCCTGAAACAGGGTTTCAGTGCCATTGACACTGATGAACGAAACTCTGGTCCA
GCCTTGACAGAATCCTTGGTCCAGACCCTGGTGAAGAACAGGACCTTCTCAGGCTCTCTG
AGCCACCTTGGGGAGTCCAGCAGTTACCAGGGCACAGGGTCAGTGCAAGTTTCCAGGGGAC
CAGGACCTCCGTTTTTGCCAGGGTCCCCTTAGCGTTACACCCGGTGGTTCGGGCAACCATTC
CTGAAGGCTGAGGGAAGCAGCAATTCTGTGGTACATGCAGAGACCAAATTGCAAACTAT
GGGGAGCTGGGGCCAGGAACCACTGGGGCCAGCAGCTCAGGAGCAGGCCTTCACTGGGGG
GGCCCAACTCAGTCTTCTGCTTATGGAAAACCTCTATCGGGGGCCTACAAGAGTCCCACCA
AGAGGGGGAAGAGGGAGAGGAGTTCTTACTAA

SEQ ID NO: 52_AA789239_H

TGAAAATGGAGATGTATGAAACCCTTGGAAGAGTGGGAGAGGGAAGTTACGGAACAGTCA
TGAAATGTAAACATAAGAATACTGGGCAGATAGTGGCCATTAAGATATTTTATGAGAGAC
CAGAACAATCTGTCAACAAAATTGCGATGAGAGAAATAAAGTTTCTAAAGCAATTTTCATC
ACGAAAACCTGGTCAATCTGATTGAAGTTTTTAGACAGAAAAAGAAAATTCATTTGGTAT
TTGAATTTATTGACCACACAGTATTAGATGAGTTACAACATTATTGTTCATGGACTAGAGA
GTAAGCGACTTAGAAAATACCTCTTCCAGATCCTTCGAGCAATTGACTATCTTCACAGTA
ATAATGTAATCATTCATCGAGATATAAAACCTGAGAATATTTTAGTATCCAGTCAGGAA
TTACTAAGCTCTGTGATTTTGGTTTTGCACGAACACTAGCAGCTCCTGGGGACATTTATA
CGGACTATGTGGCCACACGCTGGTATAGAGCTCCCGAATTAGTATTAAAGATACTTCTT
ATGGAAAGTATGTGCCTGTGGATATCTGGGCTTTGGGCTGTATGATCATTGAGATGGCCA
CTGGAAATCCCTATCTTCTTAGTAGTTCTGATTTGGATTTACTCCATAAAATTGTTTTGA
AAGTGNGATTGATGCCAGAACTGAAAGCTAAATTACTGCAGGAAGCAAAAGTCAATTCAT
TAATAAGCCAAAAGAGAGTTCTAAAGAAAATGAACTCAGGAAAGATGAAAGAAAAACAG
TTTATACCAATACACTGCTAAGTAGTTTCAGTTTGGGAAAGGAAATAGAAAAAGAGAAAA
AGCCCAAGGAGATCAAAGTCAGAGTTATTAAGTCAAAGGAGGAAGAGGAGATATCTCAG
AACCAGAAAAGAGAGATGAAGGTGGACTTGGTCAACAGGATGCAAATGAAAATGTTC
ATCCTATGTCTCCAGATACAAAACCTTGTAACCATTTGAACCAACCAACCTATCAATCCCA
GCACTAACTGTAATGGCTTGAAAGAAAATCCACATTGCGGAGGTTCTGTGACAATGCCAC
CCATCAATCTAACTAACAGTAATTTGATGGCTGCAAATCTCAGTTCAAATCTCTTTTACC
CCAGTGTGAGGTTAACTGAAAGAGCAAAAAAGAGACGCACTTCTTCACAATCTATTGGAC
AAGTTATGCCTAATAGCAGGCAAGAGGATCCAGGTCTTATTCAAAGCCAAATGGAGAAGG
GTATATTTAATGAGCGAACAGGTCACAGTGACCAAATGGCAAATGAGAACAAAAGGAAGC

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FIGURE 2QQ

TGAATTTTCCAGATCTGACAGGAAAGAATTCCATTTTCCAGAATTGCCTGTCACAATAC
AGTCAAAAGATACAAAAGGAATGGAAGTTAAACAGATAAAAATGCTGAAGAGGGAGTCAA
AGAAAACAGAGTCATCTAAGATACCAACTTTACTTAACGTGGATCAAAATCAAGAAAAAC
AAGAGTTTATTCCCTTATCTCTGCTGTCTGCCTGCTGTCCTATTTTACAAATATTTGCT
CTCAGCTAACTATCAGGGTGGAGATGGCCATTGCGAGGGGAAGAATTTGAAGAGAAACAG
GTTTTTTTTCTGGTAGTGTCTTTTCTTTTACATAGTCCAAAAAATACAAGATGACAACCTC
TTCCCGTTTTATTTATCTACAATAGAAGTGTGATGTGAGTTGTTGTTAAGACAGCCATCC
ATGTGCATGAGCATCATCCAGCTTTTTTTGTTAGCAAAACATTTACTGTTTTCTTTTCCC
TTTTAAGACTCTGTTGATGTGATAATTTGATTTGGAATTATAAAGTCATCTCTTCTCTGC
CTTGAA

SEQ ID NO: 53_AA124976_M

CTGGCAGATATAGTTTCATGCTTGTTTACAAATTGATCCTGCTGAGAGGACATCATCTACT
GATCTTTTGCCTCACGATTACTTTACTAGAGATGGATTTATTGAGAAATTCATACCAGAG
CTGAGAGCTAAATTATTACAGGAAGCAAAGGTTAATTCATTTATAAAGCCAAAAGAGAAT
TTTAAAGAAAATGAACCTGTGAGAGATGAGAAGAAATCAGTTTTTACCAACACCCTGCTC
TATGGAAATCCATCACTTTATGGCAAGGAAGTGGACAGAGACAAAAGGGCCAAGGAGCTC
AAAGTCAGAGTCATTAAGGCCAAAGGGGGCAAAGGAGATGTCCCAGACCAGAAGAAGCCA
GAGTATGAAGGCGACCACCGCCAGCAGGGCACAGCTGATGACACACAGCCCTCATCACTG
GACAAGAAGCCTTCTGTCTTGGAACTGACAAACCCTCTCAATCCCAGTGAGAATTCTGAC
GGTGTCAAAGAAGACCCACACGCTGGGGGTGTATGATAATGCCACCTATCAACCTGACA
AGCAGTAATTTGTTGGCCGCAAATCTCAGTTCAAACCTTTCCCACCCCAATTCACGGTTA
ACTGAAAGAACAAAAAGAGACGCACTTCTTACAAACTATTGGACAGACTTTGTCTAAT
AGCAGACAAGAGGACACAGGTCCCACACAAGTCAAACAGAGAAAGGTGCATTTAATGAG
CGAACAGGTCAGAATGACCAATATCGAGTGGGAACAAAAGAAAGCTGAATTTTCCCAA
TGCGACAGGAAAGAATTCCATTTCCCTGAACTGCCATTACAGTGCAGGCGAAGGAGATG
AAAGGGATGGAAGTTAAACAGATAAAAGTGCTGAAGAGAGAATCAAAGAAAACAGATTCA
TCTAAATACCAACTTTACTTAGTATGGACCCAAATCAAGAAAAACAAGAGGGTGGAGAT
GGCGATTGTGAGGGGAAGAATTTGAAGAGGAACAGATTTTTTTTTTTCCCGATAGTGCTTT
GTCTTTTAAGTAATCTTAAAAATACAAGCTTGACAATTCCTTCCTTTTTTATTTATATAC
ACTAGAATGTACATAGGTTGCTGCTAAGATAGCCACCCATCCCATCTGCATCAACATCAT
CTATTTTTTTGGTTTTTGCTAGCAAAATTTTACAAATTTTCTCTATCTTCCAAAACTGT
TATTTTGATGCTGTGATTTGAAATTATAAAGTCACCTCCTCTGTCTGCTTCCTTCCTTGC
CATGATTACTGAGTGGGTAGTCACATGATGTGCCCTGCTCGCACTGCTCTCAGACTGCTG
AGACTCAAACCTCATAAGCCAGGGGTCTCCTGGGAAGCACTGGCCTCTTCAAGTGGATGC
TCGATGAACCTTCTTATCTGTTGTCTTAGTAACCACTCGTTGCCATCACATGATGAAAGA
CATTCTATTGTCCCCAGTGAAGCATTATAGTACTTACATAACATGTTACAGTGATATGA
TGTTCCCTAGGTTAAACTCCTTGAGATGAAACTATTTCCCTGCATTCTCTGACTCCCCTAGT
CTAATAGTTCCCTCCATTTAGCCAGAAGAATTTCCCTGAAGAAGCGATGCACAACCTGGGA
AAGGTTTACTTTCTATCCTGGGCTGTTTTCTGTTGCTAAATAATATAGACTGGGTAGTTA
GTTAACAT

SEQ ID NO: 54_AA575635_M CCRK_M

AGCGCCTCAGGCCAGCTCAAGATAGCTGACTTTGGCCTGGCCCGGGTCTTCTCTCCGGAT
GGTGGTCGCCTCTACACACATCAGGTGGCCACCAGGTGGTACCGAGCTCCTGAACTCCTG
TATGGCGCTCGGCAGTATGACCAGGGCGTTGACCTATGGGCTGTGGGCTGCATCATGGGA
GAGCTGTTGAATGGGTCCCCCTGTTCCCGGGCGAAAACGACATTGAACAACCTGTGCTGT
GTGCTTCGCATCCTGGGTACCCCGAGTCCCTCGAGTCTGGCCGGAGATCACAGAGCTGCCT
GACTACAACAAGATCTCCTTCGAGGAGCAGGCACCAGTGGCCCTGGAGGAGGTGCTGCCT
GATGCCTCTCCCCAGGCCTTGGACCTGCTGGGCCAGTTCCTCCTCTACCCTCCACGACAG

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FIGURE 2RR

CGTATTGCAGCCTCCCAGGCCCTTCTGCATCAGTACTTCTTCACAGCGCCTCTGCCTGCC
CATCCATCCGAGCTGCCAATTCCTCAGCGCCAGGGGGACCTGCACCCAAGGCTCACCCA
GGGCCCCCCCCATGTCCACGACTTCCATGTGGATCGACCTATTGAGGAGTCACTGTTGAAC
CCAGAAGTGAATTCGGCCCTTCATCCCAGAGGGGTGAGATGCTGGTCCAGGCCTTCCTGCT
CGCCCTAGGAGCACCTCTTTCTGATTTGCCTCCATGGCCTCCCCACGGCTATATATACCA
CACCTGGTCTCTGCTCCTGAGTGTGCTTGAGGGCTGGGCTCTGGGAGGCAGAACCGTGAGA
TGTTTCATCCCAGCAGAGAAAGAGACTCACGTCTACAGACAAAGCCTCCAGAACTGCTA
GCTGTGTCTTCTCCAGGGCCACCCCTCAGTGGTGCCACCCGGCCTTAGAGATGATTGTC
AGGCTCTGTCCCCTCTTCAAGGACATTGGTACTACAGCACCACCTGGTGGAAGCACAGAG
TATAAGCTGTCTTCATACTGGGGACACAGCTGGGAAGTCAGACATGTTTTAGTTTTGGTT
CCACTGGGTGAGGATTTGAGGTTTCATATAAAAGCCCTGGGTGTTTTCTGTCTAATTGCACC
TTGTCTGTTGCTGTTAGGGAAAGGACAATGGTGGGCCTTGATTACAGGGGTGAGGTACT
CAGAAGGGGCCTCCTGTGAAGGCCATTTGGGTCTCAGGCTTCCCATGCTATTACGGGA
CTTGAGTGCTCATTTGGGAGCGAGGGTCCAGAAGCTGAGGCCAGGGATGGACAGTCCAG
TTCCCGAAGCCCACTTCCACATGTGGGTGGGTGAGTCAGTCAGTGAGCCTGAGGCTGCCTTG
CAGATGCGGAAGCAGGCATTCTTGAATCCACTCAGTAAATAAATTCCAGTGTGACTCAG

SEQ ID NO: 55_AA631990_H

GAACAACAATAACAGAATAAGGAAGAAAATCTCATGATTACCTCAATAAGTACAGAGAAA
TCTGGTCACACTCACTATCCATTCATGATTACAACTCTTCAATACTATCGCGGCCGAGGA
GGGAAGACGGCAGTTTGGCGACATTTCTCGGCCGAAGGGCCATTTGCTTTTGCGGAGATG
CGGCATTCCAAAAGAACTCACTGTCCTGATTGGGATAGCAGAGAAAGCTGGGGACATGAA
AGCTATCGTGGAAGTCACAAGCGGAAGAGGAGATCTCATAGTAGCACACAAGAGAACAGG
CATTGTAAACCACATCACCAGTTTAAAGAATCTGATTGTCATTATTTAGAAGCAAGGTCC
TTGAATGAGCGAGATTATCGGGACCGGAGATACGTTGACGAATACAGGAATGACTACTGT
GAAGGATATGTTCTTAGACATTATCACAGAGACATTGAAAAGCGGGTATCGAATCCACTGC
AGTAAATCTTCAGTCCGCAGCAGGAGAAGCAGTCCTAAAAGGAAGCGCAATAGACACTGT
TCAAGTCATCAGTCACGTTTCGNATGAAATCGTGACACTTTGGGTGAAGGAGCCTTTGGC
AAAGTTGTAGAGTGCATTGATCATGGCATGGATGGCATGCATGTAGCAGTGAAAATCGTA
AAAAATGTAGGCCGTTACCGTGAAGCAGCTCGTTCAGAAATCCAAGTATTAGAGCACTTA
AATAGTACTGATCCCAATAGTGTCTTCCGATGTGTCCAGATGCTAGAATGGTTTGATCAT
CATGGTCATGTTTGTATTGTGTTTGAACACTGAGGACTTAGTACTTACGATTTTATTAA
GAAAACAGCTTTCTGCCATTTCAAATTGACCACATCAGGCAGATGGCGTATCAGATCTGC
CAGTCAATAAATTTTTTACATCATAATAAATTAACCCATACAGATCTGAAGCCTGAAAAT
ATTTTGTGTTGTGAAGTCTGACTATGTAGTCAAATATAATTCTAAAATGAAACGTGATGAA
CGCACACTGAAAAACACAGATATCAAAGTTGTTGACTTTGGAAGTGCAACGTATGATGAT
GAACATCACAGTACTTTGGTGTCTACCCGGCACTACAGAGCTCCCGAGGTCATTTTGGCT
TTAGGTTGGTCTCAGCCTTGTGATGTTTGGAGCATAGGTTGCATTCTTATTGAATATTAC
CTTGGTTTCACAGTCTTTTCAGACTCATGATAGTAAAGAGCACCTGGCAATGATGGAACGA
ATATTAGGACCCATACCACAACACATGATTCAGAAAACAAGAAAACGCAAGTATTTTCAC
CATAACCAGCTAGATTGGGATGAACACAGTTCTGCTGGTAGATATGTTAGGAGACGCTGC
AAACCGTTGAAGGAATTTATGCTTTGTGATGATGAAGAACATGAGAACTGTTTGACCTG
GTTCTGAAGAATGTTAGAATATGATCCAACCTCAAAGAATTACCTTGGATGAAGCATTGCAG
CATCCTTTCTTTGACTTATTAAAAAAGAAATGAAATGGGAATCAGTGGTCTTACTATATA
CTTCTCTAGAAGAGATTACTTAAGACTGTGTCAGTCAACTAAACATTCTAATATTTTTGT
AAACATTAAATTATTTTGTACAGTTAAGTGTAATATTGTATGTTTTGTATCAATAGCAT
AATTAACCTTGTTAAGCAAGTATGGTCTTGATAATGCATTAGAAAAATTAAATTAATTTT
TCTTTTGAATTAACATTTTAAATACCTTTGAAATATCCTTTGTGTCCAGTGATAAAT
GTGATTGATCTTGCCTTTTGTACATGGAGGTCACCTCTGAAGTGATTTTTTTTGTAGTAAA
AGGAAATCTTGACTACTTTATATTCTTAAAGGAATATTCTTTATATACTTCAAATTTAGA

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FIGURE 2SS

ACTTAACTTTAAAAGTTTTTCTTCTGTAATTGTTGAACGGGTGATTATTATTAAGTCTAG
ATAAGCAGGTACTAGAAACCAAACTCAGAAAATGTTTACTGTTAGAATTCTATTAAATT
TTAAGTGTGTATTCTTTTTTCATTGGGTGATGTCAGGGTGATAACCAGACATTCATGGAA
AGGCATGCAGTTTGTCCATTGTGACAGTTTGTTTAATAAAACCACATACACACTTTATTT
AAGATTAAAATCTAACTGGAAAGTCAGCTTGGAAAATGGACATTTCCAAGTATGTTTGGT
GAGTCACAGATATAAAAATAGAAATTCTGATGAGAGGTTTCAGTTTTTAATACCAAGTCC
TTAGGAGTCTTAACATTGGCCAGCATCTGTTTATCAAATGACATAAATACGTAAACCTAT
AAGAATTAAGTTTATTAATTAGGCAATTTATGTCTGTGATAATTCTTACGGGAGAAAGAG
GATTTGATTGGAAAGCAGTTTGGGAAGAAAGTGCTGCTGAAATTTCCAGAATTTAATTGA
TTGGTTACATAAACTTTTTGACTTCAAT

SEQ ID NO: 56_AA557536_H

AGTAAGGCCCCGCGGGCGTCTGGCCGCCATGTGCACCGTAGTGGACCCCTCGCATTGTCC
GGAGATACCTACTCAGGCGGCAGCTCGGGCAGGGGAGAACATTCCGGGAAATCACGCTCC
TCCAGGTGAGTGGCCTGGGCCCTCCAGTCCAATCCCCTTGCCCAGGTACAGATCTCTCCA
GACAGGAGAGAACTGGCCTTCTTGGGCCCCAGAGCACAGCCCCTCCTGGCCTTCCAGCC
GCCTCCGACTCTCTCCCCAGGAGTTTGGGGACCATCCCAACATCATCAGCCTCCTTGACG
TGATCCGGGCAGAGAACGACAGGGACATTTACCTGGTGTGTTGAGTTTATGGACACTGACC
TGAACGCAGTCATCCGGAAGGGCGGCCTGCTGCAGGACGTCCACGTGCGCTCCATCTTCT
ACCAGCTCCTGCGGGCCACCCGGTTCCTCCACTCGGGGCACGTTGTGCACCGGGACCAGA
AGCCGTCCAATGTGCTCCTGGATGCCAACTGCACAGTGAAGCTGTGTGACTTTGGCCTGG
CCCGCTCCCTGGGCGACCTCCCTGAGGGGGCCTGAGGACCAGGCCGTGACAGAGTACGTGG
CCACACGCTGGTACCGAGCACCGGAGGTGCTGCTCTCTCGCACCGCTACACCGCTTCT
GCCCCAGATACACCCTTGGGGTGGACATGTGGAGTCTGGGCTGTATCCTGGGGGAGATGC
TGCGGGGGAGACCCCTGTTCCCCGGCACGTCCACCCTCCACCAGCTGGAGCTGATCCTGG
AGACCATCCCACCGCCATCTGAGGAGXXXAGGCCACGACAGACGCTGGATGCCCTCCTAC
CGCCAGACACCTCCCCAGAGGCCTTGGACCTCCTTAGGCGACTCCTGGTGTTCGCCCCGG
ACAAGCGGTTAAGCGCGACCCAGGCACTGCAGCACCCCTACGTGCAGAGGTTCCTACTGCC
CCAGCGACGAGTGGGCACGAGAGGCAGATGTGCGGCCCCGGGCACACGAAGGGGTCCAGC
TCTCTGTGCTGAGTACCGCAGCCGCTCTATCAGATGATCCTGGAGTGTGGAGGCAGCA
GCGGCACCTCGAGAGAGAAGGGCCCCGAGGGTGTCTCCCCAAGCCAGGCACACCTGCACA
AACCAGAGCCGACCTCAGCTGCCTTCTAGGACACCTGTGCAGGGTCCCAGACCCAGGC
CCCAGAGCAGCCAGGCCATGACCCTGCCGAGCACGAGTCCCCCGTGCAGCCAAGAACG
TTCCAGGCAGAACTCCGCTCCCCCTGCTCCAACTGCTCTCCTAGGGAATGGGGAAAGGC
CCCCCTGGGGCGAAGGAAGCGCCCCCTTGACACTCTCGCTGGTGAAGCCAAGCGGGAGGG
GAGCTGCGCCCTCCCTGACCTCCAGGCTGCGGCTCAGGTGGCCAACCAGGCCCTGATCC
GGGGTGAAGTGAACCGGGGCGGTGGGGTGAAGGTGGCCAGCGTACAACAGGTCCCTCCCC
GGCTTCTCCGGAGGCCCGGCCCGGCGGAGGATGTTTACGACCTCTGCCTTGACGGGTG
CCCAGGGGGGTGCCAGGGCTTTGCTTGGAGGCTACTCCCAAGCCTACGGGACTGTCTGCC
ACTCGGCACTGGGCCACCTGCCCTGCTGGAGGGGCACCATGTGTGAGCCGCCCTACTCC
CTTACCTGGCCCTCTGTTCCCTGCCCCAGCNCCTTCCCCAGACCCCTCTCCAGTCTCCTG
CACCCCTTAGCCCTCCCTGCTTTGCCTGGCCCGTTGAAGTTCCAGGGAGCTTGCCCCGGGT
CTCCTCGGGGGAGCAGATGAGGGCCCTGCCC

SEQ ID NO: 57_N28606_H, MOK_H

ATGAAGAACTATAAAGCAATTGGCAAAATAGGAGAGGGAACGTTTTCTGAAGTTATGAAG
ATGCAAGCCTGAGAGATGGAACTACTATGCATGTAAACAAATGAAGCAGCGCTTTGAAG
AGTATTGAGCAAGTCAACAACCTACGAGAGATCCAAGCACTGAGGCGCCTGAATCCGCAC
CCAAACATTCTTATGTTGCATGAAGTGGTTTTTGACAGAAAATCTGGTTCTCTTGCACTA
ATATGTGAAGTTATGGACATGAATATTTATGAGCTAATACGAGGGAGAAGATAACCCATTA

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FIGURE 2TT

TCAGAAAAAAAAATTATGCACTATATGTACCAGTTATGTAAGTCCCTGGATCATATTAC
AGAAATGGAATATTTACAGAGATGTAAAACCAGAAAATATACTAATAAAGCAGGATGTC
CTGAAATTAGGGGACTTTGGCTCCTGCCGGAGTGTCTATTCCAAGCAGCCGTACACGGAA
TACATCTCCACCCGCTGGTACCGGGCCCCGGAGTGTCTCCTCACTGATGGGTCTACACG
TACAAGATGGACCTGTGGAGCGCCGGCTGTGTGTTCTACGAGATCGCCAGTCTGCAGCCC
CTCTTTCTGGAGTAAATGAACTGGACCAAATCTCAAAAATCCACGATGTATCGGCACA
CCCGCTCAGAAGATCCTCACCAAGTTCAAACAGTCGAGAGCTATGAATTTTGATTTTCT
TTTAAAAGGGATCAGGAATACCTCTACTAACAACCAATTTGTCCCCACAATGCCTCTCC
CTCCTGCACGCAATGGTGGCCTATGATCCCGATGAGAGAATCGCCGCCACCAGGCCCTG
CAGCACCCCTACTTCCAAGAACAGAGGAAAACAGAGAAGCGGGCTCTGGGCAGCCACAGA
AAAGCTGGCTTTCCGGAGCACCCCTGTGGCACCGGAACCACTCAGTAACAGCTGCCAGATT
TCCAAGGAGGGCAGAAAGCAGAAACAGTCCCTAAAGCAAGAGGAGGACCGTCCCAAGAGA
CGAGGACCGGCCTATGTATGGAAGTCCCAAACCTAAAGCTTTCCGGAGTGGTCAGACTG
TCGTCTTACTCCAGCCCCACGCTGCAGTCCGTGCTTGGATCTGGAACAAATGGAAGAGTG
CCGGTGCTGAGACCCTTGAAGTGCATCCCTGCGAGCAAGAAGACAGATCCGCAGAAGGAC
CTTAAGCCTGCCCCGCAGCAGTGTGCGCTGCCACCATAGTGCGGAAAGGCGGAAGATAA

SEQ ID NO: 58_AB023153_H, ICK_H

ATGAATAGATACACAACAATCAGGCAGCTCGGGGATGGAACCTACGGTTCCGTCCTGCTG
GGAAGAAGCATTGAGTCTGGGGAGCTGATCGCTATTAAAAAATGAAAAGAAAATTTTAT
TCCTGGGAGGAATGCATGAACCAACGGGAGGTTAAGTCTTTAAAGAAGCTCAACCATGCC
AATGTAGTCAAATTAAGAAGTTATCAGGGAAAATGATCATCTTTATTTTATCTTCGAG
TACATGAAGGAAAATCTTTACCAGCTCATTAAAGAGAGAAAATAAGTTGTTTCTGAGTCT
GCTATAAGGAATATCATGTATCAGATATTACAAGGACTCGCATTTATTCACAAACTCGGC
TTCTTTCATCGAGACTTAAAGCCTGAGAACCTCCTCTGCATGGGACCAGAACTTGTGAAA
ATTGCAGACTTTGGTTTGGCCCCGAGAAATACGATCAAAACCTCCATATACAGATTATGTA
TCTACCAGATGGTACAGGGCTCCAGAAGTACTCCTGAGGTCTACCAACTACAGCTCCCC
ATTGACGTCTGGGCGGTGGGCTGCATCATGGCAGAAGTTACACCCTCAGGCCACTCTTC
CCTGGAGCCAGTGAAATTGACACAATATTCAAAATTTGCCAAGTCTGGGGACACCAAAA
AAGACTGACTGGCCTGAAGGCTATCAACTTTCAAGTGCATGAACCTCCGTTGGCCACAG
TGTGTACCCAATAACTTAAAGACCTTGATTCCCAATGCTAGCAGTGAAGCAGTCCAGCTC
CTGAGAGACATGCTTCAGTGGGATCCCAAGAACGACCAACAGCTAGTCAGGCACTTCGA
TATCCTTACTTCCAAGTTGGACACCCACTAGGCAGCACCAACACAAAACCTTCAGGATTCA
GAAAAACCACAGAAAGGCATCCTGGAAAGGGCAGGCCACCTCCTTATATTAAGCCAGTC
CCACCTGCCCAGCCACCAGCCAAGCCACACACAGCAATTTCTTCACGACAGCATCAAGCC
AGCCAGCCCCCTCTGCATCTCACGTACCCCTACAAAGCAGAGGTCTCCAGGACAGATCAC
CCAAGCCATCTCCAGGAGGACAAGCCAAGCCCCGTTGCTTTTCCCATCCCTCCACAACAAG
CATCCACAGTCGAAAATCACAGCTGGCCTGGAGCACAAAAATGGTGAGATAAAGCCAAAG
AGTAGGAGAAGGTGGGGTCTTATTTCCAGGTCAACAAAGGATTGAGATGATTGGGCTGAC
TTGGATGACTTGGATTTAGTCCATCCCTCAGCAGGATTGACCTGAAAAACAAGAAAAGA
CAGAGTGATGACACTCTCTGCAGGTTTGAGAGTGTGTTTGGACCTGAAGCCCTCTGAGCCT
GTGGGCACAGGAAACAGTGCCCCCACCAGACGTCATATCAGCGGCGAGACACGCCACC
CTGAGATCTGCAGCCAAGCAGCACTATTTGAAGCACTCTCGATACTGCCTGGGATCAGT
ATAAGAAATGGCATACTCTCGAATCCAGGCAAGGAATTTATTCACCTAATCCATGGTCT
AGTTCTGGCTTGTCTGGAAAATCTTCAGGGACAATGTCAGTAATCAGCAAAGTAAATTCA
GTTGGTTCCAGCTCTACAAGTTCTAGTGGACTGACTGGAACTATGTCCCTTCTTTCTG
AAAAAGAAATCGGTTCTGCTATGCAGAGGGTACACCTAGCACCTATTCCAGACCCTTCC
CCTGGTTATTCTCCCTGAAGGCCATGAGACCTCATCCTGGGCGACCATTCTTGGACACC
CAGCCTAGAAGCACTCCTGGGTTGATACCACGGCCTCCAGCCGCCAGCCAGTGCATGGC
CGGACAGACTGGGCTTCCAAGTACCCATCCCGGCGGTGA

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FIGURE 2UU

SEQ ID NO: 59_AA839940_M

AGCAGCAACAATGGTGGCATGAGTGCAGAGGAGGAGATAGGGCCTGGGGCTGAGCCTATG
AGAGGACCAAGCTTGGCTACAAGGGACTGGAGAGATGAGACTGTTGGGACCACAGACCTG
CAGCAAGGCATAGACCCAGGAGCAGTGAGCCCTGAGCCTGGGAAGGACCACGCAGCCCAG
GGCCCAGGAAGAACTGAAGCTGGAAGGGTATCTTCTGCTGCAGAGGCTGCCATTGTGGTT
CTAGATGACAGCGCAGCACCCCCAGCCCCCTTTGAACACCGGGTAGTGAGCATCAAAGAT
ACCCTGATCTCAGCAGGCTACACGGTATCCCAACATGAAGTCTTAGGAGGGGGTCGGTTT
GGCCAGGTGCACAGGTGTACAGAGAGGTCTACAGGCCTTGCACTGGCAGCCAAGATCATC
AAAGTGAAGAACGTAAAGGACCGGGAGGATGTGAAGAATGAGGTCAACATCATGAACCAG
CTCAGCCACGTAACTTGATCCAACCTTTATGATGCGTTTGAGAGCAAGAACAGCTTCACT
CTGATCATGGAGTATGTGGATGGAGGCGAACTCTTTGACCGGATCACGGATGAGAAGTAC
CACCTCACTGAGTTGGATGTGGTCTTGTTCACGAGGCAGATCTGTGAGGGTGTGCATTAC
CTGCATCAGCACTATATCCTGCACCTGGACCTCAAGCCTGAGAACATATTGTGTGTACAGC
CAGACAGGGCATCAAATTAAGATCATTGACTTTGGGCTGGCTAGAAGATAACAAGCCTCGG
GAGAAGCTAAAGGTGAACCTTTGGTACTCCGGAGTTCTTGCCCCAGAAGTTGTAACTAT
GAGTTTGTGTCACTTCCAACAGACATGTGGAGTGTGGGAGTTATCACCTACATGCTACTC
AGTGGTTTGTCCCCATTTCTAGGGGAGACAGATGCAGAGACCATGAATTTTATTGTGAAC
TGCAGCTGGGATTTTCGATGCTGATACCTTCAAAGGGCTGTGCGAGGAAGCCAAGGACTTT
GTTTCCCGGTTACTGGTCAAAGAGAAGAGCTGTAGGATGAGCGCCACACAGTGCCTGAAA
CACGAGTGGTTAAATCACCTGCCTGCCAAAGCCTCGGGCTCCAACGTTGCGCTCAGATCC
CAACAACCTGCTGCAGAAATATATGGCTCAGAGTAAATGGAAGAAACATTTCCACGTGGTG
GCTGCAGTCAACAGGCTACGGAAATTTCCAACGTGTCCCTAATCTTCAACTCTGGTGTTC
CACTGGGCCTGGGAATTCTTGAGGCAACACGAAGTGGTAATATGAAGAGATTACTCAAGA
TTTTATGTAGATTGGCGCTTTGCTATTATTGATTTTTCTTATTTTGCAAAGAATGATGGA
AGGAAGCAAGAAAGAAAGAAAAGAAGAAAAGGGGGAAGAAAAGGAAAAGGCAGAAAGCAA
GGAAACAGGCTACGTTGTTGCTCTTCTTGTAGGTGAAAGTGTTTTTATTAAGCCCTAG
GAATGTTTTTCTGCCTCGTAAGGTGAGCAGGTCTCATATGCTGCTTGCTACCCCGCACCC
TTCCTTTTGGTAATAAGAGCAGGCACGCTCAGGATGGGCAGGGAAATCCTACTTGGCTTT
TGGTCAAATTTGAATTCTAACTTGTGATGATTAAAGAAGCCAGTAGGGAGGGAGGTATG
GAAGAGGGAGGAATTAGGTCCAACAGTGGGGGATGAATTTGACCGAAACATTGTATAAAA
TTCTTAAAGAATTAATAAAATATATTTTTTAAAGGAG

SEQ ID NO: 60_AA460132_H

GGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAACCACTTACAGGCCGGAAG
TGTCCGGGGTGGACGCATTTCGGGTAGCCGAAGAAGTCCCAGGATTGCCGAAGAAGTCCCA
GGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAGACAGCTGATCGGTTGGAG
CTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACGCCGCGCCGATGGCGAGGAG
CCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCCCGGGAGCGGAGCAGCCGCTTCTTGAGC
GGCCTGGAGCTGGTGAAGCAGGGTGCAGAGGCGCGCGTGTTCGCTGGCCGCTTCCAGGGC
CGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGGCACCCGGCGCTGGAGGCG
CGGCTTGGCAGACGGCGGACGCTGCAGGAGGCCCCGGGCGCTCCTCCGCTGTCGCCGCGCT
GGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCCAACCTGCTTATATATGGAA
GAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGTCCACTATGGAGACTGAAAAA
ACTCCCCAGGCTCTCTCAACTTAGCCAAGACAATTGGGCAGGTTTTTGCTCGAATGCAC
GATGAAGACCTCATTGATGGTGATCTCACCACCTCCAACATGCTCCTGAAACCCCCCTG
GATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCCTCAGTACCCATCCCAACACT
GAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCCTCCAAGGAGGAGGCCA
GTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAGAGGTCCATGGTTGGGTAG
AAGAATGTGTATGACAACCACACAGTGAAGCTTTTTTTCAAAGTAAATTTGAAGAAA

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FIGURE 2VV

TGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGATATTTTTAAGTGGTATGTG
ATCGTGTCAATTATCATCTGCACTTCACTCAAGAGCTTACTATGTGTCTAAGTCATGTTCT
AGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTTCTCCCAGATTGTGACATGTA
TATCTCAGATACATGGGTGTGGCATTGAACCACATAATGAGAACATTATTCTCTTTTATG
TCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTCGCTGAGCTTACTGGCCCTCT
AACCCAGTGTTTTTTTTTTGTGTTGTTGTGTGTACATGTTATATTTATTTTGAACAGTTT
AATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATACAGCATGG

SEQ ID NO: 61_SGK034_H

CAGAGAGAGAAGGTAAACCAAGGGAACATGCCAGGGCTTCAGAGCACCTTCCTAGCCATG
GACACGGAGGAGGGGGTAGAGGTGGTGTGGAACGAGCTCCACTTCGGAGACAGGAAGGCC
TTCGCGGCGCACGAGGAGAAGATCCAGACCGTGTTCGAGCAGCTGGTGTGGTGGACCAC
CCGAACATCGTGAAGTTGCACAAGTACTGGCTGGATACCTCTGAGGCCTGCGCGAGGGTC
ATCTTCATCACAGAGTACGTGTTCATCAGGCAGCCTCAAGCAATTCCTCAAAAAGACCAAG
AAGAACCACAAGGCCATGAACGCCCGGGCCTGGAAGCGCTGGTGCACGCAGATCCTGTCT
GCGCTCAGCTTCCTGCACGCCTGCAGCCCCCAATCATCCACGGGAACCTGACCAGCGAC
ACCATCTTCATTTCAGCACAAACGGCCTCATCAAGATCGGCTCCGTGTGGCACC GAATCTTC
TCCAATGCACTTCCAGATGATCTCCGAAGCCCCATCCGCGCTGAGCGAGAGGAACCTTCGG
AACCTGCACTTCTTCCCCCAGAGTATGGAGAGGTGGCCGATGGGACCGCTGTGGACATC
TTCTCCTTTGGGATGTGTGCGCTGGAGATGGCTGTACTGGAAATCCAGACCAATGGGGAC
ACCCGGGTTCACAGAGGAGGCCATTGCTCGCGCCAGGCACTCGCTGAGTGACCCCAACATG
CGGGAGTTTCATCCTTTGCTGCCTGGCCCCGGGACCCTGCCCCGCCGGCCCTCTGCCACAGC
CTCCTCTTCCACCGCGTGTCTTTCGAGGTGCACTCGCTGAAGCTCCTGGCAGCCCACTGC
TTCATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTGGAGGAGAAGACCAAGGCCATG
GACCTGCACGCGGTCTTGGCGGAGCTTCCCCGGCCCCGCAGGCCCCCGCTGCAGTGGCGG
TACTCGGAAGTCTCCTTCATGGAGCTGGACAAATTCCTGGAGGATGTCAGGAATGGAATC
TACCCACTGATGAACTTTGCAGCCACTCGACCCCTGGGGCTGCCCCGTGTGCTGGCCCCA
CCCCCGGAGGAGGTCCAAAAGGCCAAGACCCCGACGCCAGAGCCCTTTGACTCTGAGACC
AGAAAGGTTCATCCAGATGCAGTGAACCTGGAGAGAAGCGAGGACAAGGCGCGCTGGCAT
CTCACTCTGCTTCTGGTGTGCTGGAAGACCGGCTGCACCGGCAGCTGACCTACGACCTGCTC
CCAACGGACAGCGCCAGGACCTCGCCTCGGAGCTCGTGCACATATGGCTTCTCCACGAG
GACGACCGGATGAAGCTGGCCGCCTTCTGGAGAGCACCTTCTCAAGTACCGTGGGACC
CAGGCCTGACCCGGAGCCCCAGCCCCAGGGGACCATGCCGGGGTGTGCTGCCCGGGCAGGCC
ATGTTGGGGAGACTCCAGCACCGTGGGGCTGCCCTCCTCCATGCGCCTGGGAGCACAAAG
GCCCCGTTAGTGAAGGAACCCCCGTCTCCTGAGAGTGGGGCTGACCCTGCCTTGGGCGC
CGAGGGGTGGGGGGTGGGTGTGGGGGAGCCGTTAGGCCTCCCAGGTCTTAGGATCAGG
GTTGCCCCCAGAACCCCTTCCCATATCCTCCATTCTCCGCCCTGAGTTCTTACCCAGGCT
GCCTGGCTGGGGCCACTGCCTCCTCAGCATGCAGGAGGCTGCCCTGTAGGGAACCCACAGC
TCTGGGGCTTGGGGGTGAGGGTCAGCCCTGGACAGACCTCTGCCCAGGGAAGTCTCCAT
GGGGTCTGGGAGAGCAGCCATCCCCTGTGGCACCATAGACCCACACAAGGAGCCTGCAC
AGCAAGCCAGCGGTGACACACCTGCAGGTGTGAGGCATGGCACTGGGCACAACAGGGACC
TGGCAGGAGAAACAGACCACAGAGAGGTCTGGAGTTGAGGCTGTTGTGAGCAAGCCCT
GGTCCACACAGCTCTGCCCTAGAGCCACCTCTTTGACCCTTTACCCACCCTGAGACCAG
AACTTGCAGCCCCTCTGCAGATCTCCTCTGGCCACTGCAGCCCCTCCAATGGGCTTTTTT
TCTCATGCATTCCCTGGCCTGGAGGCGTCAGGGACCCACATCCTCCCTGCTCCTCAGAC
TCACAGCCCCCTCATGTTACCTCCCGCACCTCCTCCCTGGGGCAGCTGCTCCTGGGCCT
CTGAGGATGTCAGCTCCTGGCTCCCTGCCTCTCTCCCACTCCACTCCTGGCTCAGTCTTA
GAGATTTCTATGCCCTCATGGATTCTACCCCTGCCTTCTGGCCTCTTGATTCTTGGCTT
GCCTCTCCTCCAATTCCAACTTAGTGAAATGGCCTTAAGCATTTTAAACTGTATGTATA
CATTAGCGCATTCATGCCTTTCTAAACGCATTTCAAATGTCAACCAGGAAGGCACACCAC

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TGTATTAGTTTTATACTGCCGCTGTAAAATTTACCACAACTTAGTGACTTAACACAAAT
TTATTGCAATTCTGTAGGCTGGAAGTCTGACTATGGGTCTCACTGGACTAGAATCAAGGC
TGGCAGGCTGCCTTCCTTCCTGGAGGTTCTAGGGGAGACTCTGTCTCCTGCTCCTTCAGG
CTGCTGGCAGAATCCACATCCTTTCGGTGGCAGGGCCAAGGTCCCCACTTTCTTGCTGAC
TGTAACCTAAGGCCACTTCCAGCTTGTAGAGGCTGCCTACATTCCCTGGCTCTTGGCCCC
CTCCTCCATCTTCAGAGCTAGCAGGTTTCAGTCTGTGTACGAACCATTTCTCTGGTTCCC
TGCAGACAGGAAAGGTTGTCCCTAAGGACTCATGAGATTAGGTTGGGCCCAGCCAGATAA
TACATGATAATCTCCCTCCTCAAGGTTTTTAATATTAAACACATCTGCAGGACACATTTT
GCCATGTAACTAACATTCACTGGTTCAGGGATTAAGGAATGAACCTCTTTTGTTGGGG
AAGGGTGGCATTCTGCTGACCACAGCACTCCAACCAAAGCCAAAACCAAAGCAAGACT
TACTAACGCATATCAAATAAATTAAAGGTACAAAATCGTGAATCTCAGTTATCTTAAATA
TTCCAATACTATTTACAAAATTATTCAAATTCTCACGCCTTCCAACCTCAAATTAGCAAT
CTAAAGTAATTTCCATATCCTAGATGGAAACCCTCATGCTAAACTGTCTGATTATGCATG
GTTCTAAATGGTTTCAGTGGCAAATACATAACATTGTACTACTGATTAAACTGAACTTAA
AAGC

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CCACGCGTCCGCAACCAGAGTATGGCGAAGTCAATGATGGGACTGGCTTTGTGGACATCTT
CTCCTTCGGGATGTGTGCACTGGAGATGGCTGTACTCGAGATCCAAGCCAACGGGGATAC
CAGAGTCACAGAAGAGGCCATCGCTCGAGCCAGGCACTCACTGAGTGACCCCAACATGCG
GGAATTCATCCTCTCCTGCCTGGCCCCGGGACCCTGCCCCGCCGACCCTCAGCCCACAACCT
CCTCTTCCACCGAGTGCTCTTTGAGGTGCACTCGCTGAAGCTGCTGGCAGCTCACTGCTT
CATCCAGCACCAGTACCTCATGCCTGAGAATGTGGTAGAGGAAAAGACCAAGGCCATGGA
CCTCCATGCAGTTTTGGCTGAGATGCCGCAGCCCCATGGACCCCCAATGCAGTGGCGGTA
CTCAGAGGTCTCCTTCTTGAGCTGGACAAATTCTTAGAGGATGTCAGGAACGGGATCTA
TCCACTGATGAACTTTGCGGCTGCTCGGCCCTTGGGGCTTCCCCGTGTGTTGGCCCCACC
CCCAGAGGAAGCCCCAAAAGGCCAAAACCTCCAACGCCAGAACCCTTTGACTCGGAGACCAG
GAAGGTGGTCCAGATGCAGTGCAACCTGGAAAGAAGCGAGGACAAGGCTCGGTGGCACCT
TACTCTGCTCTTGGTGCTTGAGGACCGGCTACATCGGCAGCTGACCTATGATCTGCTCCC
AACGGACAGTGCCAGGACCTCGCTGCTGAACTAGTGCAATTATGGCTTCTTGACGAGGA
TGACAGGACAAAGCTAGCAGCCTTTCTGGAGACCACCTTTTCTCAAGTACCGAGGGACGCA
AGCGTGACCTTCCCAGTCCTGACGGCCCAGCAGAGATACAGGGGCTCAGGGTTGTCCACT
TGGCAAAGAGCCCCCACACTGCTCAAAGCTGCCTTCTGCCTGTGTTCCCTGGAACCTGAAC
ACAGGCCCTGCTAGTGAAGACACCCCCACCCCCAGCTTTCTGCAGCAGTGTGGGACCCT
GGGTGGTGTATGGAGCCCTGAGCCTGGACGAGAGTGGATACAGGTCAGTTAGGGGAACCG
CTCCATCTGGTACTAGACAACAGCCATGCCTTCAGGTGGCATAGAAACCTAGGGAAGGAG
CCTGAACTCAGGTGTACAGTGCTGGGCATCAGGCAGACCAGACCTGACCTGATTGGAGA
ACTGTAGACTAGATAGCTTGGAGTTGAACCCATGGCCAGGGAATTCCTTGGTCTCTGCTCA
GACCAGTCCTGATCCCTTGACAGCCTGCCTTGAGCCCTCTTTCTGATCTTCCACACTCTT
GAGACCAGGACCTGTGTCTCCCCAAAGCCCTTGGGAAGGATCTTTCTATTCAATCATCCC
TCTGGCCTAGGGGCTCAGGGGTGAGGCATCCTCCACATTCCCTCCCTGGGGAAGTTGTGT
GTTTGAGTTGAGGATGTGGGTTCTGGCTCCCTCTTCTCCCCAGCCCCAAGTTGTCTCTT
TCTTACTGGTTTCAAAGTCCTGATGAACGCTTCCCTCAGAGCCACCCTGGTTTCTTGG
TTCTTGAAGTGCCTCTCTCCCAACTTCAAACCAGGTCTTAAACGTTTTTTTAAATGCATAT
ATAAATGTAATGCAGTCACGGTCCTTTTTTAAACACTTTGTGTATGAAACCAGGAAAGCTC
ACTATTGTATTAGGAATAGTTCCACATTGCTGCTGTTAACAGATATCATAAACCAGTG
TTTGAGACGACACACACACACACACACACACACACAGAGAGAGAGAGAGTCTGTA
CATCAAGTGTGATCCAGGCTCTCACTAGATTAATACCCAGGCTAAGTTCCTTTCTGGAAG
CTGGGACTTACCTCCTGCTCCTTCAAGCTATTGGCAGAACTCACTTCCCTGCAATGGTAA
GGCAGAAATCCCTATTTTCTCAACAGCTGCCAACTAAGAACCCTCTCAGCTTCTAGAGG

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FIGURE 2XX

CCACCAACTTTTCTTAGTTCTTCTTTCTCCCCCTCAAGACCAGCAGCGTCAAGTTGAAT
CTTTGTCCTGGGCTAGCTGACTGGCTTGCCACTGCTGGGAAGAGTTGGGGCCTTTTGTGA
GTAGGTTGGACCCACCAGGATAACCGAGGATGATCCCCCTTCTCAGGGTCTATAGATGAAC
CACACCTGCGCAGTTCCTTCTGCTGTCATCCTGGGCTTTGGTGCTTGAGAACAGCCGTG
GGCGGTGGGTGTTGTTACTGTGGTACCTACCATGCCATCTTAACCGAAACCAAGACCTAA
AATAAAACAGATTTGTTCATGGGACATCTAATAAATTAAATGAACTCTG

SEQ ID NO: 63_NEK7_H, N34132_H

CACGAATCCGAGCCCGCTCGCCTCTCTCCAGCGAACCGACCATGTCTGGCGGGCGCCGAG
AGAAGCAGAGCAGCACTCCCGGTTCCCTGTTCCTCTCGCCGCCGGCTCCTGCCCCCAAGA
ACGGCTCCAGCTCCGATTCTCCGTGGGGGAGAACTGGGAGCCGCGGGCCGCGGACGCTG
TGACCGGCAGGACCGAGGAGTACAGGCGCCGCCACACTATGGACAAGGACAGCCGTG
GGGCGGGCGGACCACTACCACCACTGAGCACCGCTTCTTCCGCCGGAGCGTCATCTGCG
ACTCCAATGCCACTGCACTGGAGCTTCCCGGCTTCTCTTTCCCTGCCCCAGCCAGCA
TCCCCGCGGCTGTCCCGCAGAGTGCTCCACCGGAGCCCCACCGGGAAGAGACCGTGACCG
CCACCGCCACTTCCCAGGTAGCCAGCAGCCTCCAGCCGCTGCCGCCCTGGGGAACAGG
CCGTGCGGGGCCCTGCCCCCTCGACTGTCCCGAGCAGTACCAGCAAAGACCGCCAGTGT
CCCAGCCTAGCCTTGTGGGGAGCAAAGAGAGCCGCCGCCGGCGAGAAGTGGCAGCGGCG
GCGGCAGCGCCAAGGAGCCACAGGAGGAACGGAGCCAGCAGCAGGATGATATCGAAGAGC
TGGAGACCAAGGCCGTGGGAATGTCTAACGATGGCCGCTTCTCAAGTTTGACATCGAAA
TCGGCAGAGGCTCCTTTAAGACGGTCTACAAAGGTCTGGACACTGAAACCACCGTGGAAG
TCGCCTGGTGTGAACTGCAGGATCGAAAATTAACAAAGTCTGAGAGGCAGAGATTTAAAG
AAGAAGCTGAAATGTTAAAAGGTCTTCAGCATCCCAATATTGTTAGATTTTATGATTCTT
GGGAATCCACAGTAAAAGGAAAGAGTGCATTGTTTTGGTGACTGAACTTATGACGTCTG
GAACACTTAAAACGTATCTGAAAAGGTTTAAAGTGATGAAGATCAAAGTTCTAAGAAGCT
GGTGCCGTGAGATCCTTAAAGGTCTTCAGTTTCTTCATACTCGAACTCCACTTATCATTC
ACCGCGATCTTAAATGTGACAACATCTTTATCACCGGCCCTACTGGCTCAGTCAAGATTG
GAGACCTCGGTCTGGCAACCCCTGAAGCGGGCTTCTTTTGCCAAGAGTGTGATAGGTACCC
CAGAGTTCATGGCCCCCTGAGATGTATGAGGAGAAATATGATGAATCCGTTGACGTTTATG
CTTTTGGAATGTGATGCTTGAGATGGCTACATCTGAATATCCTTACTCGGAGTGCCAAA
ATGCTGCGCAGATCTACCGTTCGCGTGACCAGTGGGGTGAAGCCAGCCAGTTTTGACAAAG
TAGCAATTCCTGAAGTGAAGGAAATTATTGAAGGATGCATACGACAAAACAAAGATGAAA
GATATTCATCAAAGACCTTTTGAACCATGCCTTCTTCCAAGAGGAAACAGGAGTACGGG
TAGAATTAGCAGAAGAAGATGATGGAGAAAAAATAGCCATAAAATTATGGCTACGTATTG
AAGATATTAAGAAATTAAGGGAAAATACAAAGATAATGAAGCTATTGAGTTTTGTTTTG
ATTTAGAGAGAGATGTCCAGAGATGTTGCACAAGAAATGGTAGAGTCTGGGTATGTCT
GTGAAGGTGATCACAAGACCATGGCTAAAGCTATCAAAGACAGAGTATCATTAATTAAGA
GGAAACGAGAGCAGCGGCAGTTGGTACGGGAGGAGCAAGAAAACAAAAGCAGGAAGAGA
GCAGTCTCAAACAGCAGGTAGAACAATCCAGTGCTTCCAGACAGGAATCAAGCAGCTCC
CTTCTGCTAGCACCGGCATACCTACTGCTTCTACCACTTCAGCTTCAGTTTCTACACAAG
TAGAACCTGAAGAACCTGAGGCAGATCAACATCAACAACCTACAGTACCAGCAACCCAGTA
TATCTGTGTTATCTGATGGGACGGTTGACAGTGGTCAGGGATCCTCTGTCTTCACAGAAT
CTCGAGTGAGCAGCCAACAGACAGTTTCATATGGGTTCCTCAANNCATGAACAGGCACATT
CTACAGGCACAGTCCAGGGCATATACCTTCTACTGTCCAAGCACAGTCTCAGCCCCATG
GGGTATATCCACCCTCAAGTGTGCAGCAGGGAATACAGCAGACAGCCCCCTCCTCAACAGA
CAGTGCAGTATTCACTTTCACAGACATCAACCTCCAGTGAGGCCACTACTGCACAGCCAG
TGAGTCAGCCTCAAGCTCCACAAGTCTTGCTCAAGTATCAGCTGGAAAACAGAGTACTC
AGGGAGTCTCTCAGGTTGCTCCTGCAGAGCCAGTTGCAGTAGCACAGCCCCAAGCTACCC
AGCCGACCACTTTGGCTTCTCTGTAGACAGTGCACATTGAGATGTTGCTTCAGGTATGA
GTGATGGCAATGAGAACGTCCCATCTTCCAGTGGAAGGCATGAAGGAAGAACTACAAAAC

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FIGURE 2YY

GGCATTACCGAAAATCTGTAAGGAGTCGCTCTCGACATGAAAAAACTTCACGCCCAAAT
TAAGAATTTTGAATGTTTCAAATAAAGGAGACCGAGTAGTAGAATGTCAATTAGAGACTC
ATAATAGGAAAATGGTTACATTCAAATTTGACCTAGATGGTGACAACCCCGAGGAGATAG
CAACAATTATGGTGAACAATGACTTTATTCTAGCAATAGAGAGAGAGTTCGTTTGTGGATC
AAGTGCGAGAAAATTATTGAAAAAGCTGATGAAATGCTCAGTGAGGATGTGAGTGTGGAAC
CAGAGGGTGATCAGGGATTGGAGAGTCTACAAGGAAAGGATGACTATGGCTTTTTCAGGTT
CTCAGAAATTGGAAGGAGAGTTCAAACAACCAATTCCTGCGTCTTCCATGCCACAGCAAA
TAGGCATTCTACCACTTCTTTAACTCAAGTTGTTCAATTCTGCGGGAAGGCGGTTTATAG
TGAGTCCTGTGCCAGAAAGCCGATTACGAGAATCAAAGTTTTCCCCAGTGAAATAACAG
ATACAGTTGCTGCCTCTACAGCTCAGAGCCCTGGAATGAACTTGTCTCACTCTGCATCAT
CCCTTAGTCTACAACAGGCCTTTTCTGAACTTAGACGTGCCCAAATGACAGAAGGACCCA
ATACAGCACCTCCAACTTTAGTCATACAGGACCAACATTTCCAGTAGTACCTCCTTTCT
TAAGTAGCATTGCTGGAGTCCCAACCACAGCAGCAGCCACAGCACCAGTCCCTGCAACAA
GCAGCCCTCCTAATGACATTTCCACATCAGTAATTCAGTCTGAGGTTACAGTGCCCACTG
AAGAGGGGATTGCTGGAGTTGCCACCAGCACAGGTGTGGTAACTTCAGGTGGTCTCCCCA
TACCACCTGTGTCTGAATCACCAGTACTTTCCAGCGTAGTTTCAAGTATCACAATACCTG
CAGTTGTCTCAATATCTACTACATCCCCGTCACTTCAAGTCCCCACATCCACATCTGAGA
TCGTTGTTTCTAGTACAGCACTGTATCCTTCAGTAACAGTTTCAGCAACTTCAGCCTCTG
CAGGGGGCAGTACTGCTACCCAGGTCTTAAGCCTCCAGCTGTAGTATCTCAGCAGGCAG
CAGGCAGCACTACTGTGGGAGCCACATTAACATCAGTTTCTACCACCACTTCATTCCCAA
GCACAGCTTCACAGCTGTCCATTACAGCTTAGCAGCAGTACTTCTACTCCTACTTTAGCTG
AAACCGTGGTAGTTAGCGCACACTCACTAGATAAGACATCTCATAGCAGTACAACCTGGAT
TGGCTTTTCTCCCTCTCTGCACCATCTTCCTCTTCCTCTCCTGGAGCAGGAGTGTCTAGTT
ATATTTCTCAGCCTGGTGGGCTGCATCCTTTGGTCAATCCATCAGTGATAGCTTCTACTC
CTATTCTTCCCCAAGCAGCAGGACCTACTTCTACACCTTTATTACCCCAAGTACCTAGTA
TCCCACCTTGGTACAGCCTGTTGCCAATGTGCCTGCTGTACAGCAGACACTAATTCATA
GTCAGCCTCAACCAGCTTTGCTTCCCAACCAGCCCCATACTCATTGTCCTGAAGTAGATT
CTGATACACAACCCAAAGCTCCTGGAATTGATGACATAAAGACTCTAGAAGAAAAGCTGC
GGTCTCTGTTCAGTGAACACAGCTCATCTGGAGCTCAGCATGCCTCTGTCTCACTGGAGA
CCTCACTAGTCATAGAGAGCACTGTACACCAGGCATCCCAACTACTGCTGTTGCACCAA
GCAAACCTCCTGACTTCTACCACAAGTACTTGCTTACCACCAACCAATTTACCACTAGGAA
CAGTTGCTTTGCCAGTTACACCAGTGGTCACACCTGGGCAAGTTTCTACCCAGTCAGCA
CTACTACATCAGGAGTGAAACCTGGAACCTGCTCCCTCCAAGCCACCTCTAACTAAGGCTC
CGGTGCTGCCAGTGGGTAAGTCTCAGCAGGTACTCTACCCAGCGAGCAGCTGCCAC
CTTTTCCAGGACCTTCTCTAACCAGTCCCAGCAACCTCTAGAGGATCTTGATGCTCAAT
TGAGAAGAACACTTAGTCCAGAGATGATCACAGTGACTTCTGCGGTTGGTCTGTGTCCA
TGGCGGCTCCAACAGCAATCACAGAAGCAGGAACACAGCCTCAGAAGGGTGTCTTCTCAAG
TCAAAGAAGGCCCTGTCTAGCAACTAGTTCAAGGAGCTGGTGTCTTTTAAGATGGGACGAT
TTCAGGTTTCTGTTGCAGCAGACGGTGCCAGAAAGAGGGTAAAAATAAGTCAGAAGATG
CAAAGTCTGTTCAATTTTGAATCCAGCACCTCAGAGTCTCAGTGCTATCAAGTAGTAGTC
CAGAGAGTACCTTGGTGAAACCAGAGCCGAATGGCATAACCATCCCTGGTATCTCTTCAG
ATGTGCCAGAGAGTGCCCAAAAACCTACTGCCTCAGAGGCAAAGTCAGACACTGGGCAGC
CTACCAAGGTTGGACGTTTTTCAGGTGACAACCTACAGCAAACAAAGTGGGTGCTTTCTCTG
TATCAAAAACCTGAGGACAAGATCACTGACACAAAGAAAGAGGACCAGTGGCATCTCCTC
CTTTTATGGATTTGGAACAAGCTGTTCTTCTGCTGTGATACCAAAGAAAGAGAAGCCTG
AACTGTCAGAGCCTTCACATCTAAATGGGCCGTCTTCTGACCCGAGGCGCTTTTTTAA
GTAGGGATGTGGATGATGGTTCCGGTAGTCCACACTCGCCCCATCAGCTGAGCTCAAAGA
GCCTTCCTAGCCAGAATCTAAGTCAAAGCCTTAGTAATTCATTTAACTCCTCTTACATGA
GTAGCGACAATGAGTCAGATATCGAAGATGAAGACTTAAAGTTAGAGCTGCGACGACTAC
GAGATAAACATCTCAAAGAGATTCAAGACCTGCAGAGTCGCCAGAAGCATGAAATTGAAT

FIGURE 2ZZ

CTTTGTATACCAAACCTGGGCAAGGTGCCCCCTGCTGTTATTATTCCCCCAGCTGCTCCCC
TTTCAGGGAGAAGACGACGACCCACTAAAAGCAAAGGCAGCAAATCTAGTCGAAGCAGTT
CCTTGGGGAATAAAAGCCCCCAGCTTTCAGGTAACCTGTCTGGTCAGAGTGCAGCTTCAG
TCTTGCACCCCCAGCAGACCCTCCACCCTCCTGGCAACATCCCAGAGTCCGGGCAGAATC
AGCTGTTACAGCCCCCTTAAGCCATCTCCCTCCAGTGACAACCTCTATTTCAGCCTTCACCA
GTGATGGTGCCATTTTCAGTACCAAGCCTTTCTGCTCCAGGTCAAGGTAATAAAGCAACCA
TCATCGTCCAAAAACAATAAAATGGAGATGTTGCCATACCTGGGACAAAAGCCTGTTAAG
GCGGGTTGGGAGACTAGCTGACCAGAACACAGCCTGTGTGTTGTACACTGAAGAATCTGG
GTGAAAAGGGAAGTGGAGTGATAATGAGAATCGGTGGGCTCACTGCTCCCATTAGGTGAA
ATTACTTTTTTTTCAAGGAATTACAGTGAAAAGTTACATCTGTGTGGCCTATATGACTTGC
TCATTTGGGATTGGAAGTTAGGCTTTAATATTAGGCTGAGATTTCTGGATGAAATTCT
AAGGTGTTTTAGCAGTTTCTGAAGCTAATACATTTTCTTAGCCATTGTAGAATTTTGTTA
CTTTTAAGTATGGGAGTGGCATACTAAAATGAATAACCTTACAATTCAGTTTTTTATCCA
TAATCTACTTTCCAAATATAGCTCTGTTTATTAGTGATTGCTGAAAAAATCCCCACAGAG
GAAAGAGCTTTTAGTCATATTAGAACAAGAATTGAAAAGACTTGGGCATCTGGGTGAGAA
GAATGAAAAAATATAGGTACTGGCTTATGTGCCTTTGCCACAGTTTCACAGAAATTAGA
GATCAGTCTCTTCACAGGAAGAATGCACTTGATTGGTAAGGAGGGCAAACCTAGCTAGCAT
TATTCGAACCTAAGAAAAGCTTCCGCATTTTGCAGATGGGTAGAATTAAGACCTAATATTT
CATCTCTTACATATCTGACCTTCCCCCCAGAAGCTTGTTCTTCTGTGTGCCATCTTAGTG
CATTTACACACTCCAGCCTCAAGTTTCTAACATCTTGATGTTGTGTTCTGTCTCTTCTCC
TCTCTCTGTTCTACCCTGTTTTTTCCCTCTCACAGGCTGTGCGAAGTTTAACTGTGCATC
TGAACAGGTGACATTCAAACCTGGTGGCAGGAGGACCCGATTCTGAGTACGCCCTGCTT
GGCTCTTTGTGTGTAACACCTTTACTCCTTCCTTGTCCTTGTTGTTCTGCTGCTTGGATC
TGATGTTTCACGCAGTCCATTTTTCATTTGTCTCTTTTTTGTATATCATCTACTCAGTGGCT
TGGCTGAATTACTGTTACCCTCAGAAGTTTGGGCCCCCACATTAATTATGATAAAAAATG
TCAAAATAACAAGTTATCTACAAATTTCAATGTAACCTTCTGGTAGAAGTGCTTCTTCAT
GGATCTGTGACAGAGAGTGGATATGGTATCTAGGCAATAGATTGCTGGGTCAATTTAGAAT
AATGAAGACTGAACTCCACAGTCGTAGTCAGTGCTGTCTGTCTGCCCTAGCATTAGAAAT
GAGAGAAATCAGCCAGACACGGTGGCGTACACCTGTAATCCCAGCACTTTGGGAGGCCGA
GGCGGGAAGATTGCTTGAGGCCAGGAGCTCGAGACCAACCCTGGGCAACATGGTGATACC
CCATCTCT

SEQ ID NO: 64_BCON3_H

GCGGAGCGCAGCTGTGAGGGAGTCGCTGTGATCCGGGGCCCCGGAACCCGAGCTGGAGCT
GAAGCGCAGGCTGCGGGGCGCGGAGTCGGGAGGCCTGAGTGTTCCCTTCAGCATGTCGGA
GGGGGAGTCCCAGACAGTACTTAGCAGTGGCTCAGACCCAAAGGTAGAATCCTCATCTTC
AGCTCCTGGCCTGACATCAGTGTACCTCCTGTGACCTCCACAACCTCAGCTGCTTCCCC
AGAGGAAGAAGAAGAAAGTGAAGATGAGTCTGAGATTTTGAAGAGTCGCCCTGTGGGCG
CTGGCAGAAGAGGCGAGAAGAGGTGAATCAACGGAATGTACCAGGTATTGACAGTGCATA
CCTGGCCATGGATACAGAGGAAGGTGTAGAGGTTGTGTGGAATGAGGTACAGTTCTCTGA
ACGCAAGAATAACAAGCTGCAGGAGGAAAAGGTTCTGTGCTGTGTTTGATAATCTGATTCA
ATTGGAGCATCTTAACATTGTTAAGTTTCAAAATATTGGGCTGACATTAAAGAGAACAA
GGCCAGGGTCATTTTTATCACAGAATACATGTCTATCTGGGAGTCTGAAGCAATTTCTGAA
GAAGACCAAAAAGAACCACAAGACGATGAATGAAAAGGCATGGAAGCGTTGGTGACACA
AATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCCCCATCATCCATGGGAACCT
GACCTGTGACACCATCTTCATCCAGCACAAACGGAATCATCAAGATTGGCTCTGTGGCTCC
TGACACTATCAACAATCATGTGAAGACTTGTGAGAAGAGCAGAAGAATCTACACTTCTT
TGCACCAGAGTATGGAGAAGTCACTAATGTGACAACAGCAGTGGACATCTACTCCTTTGG
CATGTGTGCACTGGAGATGGCAGTGCTGGAGATTACGGGCAATGGAGAGTCCTCATATGT
GCCACAGGAAGCCATCAGCAGTGCCATCCAGCTTCTAGAAGACCCATTACAGAGGGAGTT

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FIGURE 2AAA

CATTCAAAAGTGCCTGCAGTCTGAGCCTGCTCGCAGACCAACAGCCAGAGAACTTCTGTT
CCACCCAGCATTTGTTTGAAGTGCCCTCGCTCAAACCTCTTGCGGCCCCACTGCATTGTGGG
ACACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACCAAAAACATGGATACTAG
TGCCGTACTGGCTGAAATCCCTGCAGGACCAGGAAGAGAACCAGTTTCAGACTTTGTACTC
TCAGTCACCAGCTCTGGAATTAGATAAAATTCCTTGAAGATGTCAGGAATGGGATCTATCC
TCTGACAGCCTTTTGGGCTGCCTCGGCCCCAGCAGCCACAGCAGGAGGAGGTGACATCACC
TGTCGTGCCCCCTCTGTCAAGACTCCGACACCTGAACCAGCTGAGGTGGAGACTCGCAA
GGTGGTGCTGATGCAGTGCAACATTGAGTCGGTGGAGGAGGAGTCAAACACCACCTGAC
ACTTCTGCTGAAGTTGGAGGACAACTGAACCGGCACCTGAGCTGTGACCTGATGCCAAA
TGAGAATATCCCCGAGTTGGCGGCTGAGCTGGTGCAGCTGGGCTTCATTAGTGAGGCTGA
CCAGAGCCGGTTGACTTCTCTGCTAGAAGAGACCTTGAACAAGTTCAATTTTGCCAGGAA
CAGTACCCTCAACTCAGCCGCTGTCACCGTCTCCTCTTAGAGCTCACTCGGGCCAGGCC
TGATCTGCGCTGTGGCTGTCCCTGGACGTGCTGCAGCCCTCCTGTCCCTTCCCCCAGTC
AGTATTACCCTGTGAAGCCCCTTCCCTCCTTTATTATTTCAGGAGGGCTGGGGGGGCTCCC
TGGTTCTGAGCATCATCCTTTCCCTCCCTCTCTTCCCTCCCTCTGCACTTTGTTTACT
TGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCGCCTTCTAGTTGGGGGGCTAGT
CGCTGATCTGCCGGCTCCCGCCCAGCCTGTGTGGAAAGGAGGCCACGGGCACTAGGGGA
GCCGAATTCTACAATCCCGCTGGGGCGGCCGGGGCGGGAGAGAAAGGTGGTGCTGCAGTG
GTGGCCCTGGGGGGCCATTGATTGCGCTCAGTTGCTGCTGTAATAAAAGTCTACTTTTT
GCT

SEQ ID NO: 65_AA711829_M

CTTAAGCAGTTTCTGAAGAAGACCAAAAAGAACCACAAGACTATGAATGAAAAGGCTTGG
AAACGCTGGTGTACACAGATCCTCTCTGCCCTAAGCTACCTGCACTCCTGTGACCCTCCC
ATCATCCATGGGAACCTGACCTGTGACACCATCTTCATCCAGCACAAACGGACTCATCAAG
ATTGGCTCTGTGGCTCCTGACACTATCAACAATCACGTGAAGACTTGCCGGGAAGAAGAG
AAGAACCTACACTTTTTTGCACCAGAGTATGGAGAAGTCAAAACGTGACAAACAGCAGTG
GACATCTACTCCTTTGGCATGTGTGCACTGGAGATGGCAGTGCTGGAGATTTCAGGGCAAT
GGCGAGTCCTCATATGTGCCACAGGAAGCCATCAGCAGTGCCATCCAGCTACTAGAAGAC
TCATTACAGAGGGAGTTTATTCAAAGTGCCCTGCAGTCTGAGCCTGCTCGGAGACCAACA
GCCAGAGAACTTCTGTTCCACCCAGCACTGTTTGAAGTGCCCTCACTCAAGCTTCTTGCT
GCTCACTGTATCGTGGGGCACCAACACATGATCCCAGAGAACGCTCTAGAGGAGATCACC
AAGAACATGGATAACAGTGCTGTACTAGCTGAAATTCCCGCAGGGCCAGGACGAGAACCA
GTTTCAGACTTTGTACTCTCAGTEACCAGCCCTAGAATTAGACAAATTCCTTGAAGATGTC
AGGAATGGGATCTACCCTCTGACAGCCTTTGGGCTACCTCGGCCTCAGCAGCCACAGCAG
GAGGAGGTGACATCACCTGTTGTGCCCCCTCTGTCAAGACTCCAACCTCCTGAGCCAGCT
GAAGTGGAGACACGAAAGGTGGTGTGATGCAGTGCAACATCGAATCTGTGGAGGAGGGA
GTCAAACACCATCTAACACTTCTGCTGAAGCTGGAGGACAAATTGAACCGGCACCTGAGC
TGTGACCTGATGCCAAATGAGAGCATCCCGGACTTGGCAGCTGAGCTGGTGCAGCTGGGC
TTCATTAGTGAGGCTGATCAGAGCCGCCTGACTTCTCTGCTGGAGGAGACGCTCAACAAG
TTCAACTTCACCAGGAACAGTACACTCAACACAGCCACTGTCACCGTCTCCTCGTAGAGC
TCACTTGAGCCAGGCCCTTAGCCAGGCTGTGGCTGTCCCTGGGCATGCTGCAGTCCTCCT
GTCCCTTCTCCCCAGTCAGTATTACCTTTCGCGCCCATATTATTTAGGAGGGCTTTAGGG
GCTCCCTGTTGAGTATCACCTGCCCCCTTCCCCTCTCTTCCCTCCCCCTCTGCACTTTGTT
TACTTGTTTTGCACAGACGTGGGCCTGGGCCTTCTCAGCAGCCACCTTCTAGCTGGGGGC
TAGTAGCTGACCTGCTGCCCTCCTGCCCTACTTGTGTGGACAGGAGGCCACGGGCACTGG
GGAAGCTGAGTTCTACAATCCCGCTGGGGCGCATGGGCAGGAGAGAAAGGTGGTGCTGCA
GGGGTGGCCCCCGGGGGGGGCATTGGAATCACCTCAGTTGCTGCTGTAATAAAAGTCTAC
TTTTTGCT

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FIGURE 2BBB

SEQ ID NO: 66_AA099102_H

ATGTCATCATGTGTCTCTAGCCAGCCCAGCAGCAACCGGGCCGCCCCCAGGATGAGCTG
GGGGGCAGGGGCAGCAGCAGCAGCGAAAGCCAGAAGCCCTGTGAGGCCCTGCGGGGCCCTC
TCATCCTTGAGCATCCACCTGGGCATGGAGTCCTTCATTGTGGTCACCGAGTGTGAGCCG
GGCTGTGCTGTGGACCTCGGCTTGGCGCGGGACCGGCCCTGGAGGCCGATGGCCAAGAG
GTCCCCCTTGACACCTCCGGGTCCCAGGCCCGGCCACCTCTCCGGTCGCAAGCTGTCT
CTGCAAGAGCGGTCCCAGGGTGGGCTGGCAGCCGGTGGCAGCCTGGACATGAACGGACGC
TGCATCTGCCCCGTCCCTGCCCTACTCACCCGTACAGCTCCCCGCAGTCTCGCCTCGGCTG
CCCCGGCGGCCGACAGTGGAGTCTCACACGTCTCCATCACGGGTATGCAGGACTGTGTG
CAGCTGAATCAGTATACCCTGAAGGATGAAATTGGAAAGGGCTCCTATGGTGTGCTCAAG
TTGGCCTACAATGAAAATGACAATACCTACTATGCAATGAAGGTGCTGTCCAAAAGAAG
CTGATCCGGCAGGCCGCTTTTCCACGTGCCCCCTCACCCCCGAGGCACCCGGCCAGCTCCT
GGAGGCTGCATCCAGCCCAGGGGCCCATTTGAGCAGGTGTACCAGGAAATTGCCATCCTC
AAGAAGCTGGACCACCCAATGTGGTGAAGCTGGTGGAGGTCTGGATGACCCAATGAG
GACCATCTGTACATGGTGTTCGAACTGGTCAACCAAGGGCCCGTGATGGAAGTGCCACC
CTCAAACCACTCTCTGAAGACCAGGCCCGTTTCTACTTCCAGGATCTGATCAAAGGCATC
GAGTACTTACACTACCAGAAGATCATCCACCGTGACATCAAACCTTCCAACCTCCTGGTC
GGAGAAGATGGGCACATCAAGATCGCTGACTTTGGTGTGAGCAATGAATTCAAGGGCAGT
GACGCGCTCCTCTCCAACCTACGTGGGCACGCCCGCCTTCATGGCTCCCGAGTCGCTCTCT
GAGACCCGCAAGATCTTCTCTGGGAAGGCCAAGGATGTTTGGGCCATGGGTGTGACACTA
TACTGCTTTGTCTTTGGCCAGTGCCCATTCATGGACGAGCGGATCATGTGTTTACACAGT
AAGATCAAGAGTCAGGCCCTGGAATTTCCAGACCAGCCCGACATAGCTGAGGACTTGAAG
GACCTGATCACCCGTATGCTGGACAAGAACCCCGAGTCGAGGATCGTGGTGCCGGAATC
AAGCTGCACCCCTGGGTACGAGGCATGGGGCGGAGCCGTTGCCGTGCGAGGATGAGAAC
TGCACGCTGGTCAAGTGACTGAAGAGGAGGTGAGAACTCAGTCAAACACATTCCCAGC
TTGGCAACCGTGATCCTGGTGAAGACCATGATACGTAAACGCTCCTTTGGGAACCCATTC
GAGGGCAGCCGGCGGGAGGAACGCTCACTGTGAGCGCCTGGAACTTGCTCACCAAAAAA
CCAACCAGGGAATGTGAGTCCCTGTCTGAGCTCAAGGAAGCAAGGCAGCGAAGACAACCT
CCAGGGCACCGACCCGCCCGCCCGTGGGGGAGGAGGAAGTGCTCTTGTGAGAGGCAGTCCC
TGCGTGGAAGTTGCTGGGCCCCCGCCCCGGCTCCCCCGCACGCATGCATCCACTGCGG
CCGGAGGAGGCCATGGAGCCCGAGTAG

SEQ ID NO: 67_5R69_17_2_H

CCGGGATGTGAGCCTGGTGGTTGGCAGCTGGAGCCACGTCCGAGGGGGGAAGTGTGCGAGC
ATTCTCTGCAGGCATCACAGACCTGAGGCAGTGGCCTCCGGAGGGCACTGGACAGAAACA
GCCATCCAAGTGGCTGAGTGGAGGGACCTGCTCAAGTGCAGCTGCAGTGGCCGGGGTTT
CCCTCAGGTAGGGATCGGGGCGCCTTGTGCGCCGACGCCACGTGTGGCGTCCGGTACAGT
CAGCAGAGTGCAGGGTGCGGGCACCAGGAAAGGGGGCGCAGGGGAACTCCCGCGGGCCTC
GCGTTTGCAAACCTTCTCGCCTGGGCAGGAGGCGGTGCTGGGAAAGAAGGTGGAAGAGCGA
GCTTTTGGAACTGTGCACGGGACAGATTGGACGCACACCCCTCGGGAGGCGCGAAGGCA
TGGAATAATTTGAAGCATATTATCACCCCTTGCCAGGTATCCACAAACGGTGTGAAGAGA
TGAAATACTGCAAGAAACAGTGCCGGCGCCTGGGCCACCGCGTCCTCGGCCTGATCAAGC
CTCTGGAGATGCTCCAGGACCAAGGAAAGAGGAGCGTGCCCTCTGAGAAGTTAACCACAG
CCATGAACCGCTTCAAGGCTGCCCTGGAGGAGGCTAATGGGGAGATAGAAAAGTTTCAAGCA
ATAGATCCAATATCTGCAGGTTTCTAACAGCAAGCCAGGACAAAATACTCTTCAAGGACG
TGAACAGGAAGCTGAGTGATGTCTGGAAGGAGCTCTCGCTGTTACTTCAAGTTGAGCAAC
GCATGCCTGTTTACCCATAAAGCCAAGGAGCGTCCTGGGCACAGGAAGATCAGCAGGATG
CAGACGAAGACAGGCGAGCTTTCCAGATGCTAAGAAGAGATAATGAAAAAATAGAAGCTT
CACTGAGACGATTAGAAATCAACATGAAAGAAATCAAGGAACTTTGAGGCAGTGTAAGT
TATCATGTGCCCTGCTGTTTCTGATGGCCCCCAAACCTAGAAGTCATCAGTTTACTGGGAC

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FIGURE 2CCC

CCCAGCCTCCCGCTACCCCTGCATTTGTCCATTTTCTGTGCTGGATGGCTGGAAGCAGCC
CACAGGTTTGGGGATCCATTCATGGCTAGCCCAGGCTTCTGTCCATGGAATAACATGTGG
AGAGAGCTTCTTGACCAGTAAGATACCTTCTAGCAGCTGTCAAAGTACTTAAAAACCTCT
ATGAATAGAATCAAAGCTTCAGTTCAGTTGCTGAATTTCCAAGAAGAAATTCAAATCAAA
TTTAAATGCCCACTCATTCATTCAACAAAACCTGTGAGTATCTGGTTTATGCCAGA
GGCCATGCAAAGAGGTAACATAAGATGCAGAGAAGGACACTGCCTTCCAGGAGCTCACGGG
GTGGAGGAGGAAAGAGGAAAGACAGACAGTGAACACACAACAGCAAGGTTACTGAGCTTG
AACTATGTCCCTAACTACTAGATCTGAAATGACTACGCCAGATGCCAGATGCTCAAGTGC
CAAGCTCTGGGTAAACAGGAATAGACATCCTTCCAGGATGAGAGAGATGAGTCTGGATGAG
GGTTAAGGCTGGAGGGACAGGCGGGATTGTAAGAGGAGGGAAAGGAAGTGGATGACACAT
TCTGTAACTGTCCAGCTGTGTCTCTACTGGTCACTCAGAGGCACGGGAGCCGCTCCCTT
GGGCTGAGTCCATCAGAAGCCCCAGCCACCACAGCTCTGGTTCATGTAGTAGAGCTTCC
CACTCACACATCACAATATGCCACCTCCCTTAGGACCCCTTCTCTGTCTATTGACTCT
TTTGTCTTCTTCTCTCGGGGGTGAGGTCAGATTTACCACCAAAATGCATGCAGGAGAT
CCCGCAAGAGCAAATCAAGGAGATCAAGAAGGAGCAGCTTTCAGGATCCCCGTGGATTCT
GCTAAGGGAAAATGAAGTCAGCACACTTTATAAAGGAGAATACCACAGAGCTCCAGTGGC
CATAAAAGTATTCAAAAACTCCAGGCTGGCAGCATTGCAATAGTGAGGCAGACTTTCAA
TAAGGAGATCAAAACCATGAAGAAATTCGAATCTCCCAACATCCTGCGTATATTTGGGAT
TTGCATTGATGAAACAGTGAAGTCCGCCTCAATTCTCCATTGTCTGAGTACTGTGAAGT
CGGGACCTTGAGGAGCTGTTGGATAGGGAAAAAGACCTCACACTTGGAAGCGCATGGT
CCTAGTCTTGGGGCAGCCCGAGGCCTATACCGGCTACACCATTGAGAAGCACCTGAAGT
CCACGGAAAAATCAGAAGCTCAAACCTTCTGGTAACTCAAGGCTACCAAGTGAAGCTTGC
AGGATTTGAGTTGAGGAAAAACAGACTTCCATGAGTTTGGGAACTACGAGAGAAAAGAC
AGACAGAGTCAAATCTACAGCATATCTCTCACCTCAGGAAGTGAAGATGTATTTTATCA
ATATGATGTAAAGTCTGAAATATACAGCTTTGGAATCGTCTCTGGGAAATCGCCACTGG
AGATATCCCGTTTCAAGGTGAAGAAATGTGAAGACTGGCTCAGCCAGTGGCTGTAATTCTG
AGAAGATCCGCAAGCTGGTGGCTGTGAAGCGGCAGCAGGAGCCACTGGGTGAAGACTGCC
CTTCAGAGCTGCGGGAGATCATTGATGAGTGCCGGGCCCATGATCCCTCTGTGCGGCCCT
CTGTGGATGAAATCTTAAAGAACTCTCCACCTTTTCTAAGTAGTGATCAAAATCTAAA
CCAAGGAGTCTCTGGACAAGAAGCTGGGAGAGGCACGAAGTGGACATCTCTCTCTCAT
ATCCTTCGGCATTGGGTTATCTATGGGTGCAAGGAGTGGGCACGCTTCTCTGTACAAAT
AGAAAACGATTCCAGTCATACAGGACACATCCCACTCCAAATGATATTTCCAAAAACATA
CCTCTGACAGTAACTTTGATAGATGGTTTGTCAAATGTATCTTTCTGGGTATCCACACCT
CTTGGCAATGAAATTTGCAGCTCCTCCCTTCCATAAATGAAGTCTCTTTCCCCACCATTT
GAATCTGGGCTGGCACTGTGACTTGATTTGATCAATAGAATGTGGAAGAAGTGAAGTGTAT
GCCAGTTCCAAGCCTAGGTTTCAAGAGGCCTTATAAATGTCTGTTGGAACCTTACCCAGC
CATGGACATGTTGAGTGAGCATGCTGGAGAATGAGAGACCACATGAAGCAGAAACATGCT
TTCCTAGCTGAAGTCATACTAGCCCAACCAACATGGCAGCTAACACATGAATGAGGCCAA
TCAAGACCAGAAGAACCCTCAAGCAGATCCAGCCCAATTGCCCATTCACACAATCAG
GAGCTAAATAAATTACTGTTGTCTTTT

SEQ ID NO: 68_H85811_H

CGCCCCGGCCCCCTCCCCGGCGCCGGCCACGGGAGGCGGTGATGCGGGCGCGGGCGGCCT
CGGCTGCGCCGAGAGCGGAGACACAGGCTCAAGATGGCAGATTCCGACTGAGGCTGGGGG
GGCCGAGCTCGCGCGCCGCTTTCCCGTCCCCGTGTCATGAACCGCGGACACCCCGGCC
CGATGGCCCCCGTGTACGAAGGTATGGCCTCACATGTGCAAGTTTTCTCCCCTCACACCC
TTCAATCAAGTGCCTTCTGTAGTGTGAAGAACTGAAAATAGAGCCGAGTTCCAAGTGGG
ACATGACTGGGTACGGCTCCACAGCAAAGTGTATAGCCAGAGCAAGAACATCCCCCTGT
CGCAGCCAGCCACCACAACCGTCAGCACCTCCTTGCCGGTCCCAAACCAAGCCTACCTT
ACGAGCAGACCATCGTCTTCCCAGGAAGCACCGGGCACATCGTGGTCACTCAGCAAGCA

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FIGURE 2DDD

GCACCTTCTGTCACCGGGCAAGTCCTCGGCGGACCACACAACCTAATGCGTTCGAAGCACTG
TGAGCCTCCTTGATACCTACCAAAAATGTGGACTCAAGCGTAAGAGCGAGGAGATCGAGA
ACACAAGCAGCGTGCAGATCATCGAGGAGCATCCACCCATGATTGAGAATAATGCAAGCG
GGGCCACTGTCGCCACTGCCACCACGTCTACTGCCACCTCCAAAAACAGCGGCTCCAACA
GCGAGGGCGACTATCAGCTGGTGCAGCATGAGGTACTGTGCTCCATGACCAACACCTACG
AGGTCTTAGAGTTCTTGGGCGGAGGGACGTTTGGGCAAGTGGTCAAGTGCTGGAAACGGG
GCACCAATGAGATCGTAGCCATCAAGATCCTGAAGAACCACCCATCCTATGCCCGACAAG
GTCAGATTGAAGTGAGCATCCTGGCCCGGTTGAGCACGGAGAGTGCCGATGACTATAACT
TCGTCCGGGCCTACGAATGCTTCCAGCACAAGAACCACACGTGCTTGGTCTTCGAGATGT
TGGAGCAGAACCTCTATGACTTTCTGAAGCAAAAACAAGTTTAGCCCCCTTGCCCCCTCAAAT
ACATTCGCCCCAGTTCTCCAGCAGGTAGCCACAGCCCTGATGAAACTCAAAGCCTAGGTC
TTATCCACGCTGACCTCAAACCAGAGAACATCATGCTGGTGGATCCATCTAGACAACCAT
ACAGAGTCAAGGTCATCGACTTTGGTTCAGCCAGCCACGTCTCCAAGGCTGTGTGCTCCA
CCTACTTGCAGTCCAGATATTACAGGGCCCCCTGAGATCATCCTTGGTTTACCATTTTGTG
AGGCAATTGACATGTGGTCCCTGGGCTGTGTTATTGCAGAATTGTTCTGGGTTGGCCGT
TATATCCAGGAGATTCCGAGTATGATCAGATTCCGTATATTTACAAACACAGGGTTTGC
CTGCTGAATATTTATTAAGCGCCGGGACAAAGACAACCTAGGTTTTTCAACCGTGACACGG
ACTCACCATATCCTTTGTGGAGACTGAAGACACCAGATGACCATGAAGCAGAGACAGGGA
TTAAGTCAAAGAAGCAAGAAAGTACATTTTCAACTGTTTAGATGATATGGCCAGGTGA
ACATGACGACAGATTTGGAAGGGAGCGACATGTTGGTAGAAAAGGCTGACCGGCGGGAGT
TCATTGACCTGTTGAAGAAGATGCTGACCATTGATGCTGACAAGAGAATCACTCCAATCG
AAACCCTGAACCATCCCTTTGTACCATGACACACTTACTCGATTTTCCCCACAGCACAC
ACGTCAAATCATGTTTCCAGAACATGGAGATCTGCAAGCGTCGGGTGAATATGTATGACA
CGGTGAACCAGAGCAAACCCCTTTATCACGCACGTGGCCCCCAGCACGTCCACCAACC
TGACCATGACCTTTAACAACCAGCTGACCACTGTCCACAACCAGCCCTCAGCGGCATCCA
TGGCTGCAGTGGCCCAGCGGAGCATGCCCCTGCAGACAGGAACAGCCCAGATTTGTGCCC
GGCTGACCCGTTCCAGCAAGCTCTCATCGTGTGTCCCCCGGCTTCCAAGGCTTGCAGG
CCTCTCCCTCTAAGCACGCTGGCTACTCGGTGCGAATGGAAAATGCAGTTCCCATCGTCA
CTCAAGCCCCAGGAGCTCAGCCTCTTCAGATCCAACCAGGTCTGCTTGCCAGCAGGCTT
GGCCAAGTGGGACCCAGCAGATCCTGCTTCCCCCAGCATGGCAGCAACTGACTGGAGTGG
CCACCCACACCTCAGTGCAGCATGCCACCGTGATTCCCGAGACCATGGCAGGCACCCAGC
AGCTGGCGGACTGGAGAAATACGCATGCTCACGGAAGCCATTATAATCCCATCATGCAGC
AGCCTGCACTATTGACCGGTGATGTGACCCTTCCAGCAGCACAGCCCTTAAATGTGGGTG
TGGCCACGTGATGCGGCAGCAGCCAACCAGCACCACCTCCTCCCGGAAGAGTAAGCAGC
ACCAGTCATCTGTGAGAAATGTCTCCACCTGTGAGGTGTCTCCTCTCAGGCCATCAGCT
CCCCACAGCGATCCAAGCGTGTCAAGGAGAACACACCTCCCCGCTGTGCCATGGTGCACA
GTAGCCCGGCCTGCAGCACCTCGGTACCTGTGGGTGGGGCGACGTGGCCTCCAGCACC
CCCGGGAACGGCAGCGGCAGACAATTGTCATTCCCGACACTCCAGCCCCACGGTCAGCG
TCATCACCATCAGCAGTGACACGGACGAGGAGGAGGAACAGAAACACGCCCCCACCAGCA
CTGTCTCCAAGCAAAGAAAAAACGTATCAGCTGTGTACAGTCCACGACTCCCCCTACT
CCGACTCCTCCAGCAACACCAGCCCCTACTCCGTGCAGCAGCGTGCTGGGCACAACAATG
CCAATGCCTTTGACACCAAGGGGAGCCTGGAGAATCACTGCACGGGGAACCCCCGAACCA
TCATCGTGCCACCCCTGAAAACCCAGGCCAGCGAAGTATTGGTGGAGTGTGATAGCCTGG
TGCCAGTCAACACCAGTCACTACTCGTCTCTACAAGTCCAAGTCTCCTCAGCAACGTGA
CCTCCACCAGCGGTCACTCTTTCAGGGAGCTCATCTGGAGCCATCACCTACCGGCAGCAGC
GGCCGGGCCCCCACTTCCAGCAGCAGCAGCCACTCAATCTCAGCCAGGCTCAGCAGCACA
TCACCACGGACCGCACTGGGAGCCACCGAAGGCAGCAGGCCTACATCACTCCCACCATGG
CCCAGGCTCCGTACTCCTTCCCGCACAACAGCCCCAGCCACGGCACTGTGCACCCGCATC
TGGCTGCAGCCGCTGCCGCTGCCACCTCCCCACCCAGCCCCACCTCTACACCTACACTG
CGCCGGCGGCCCTGGGCTCCACCGGCACCGTGGCCCACTGGTGGCCTCGCAAGGCTCTG

FIGURE 2EEE

CGCGCCACACCGTGCAGCACACTGCCTACCCAGCCAGCATCGTCCACCAGGTCCCCGTGA
GCATGGGCCCCCGGGTCCTGCCCTCGCCACCATCCACCCGAGTCAGTATCCAGCCCAAT
TTGCCACACAGACCTACATCAGCGCCTCGCCAGCCTCCACCGTCTACACTGGATACCCAC
TGAGCCCCCGCAAGGTCAACCAGTACCCTTACATATAAACTGGAGGGGAGGGAGGGAG
GGAGGGAGGGAGAGAATGGCCCCGAGGGAGGAGGGAGAGAAGGAGGGAGGCGCTCCTGGGA
CCGTGGGCGCTGGCCTTTTATACTGAAGATGCCGCACACAAACAATGCAAACGGGGCAGG
GGCGGGGGGGGGGGGGCAGAGGGCAGGGGGACGGGTCTGGGACACCAGTGAACCTTGAACC
GGGAAGTGGGAGGACGTAGAGCAGAGAAGAGAACATTTTAAAAGGAAGGGATTAAAGAG
GGTGGGAAATCTATGGTTTTTATTTTAAAAAAG

SEQ ID NO: 69_DYRK3_H

CGGGAGCGAAAGTGCCTGAGCTGCAGTGTCTGGTCGAGAGTACCCGTGGGAGCGTCGCG
CCGCGGAGGCAGCCGTCCCGGCGTAGGTGGCGTGGCCGACCGGACCCCCAACTGGCGCCT
CTCCCCGAGCGGGGTCCCCGAGCTAGGAGATGGGAGGCACAGCTCGTGGGCCTGGGCGGAA
GGATGCGGGGCGCCTGGGGCCGGGCTCCCGCCCCAGCAGCGGAGTTGGGGGATGGTGTCT
TATGACACCTTCATGATGATAGATGAAACCAATGTCCCCCTGTTCAAATGTACTCTGC
AATCCTTCTGAACCACCTCCACCCAGAAGACTAAATATGACCGCTGAGCAGTTTACAGGA
GATCATACTCAGCACTTTTTGGATGGAGGTGAGATGAAGGTAGAACAGCTGTTTCAAGAA
TTTGGAACAGAAAATCCAATACTATTTCAGTCAGATGGCATCAGTACTCTGAAAAATGC
TCTCCTACTGTTTCTCAGGGTAAAAGTTTCAGATTGCTTGAATACAGTAAAATCCAACAGT
TCATCCAAGGCACCCAAAGTGGTGCCTCTGACTCCAGAACAAGCCCTGAAGCAATATAAA
CACCACCTCACTGCCTATGAGAACTGGAAATAATTAATTATCCAGAAATTTACTTTGTGTA
GGTCCAAATGCCAAGAAAAGACATGGAGTTATTGGTGGTCCCAATAATGGAGGGTATGAT
GATGCAGATGGGGCCTATATTTCATGTACCTCGAGACCATCTAGCTTATCGATATGAGGTG
CTGAAAATTATTGGCAAGGGGAGTTTGGGCAGGTGGCCAGGGTCTATGATCACAACTT
CGACAGTACGTGGCCCTAAAAATGGTGCCTCAATGAGAAGCGCTTTCATCGTCAAGCAGCT
GAGGAGATCCCGATTTTGGAGCATCTTAAGAAACAGGATAAACTGGTAGTATGAACGTT
ATCCACATGCTGGAAAGTTTCACATTCCGGAACCATGTTTGCATGGCCTTTGAATTGCTG
AGCATAGACCTTTATGAGCTGATTAAAAAAATAAGTTTTCAGGGTTTTAGCGTCCAGTTG
GTACGCAAGTTTGCCAGTCCATCTTGCAATCTTTGGATGCCCTCCACAAAAATAAGATT
ATTCATGCGATCTGAAGCCAGAAAACATTCTCCTGAAACACCACGGGCGCAGTTCAACC
AAGGTCATTGACTTTGGGTCCAGCTGTTTTCGAGTACCAGAAGCTCTACACATATATCCAG
TCTCGGTTCTACAGAGCTCCAGAAATCATCTTAGGAAGCCGCTACAGCACACCAATTGAC
ATATGGAGTTTTCGCTGCATCCTTGCAAACTTTTAAACAGGACAGCCTCTCTTCCCTGGA
GAGGATGAAGGAGACCAGTTGGCCTGCATGATGGAGCTTCTAGGGATGCCACCACCAAAA
CTTCTGGAGCAATCCAAACGTGCCAAGTACTTTATTAATTCCAAGGGCATACCCCGCTAC
TGCTCTGTGACTACCCAGGCAGATGGGAGGGTTGTGCTTGTGGGGGGTCTGCTCACGTAGG
GGTAAAAAGCGGGGTCCCCCAGGCAGCAAAGACTGGGGGACAGCACTGAAAGGGTGTGAT
GACTACTTGTATATAGAGTTCTTGAAAAGGTGTCTTCACTGGGACCCCTCTGCCCGCTTG
ACCCAGCTCAAGCATTAAAGACACCCTTGATTAGCAAGTCTGTCCCAGACCTCTCACC
ACCATAGACAAGGTGTCAGGGAAACGGGTAGTTAATCCTGCAAGTGCTTTCCAGGGATTG
GGTTCTAAGCTGCCTCCAGTTGTTGGAATAGCCAATAAGCTTAAAGCTAACTTAATGTCA
GAAACCAATGGTAGTATACCCCTATGCAGTGTATTGCCAAAACCTGATTAGCTAGTGGACA
GAGATATGCCAGAGATGCATATGTGTATATTTTTATGATCTTACAAACCTGCAAAATGGA
AAAAATGCAAGCCCATTTGGTGGATGTTTTTGTAGAGTAGACTTTTTTTAAACAAGACAA
AACATTTTTATATGATTATAAAAGAATTCTTCAAGGGCTAATTACCTAACCAGCTTGTAT
TGCCCATCTGGAATATGCATTAAATGACTTTTTATAGGTCA

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FIGURE 2FFF

SEQ ID NO: 70_AA589241_M_DYRK3_M

CCACGCGTCCGGAGTTGCTAGGAATGCCACCGCAGAACTTCTGGAGCAATCCAAGCGTG
CCAAGTACTTTATTAACTCCAAAGGCTTGCTCGATACTGCTCCGTATCTACCCAGACGG
ACGGGAGGGTGGTGGCTTCTCGGGGGTCTGCTCACGCAGGGGTAAAAAGCGAGGCCCCGCCAG
GCAGCAAAGACTGGGCAACCGCACTGAAGGGCTGTGGTGACTACTTGTTCATAGAGTTTC
TGAAACGATGCCTCCAGTGGGACCCCTCTGCCCCGCTCACCCCGGCTCAAGCATTAAAGAC
ATCCTTGATTAGCAAGTCTACACCCAAACCTCTCACCATGGACAAGGTGCCAGGGAAGC
GGGTAGTTAACCCTACAAATGCTTTCCAGGGACTGGGTTCCAAGCTGCCTCCAGTCGTTG
GGATAGCCAGTAAGCTTAAAGCTAACCTAATGTCCGAAACCAGTGGTAGTATACCTCTGT
GCAGTGTATTGCCAAAGCTGATTAGCTAGTGGACCACTCAGAGACTGATACATATCATAT
GTATTTTTTAATTACCTTGCAAACATGCAAATGGAAAACGGAATAATTGAAGCCCATTAC
TGATGGATATGTTTTTGTAGACTTTTTTTTAAACAAGGCAGAACATTTTTTATATGACTAT
AAAAGAACGCTTCAAGGGCTAATGTCAAACCAGCTTGTATTGGCCATCTGGAGTATACAT
TAAATGACTTTTTTCATAGGTC

SEQ ID NO: 71_5R72_16_2_H

GTCGAGGCGCAGCGCTGCCATGGCTGGGGGCCGTGGGGCCCCCGGGCGCGGCCGGGACGA
GCCTCCGGAGAGCTACCCGCAACGACAGGACCACGAGCTACAGGCCCTGGAGGCCATCTA
CGGCGCGGACTTCCAAGACCTGCGGCCGGACGCTTGCGGACCGGTCAAAGAGCCCCCTGA
AATCAATTTAGTTTTGTACCCCTCAAGGCCTAACTGGTGAAGAAGTATATGTAAAAGTGGA
TTTGAGGGTTAAATGCCACCTACCTATCCAGATGTAGTTCCTGAAATAGAGTTAAAAAA
TGCCAAAGGTCTATCAAATGAAAGTGTCAATTTGTTAAATCTCGCCTAGAAGAACTGGC
CAAGAAACACTGTGGGGAGGTGATGATCTTTGAACTGGCTTACCACGTGCAGTCATTTCT
CAGCGAGCATAACAAGCCCCCTCCCAAGTCTTTTCATGAAGAAATGCTGGAAAGGCGGGC
TCAGGAGGAGCAGCAGAGGCTGTTGGAGGCCAAGCGGAAAGAAGAGCAGGAGCAACGTGA
AATCCTGCATGAGATTCAGAGAAGGAAAGAAGAGATAAAAGAAGAGAAAAAAGGAAAGA
AATGGCTAAGCAGGAACGTTTGGAATTGCTAGTTTGTCAAACCAAGATCATACTCTAA
GAAGGACCCAGGAGGACACAGAACGGCTGCCATTCTACATGGAGGCTCTCCTGACTTTGT
AGGAAATGGTAAACATCGGGCAAACCTCCTCAGGAAGGTCTAGGCGAGAACGTCAGTATTC
TGTATGTAATAGTGAAGATTCTCCTGGCTCTTGTGAAATTCTGTATTTCAATATGGGGAG
TCCTGATCAGCTCATGGTGCACAAAGGGAAATGTATTGGCAGTGATGAACAACTTGGA
ATTAGTCTACAATGCTTTGGAAACAGCCACTGGTGGCTTTGTCTTGTTGTATGAGTGGGT
CCTTCAGTGGCAGAAAAAATGGGTCCATTCCCTTACCAGTCAAGAAAAAGAGAAGATTGA
TAAGTGCAAAAAGCAGATTCAAGGAACAGAAACAGAATTCAACTCACTGGTAAAATTGAG
CCATCCAAATGTAGTACGCTACCTTGCAATGAATCTCAAAGAGCAAGACGACTCCATCGT
GGTGGACATTTTAGTGGAGCACATTAGTGGGGTCTCTCTTGCTGCACACCTGAGCCACTC
AGGCCCCATCCCTGTGCATCAGCTTCGCAGGTACACAGCTCAGCTCCTGTCAGGCCTTGA
TTATCTGCACAGCAATTCTGTGGTGCATAAGGTCCTGAGTGCATCTAATGTCTTGGTGA
TGCAGAAGGCACCGTCAAGATTACGGACTATAGCATTTCTAAGCGCCTCGCAGACATTTG
CAAGGAGGATGTGTTTGAGCAAACCCGAGTTCGTTTTAGTGACAATGCTCTGCCTTATAA
AACGGGGAAGAAAGGAGATGTTTGGCGTCTTGGCCTTCTGCTGCTGTCCCTCAGCCAAGG
ACAGGAATGTGGAGAGTACCCTGTGACCATCCCTAGTGACTTACCAGCTGACTTTCAAGA
TTTTCTAAAGAAATGTGTGTGCTTGGATGACAAGGAAAGATGGAGTCCCCAGCAGTTGTT
GAAACACAGCTTTATAAATCCCCAGCCAAAAATGCCTCTAGTGGAACAAAGTCTGAAGA
TTCTGGAGGACAAGATTATGTTGAGACTGTTATTCCTAGCAACCGGCTACCCAGTGCTGC
CTTCTTTAGTGAGACACAGAGACAGTTTTCCCGATACTTCATTGAGTTTGAAGAATTACA
ACTTCTTGGTAAAGGAGCTTTTGGAGCTGTCAAGGTGCAGAACAAAGTTGGACGGCTG
CTGCTACGCAGTGAAGCGCATCCCCATCAACCCGGCCAGCCGGCAGTTCCGCAGGATCAA
GGGCGAAGTGACACTGCTGTACGGCTGCACCATGAGAACATTGTGCGCTACTACAACGC
CTGGATCGAGCGGCACGAGCGGCCGGCGGGACCGGGGACGCCGCCCCCGGACTCCGGGCC

FIGURE 2GGG

CCTGGCCAAGGATGACCGAGCTGCACGCGGGCAGCCGGCGAGCGACACAGACGGCCTGGA
CAGCGTAGAGGCCCGCCGCGCCGCCACCCATCCTCAGCAGCTCGGTGGAGTGGAGCACTTC
GGGCGAGCGCTCGGCCAGTGCCCGTTTCCCCGCCACCGGCCCGGGCTCCAGCGATGACGA
GGACGACGACGAGGACGAGCACGGTGGCGTCTTCTCCAGTCCTTCTGCCTGCTTCAGA
TTCTGAAAGTGATATTATCTTTGACAATGAAGATGAGAACAGTAAAAGTCAGAATCAGGA
TGAAGATTGCAATGAAAAGAAATGGCTGCCATGAAAGTGAGCCATCAGTGACGACTGAGGC
TGTGCACTACCTATACATCCAGATGGAGTACTGTGAGAAGAGCACTTTACGAGACACCAT
TGACCAGGGACTGTATCGAGACACCGTCAGACTCTGGAGGCTTTTTTCGAGAGATTCTGGA
TGGATTAGCTTATATCCATGAGAAAGGAATGATTCACCGGGATTTGAAGCCTGTCAACAT
TTTTTTGGATTCTGATGACCATGTGAAAATAGGTGATTTTGTTTGGCGACAGACCATCT
AGCCTTTTCTGCTGACAGCAAACAAGACGATCAGACAGGAGACTTGATTAAGTCAGACCC
TTCAGGTCACCTAACTGGGATGGTTGGCACTGCTCTCTATGTAAGCCCAGAGGTCCAAGG
AAGCACCAAATCTGCATACAACCAGAAAGTGGATCTCTTCAGCCTGGGAATTATCTTCTT
TGAGATGTCCTATCACCCCATGGTCACGGCTTCAGAAAGGATCTTTGTTCTCAACCAACT
CAGAGATCCCACCTTCGCCTAAGTTTCCAGAAGACTTTGACGATGGAGAGCATGCAAAGCA
GAAATCAGTCATCTCCTGGCTGTTGAACCACGATCCAGCAAACGGCCCCACAGCCACAGA
GCTGCTCAAGAGTGAGCTGCTGCCCCCACCCAGATGGAGGAGTCAGAGCTGCATGAAGT
GCTGCACCACACGCTGACCAACGTGGATGGGAAGGCCCTACCGCACCATGATGGCCCAGAT
CTTCTCGCAGCGCATCTCCCCTGCCATCGATTACACCTATGACAGCGACATACTGAAGGG
CAACTTCTCAATCCGTACAGCCAAGATGCAGCAGCATGTGTGTGAAACCATCATCCGCAT
CTTTAAAAGACATGGAGCTGTTCAAGTTGTGTACTCCACTACTGCTTCCCCGAAACAGACA
AATATATGAGCACAACGAAGCTGCCCTATTTCATGGACCACAGCGGGATGCTGGTGATGCT
TCCTTTTGGACCTGCGGATCCCTTTTGAAGATATGTGGCAAGAAATAATATATTGAATTT
AAAACGATACTGCATAGAACGTGTGTTTCAAGCCGCGCAAGTTAGATCGATTTTCATCCCAA
AGAACTTCTGGAGTGTGCATTTGATATTGTCACTTCTACCACCAACAGCTTTCTGCCCCAC
TGCTGAAATTATCTACACTATCTATGAAATCATCCAAGAGTTTCCAGCACTTCAGGAAAG
AAATTACAGTATTTATTTGAACCATACCATGTTATTGAAAGCAATACTCTTACACTGTGG
GATCCCAGAAGATAAACTCAGTCAAGTCTACATTATTCTGTATGATGCTGTGACAGAGAA
GCTGACGAGGAGAGAAGTGGAAGCTAAATTTTGTAACTCTGTCTTTGTCTTCTAATAGTCT
GTGTGCACTCTACAAGTTTATTGAACAGAAGGGAGATTTGCAAGATCTTATGCCAACAAAT
AAATTCATTAATAAAACAGAAAACAGGTATTGCACAGTTGGTGAAGTATGGCTTAAAGA
CCTAGAGGAGGTTGTTGGACTGTTGAAGAACTCGGCATCAAGTTACAGGTCTTGATCAA
TTTGGGCTTGTTTACAAGGTGCAGCAGCACAATGGAATCATCTTCCAGTTTGTGGCTTT
CATCAAACGAAGGCAAAGGGCTGTACCTGAAATCCTCGCAGCTGGAGGCAGATATGACCT
GCTGATTCCCCAGTTTGAAGGGCCACAAGCTCTGGGGCCAGTTCCCACTGCCATTGGGGT
CAGCATAGCTATAGACAAGATATCTGCTGCTGTCCTCAACATGGAGGAATCTGTTACAAT
AAGCTCTTGTGACCTCCTGGTTGTAAGTGTTGGTCAGATGTCTATGTCCAGGGCCATCAA
CCTAACCAGAACTCTGGACAGCAGGCATCACAGCAGAAATCATGTACGACTGGTCACA
GTCCCAAGAGGAATTACAAGAGTACTGCAGACATCATGAAATCACCTATGTGGCCCTTGT
CTCGGATAAAGAAGGAAGCCATGTCAAGGTTAAGTCTTTCGAGAAGGAAAGGCAGACAGA
GAAGCGTGTGCTGGAGACTGAACTTGTGGACCATGTACTGCAGAACTGAGGACTAAAGT
CACTGATGAAAGGAATGGCAGAGAAGCTTCCGATAATCTTGCAAGTGCAAAATCTGAAGGG
GTCATTTTCTAATGCTTCAGGTTTGTGTTGAAATCCATGGAGCAACAGTGGTTCCCATTTGT
GAGTGTGCTAGCCCCGAGAAGCTGTGAGCCAGCACTAGGAGGCGCTATGAAACTCAGGT
ACAACTCGACTTCAGACCTCCCTTGCCAACCTTACATCAGAAAAGCAGTGAAATTGAAAT
TCTGGCTGTGGATCTACCCAAAGAAACAATATTACAGTTTTTATCATTAGAGTGGGATGC
TGATGAACAGGCATTTAACACAACCTGTGAAGCAGCTGCTGTACGCTGCCAAAGCAAAG
ATACCTCAAATTAGTCTGTGATGAAATTTATAACATCAAAGTAGAAAAAAGGTGTCTGT
GCTATTTCTGTACAGCTATAGAGATGACTACTACAGAATCTTATTTTAAACCCTAAAGAAC
TGTCGTTAACCTCATTCAAACAGACAGAGGCTTATACTGGAATAATGGAATGTTGTACAT

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FIGURE 2HHH

TCATCATAATTTAAAATTAAATTCTAAGAAGAGGCTGGGTGCAGTGGCTCACACCTTTAA
TCCCAGCACTTTGGGAAGCCAAGGCAGGAAGACTGCTTGAACCAGGAGTTTGAGACCAG
CCT

SEQ ID NO: 73_R43524_H, HRI_H

ATGCTGGGGGGCAACTCCGGGGTCCGCAAGCGCGAAGAGGAGGGCGACGGGGCTGGGGCT
GTGGCTGCGCCCGCGGCCATCGACTTTCCCGCCGAGGGCCCGGACCCCGAATATGACGAA
TCTGATGTTCCAGCAGAAATCCAGGTGTTAAAGAACCCTACAACAGCCAACCTTCCCT
TTTGCAGTTGCAAACCAACTCTTGCTGGTTTCTTTGCTGGAGCACTTGAGCCACGTGCAT
GAACCAAACCCACTTCGTTCAAGACAGGTGTTTAAGCTACTTTGCCAGACGTTTATCAAA
ATGGGGCTGTTGTCTTCTTTCACTTGTAAGTACGAGTTTAGCTCATTGAGACTACATCAC
AACAGAGCTATTACACACTTAATGAGGTCTGCTAAAGAGAGAGTTTCGTCAGGATCCTTGT
GAGGATATTTCTCGTATCCAGAAAATCAGATCAAGGGAAGTAGCCTTGAAGCACAAACT
TCACGTTACTTAAATGAATTTGAAGAACTTGTCATCTTAGGAAAAGGTGGATACGGAAGA
GTATACAAGGTCAGGAATAAATTAGATGGTCAGTATTATGCAATAAAAAAATCCTGATT
AAGGGTGCAACTAAAACAGTTTGCATGAAGGTCTACGGGAAGTGAAGGTGCTGGCAGGT
CTTCAGCACCCCAATATTGTTGGCTATCACACCGCGTGGATAGAACATGTTTCATGTGATT
CAGCCACGAGCAGACAGAGCTGCCATTGAGTTGCCATCTCTGGAAGTGCTCTCCGACCAG
GAAGAGGACAGAGAGCAATGTGGTGTTAAAAATGATGAAAGTAGCAGCTCATCCATTATC
TTTGCTGAGCCCAACCCAGAAAAAGAAAAACGCTTTGGAGAATCTGACACTGAAATCAG
AATAACAAGTCGGTGAAGTACACCACCAATTTAGTCATAAGAGAATCTGGTGAACCTTGAG
TCGACCCTGGAGCTCCAGGAAAATGGCTTGGCTGGTTTGTCTGCCAGTTCAATTGTGGAA
CAGCAGCTGCCACTCAGGCGTAATTCCCACCTAGAGGAGAGTTTCACATCCACCGAAGAA
TCTTCCGAAGAAAATGTCAACTTTTTGGGTGAGACAGAGGCACAGTACCACCTGATGCTG
CACATCCAGATGCAGCTGTGTGAGCTCTCGCTGTGGGATTGGATAGTCGAGAGAAACAAG
CGGGGCCGGGAGTATGTGGACGAGTCTGCCTGTCTTATGTTATGGCCAATGTTGCAACA
AAAATTTTTCAAGAATTGGTAGAAGGTGTGTTTTACATACATAACATGGGAATTGTGCAC
CGAGATCTGAAGCCAAGAAATATTTTTCTTCATGGCCCTGATCAGCAAGTAAAAATAGGA
GACTTTGGTCTGGCCTGCACAGACATCCTACAGAAGAACACAGACTGGACCAACAGAAAC
GGGAAGAGAACACCAACACATACGTCCAGAGTGGGTACTTGTCTGTACGCTTCACCCGAA
CAGTTGGAAGGATCTGAGTATGATGCCAAGTCAGATATGTACAGCTTGGGTGTGGTCTTG
CTAGAGCTCTTTCAGCCGTTTGGAAACAGAAATGGAGCGAGCAGAAAGTTCTAACAGGTTTA
AGAACTGGTCAGTTGCCGGAATCCCTCCGTAAAAGGTGTCCAGTGCAAGCCAAGTATATC
CAGCACTTAACGAGAAGGAACTCATCGCAGAGACCATCTGCCATTGAGCTGCTGCAGAGT
GAACTTTTCCAAAATTCTGGAAATGTTAACCTCACCCCTACAGATGAAGATAATAGAGCAA
GAAAAAGAAATTGCAGAACTAAAGAAGCAGCTAAACCTCCTTTCTCAAGACAAAGGGGTG
AGGGATGACGGAAAGGATGGGGGCGTGGGATGA

SEQ ID NO: 74_17000057519457_H

CACAAGAGCCCTTCTGTCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGT
AACCCTTACAGGCCGGAAGTGTCCGGGGTGGACGCATTCCGGGTAGCCGAAGAAGTCCCA
GGATTGCCGAAGAAGTCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAG
AGACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTA
CGCCGGCCGATGGCGAGGAGCCCGCCCCGGAGGCTGAGGCTCTGGCCGCAGCCGGGAGC
GGAGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCGTGT
TCCGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACC
GGCACC CGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGCAGGAGGCCCGGGCGC
TCCTCCGCTGTGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTTGTGGACTATGCTT
CCAAGTCTTATATATGGAAGAAATTGAAGGCTCAGTGACTGTTTCGAGATTATATTCAGT
CCACTATGGAGACTGAAAAAACTCCCAGGGTCTCTCCAACCTTAGCCAAGACAATTGGGC

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FIGURE 2III

AGGTTTTGGCTCGAATGCACGATGAAGACCTCATTTCATGGTGATCTCACCACCTCCAACA
TGCTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTT
TCATTTTCAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCC
TCAGTACCCATCCCAACACTGAAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCT
CCTCCAAAAGGCCAGGCCAGTGCTAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAA
AGAGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACCACACACAGTGAAGCTCTTTTT
TCAAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAG
ATATTTTTTAAGTGGTATGTGATCGTGTTCATTATCATCTGCACTTCACTCAAGAGCTTACT
ATGTGTCTAAGTCATGTTCTAGGCAGAATTGGGTATTTAAAGTAAATTGAGGACAGGCTT
CTCCCAGATTGTGACATGTATATCTCAGATACATGGGTGTGGCATTGAACCACATAATGA
GAACATTATTCTCTTTTTAGTCCTTGTGAGACAAGGATGAAGTCTCAGTTGCTGATACTC
GCTGAGCTTACTGGCCCTCTAACCAGTGTTTTTTTTTGTGTTGTTGTTGTGTACATGTTAT
ATTTATTTTGAACACAGTTTAATGGGATACAACCAGCATTTTAAAAAATGAAATAGAATA
CAGCATGGAAAATATCAGTGTATTGTTTTATGAACTTTCACGTGTATATATAGACCAAG
GATATGTGCTGAGTTTTGATGTCAAATATATTTCTCTTTCAGGGTCATGATCAAAAAATG
AAAAGTCTGCTTAACTCCAATTTCTCTTTTAAAAAAGCAGACTTACAGCTTTCAGGCAAC
TGAAATTCATGTTAACATGTTTTTATTTTTATTGCTTTGTATTTTTGTGGTTACCTTCTA
AGACAAGTGATTGATCTAAAGTTCCTTTTAAAGTTTATACCGCTAAACAAACTGAGTTGAT
TTCTATCACAGGCAGTAAGTAGGTAGAGCAAAAATGGTGAAGTGACTTGTGAAGACTGAA
GTTTGATGAAGTCTGGTTTAAAGGCACAGGTAACTGAGTGTGGATGCAAAAGTACCAGGA
GCTAGCTTTTAACTTGCCCAGCCTCAGTTTCTTTTCTTAGAAGAAGCTATGTTTGGGTG
GGAAGGGAAGAGAGGGATAAGAAAATACCTTTCTTCCTTGTAACCTCCAATCAACAAACA
TATTTTGAGTGCCTTTTGTGTTCTTGGCACCCCTGTTGGGTATTGGGTACTTGGCACCCCT
GTTGGGTATTGGGTACAATGGTGAGCCAGACAGACACAGCGCCTGTCTTTTGTAAAGAAT
ATTTATTTTTTATAAAAAAGTATAAAGTATACAGTGGGATGTTTTGATATACATTATGAAA
TGATTGCTACAGCTGAGCTAATTAACACCCATCACCTCACATAGTTACTGTCTTGTCTTCT
TAATATGGACATTTGCAGCTATGAATTTCCCTCTGCACACTGTTGTCATCACACACTCTC
AGTTTTGGTATTTTGTGTTTTTGTTTTCATTCTCAAGTATTTTCTAATTTCCCTTG
TGATTTCTTCTTTGACCCCTTGATTGTTTAGAAATCTGTAAATTTCCACACATTTGTAAA
TGTTCCAATTTTTCTTTTGTATTGCCAGCTTCATTCCATTGTGTTTCAGAGATGATACAG
TCAGTGCCTGTTCTTATGAAGCAAACATTCTATAATAGTAGGACCAGTACCCTGTCTGTT
TCATTACCACAGTCAGCATGCCCAAGTGCCAGCATGGGGCGGATGGCCAGGAATGAG
TGAAAACCTCCCTTCTGGGTAGTTGTGACTAGTAGAGAGGAAAAATAATATAATTGCCT
GCTTACTGCATGCCAGGCATTGGGCTGGGAATTTTTATATTGGATCTAAAATAACTCTTA
AGTTAGGCATTATCCCCATTTTATAGATGGAGAACTGGCCCCAAAAGGTGGGAACCTTGT
CCAAGACGTCACAGGTAGCAAGAGGTACTTTTACCTGGCTCCAAATCTGTGTTCTTTCCA
CTGACAAATGAGATATGGGATATGGTGCATCTTTACAGTACTATAATAAGTATTGGCGTA
TAACATTATTTTTCAAGGAACTCCAAGGGCCACAGGAGCTGACAGGTTTTTCAATTAATAT
TCCCAACATGAATGAGATGCCTCATTCTCAGTTTCTCAGTGTACTATAAGGCTAGTA
CCTGCTTTGTTGGGGTATGGTTGGCTCGTGTGCATTAAGTCAACAAATCCCTAGT

SEQ ID NO: 75_AA013524_M

CTGGTGCAGCAGGGCGCCGAGGCGCGCGTTTTCCGTGGCCGCTTCCAGGGCCGCGCGGCC
GTGGTGAAGCACCCTTCCCGAAGAGTTACCGGCACCCGGAGCTGGAGGCGCGGCTCGGC
CGTCGGCGGACGGTGCAGGAGGCGCGCGCTGCTCCGCTGCCGCCGTGCGGGGATAGCT
GCCCCAGTCGTCTTCTTTGTGGACTATGCGTCTAACTGCTTATATATGGAAGAAATCGAA
GACTCGGTGACTGTTGCGGATTATATCCAATCCACTATGGAGACTGAAAAGGACCCCCAG
TGCTCTTGGACCTGGCCAGGAGGATGGGGCAGGTTCTGGCCGGAATGCACGACCAAGAC
CTCATTACGGGGACCTCACACCTCCAACATGCTCCTGAGGCGGCCCTGGCGCAGCTG
CACATCGTGCTCATCGACTTTGGGCTGAGCTTTGTCTCAGGACTGCCGGAAGATAAAGGC

FIGURE 2JJJ

GTCGACCTCTATGTCCTGGAGAAGGCCTTCCTCAGCACGCACCCCCACACCGAGACCGCG
TTTGAAGCCTTTCTGAAGAGTTACGGGGCCTCGTCCAAGAAGTCCAGTCCAGTGCTGAAG
AAGTTAGATGAGGTGCGCCTGAGAGGGCGAAAGCGGTCCATGGTCGGGTAGTGGAGCTGT
GGTGAAGTGGCTCACGGTGAAGGATGATGTAGACGAGGCTGGACCCCTCAGCAAAGCATG
GGTTGTTAAGTGGTCTGTGATCGTGCTGGGCCACCACCATCCATGGCTCACTGTTCTCAG
GGGCTTCATGTACATGAGGTTTATTCTGGGCAGAACTGGGTAGGTAGCCAGGCTAGCCT
TGAATTTATGGCAACATCCTACCTCAGCTTGCTTGGAAGAGGTTATAAGCCACCATACT
GACTTTGCACTGATTCTGTCAGAAAC

SEQ ID NO: 76_17000139801197_H, IRAKM_H
ATGGCGGGGAACTGTGGGGCCCGCGCGCGCTGTCGGCGCACACGCTGCTGTTTCGACCTG
CCGCCCCGCGCTGCTCGGAGAGCTCTGCGCTGTTCTGGACAGCTGCGACGGCGCGCTGGGC
TGGCGCGGCTGGCAGAGAGACTTTCAAGCAGCTGGCTGGATGTTTCGTCATATTGAAAAG
TATGTAGACCAAGGTAAAAGTGAACAAGAGAATTACTTTGGTCTTGGGCACAGAAAAAC
AAGACCATCGGTGACCTTTTACAGGTCCTCCAGGAGATGGGACATCGTCGAGCTATTTCAT
TTAATTACAACTATGGAGCAGTGTTGAGTCCTTCAGAGAAGAGTTATCAGGAAGGTGGA
TTTCCAAATATATTATTCAAGGAAACAGCCAATGTCACCGTGGATAATGTTCTTATTCT
GAACATAATGAAAAAGGAGTACTGCTTAAATCTTCCATCAGCTTTCAAAATATCATAGAA
GGAAGTAGAAATTTCCACAAAGACTTCCTAATTGGAGAAGGAGAGATTTTTGAGGTATAC
AGAGTGGAGATTCAAAACCTAACATATGCTGTCAAATTTTAAACAGGAGAAAAAATG
CAGTGTAAGAAGCATTGGAAGAGGTTTTTATCTGAGCTTGAAGTTTTACTACTGTTTCAT
CACCCAAACATACTAGAGTTGGCTGCATATTTTACAGAGACTGAGAAGTTCTGTCTGATT
TATCCATACATGAGAAATGGAACACTTTTTTGACAGATTGCAGTGTGTAGGTGACACGGCC
CCACTCCCTTGGCACATTCGAATCGGTATATTAATAGGAATATCCAAAGCCATTCACTAC
CTGCACAACGTTCAACCATGCTCGGTATCTGTGGCAGTATATCAAGTGCAAACATCCTT
TTGGATGATCAGTTTTCAACCCAACTAAGTATTTTGCCATGGCACACTTCCGGTCCCAC
CTAGAACATCAGAGTTGTACCATAAATATGACCAGCAGCAGCAGTAAACATCTGTGGTAC
ATGCCAGAAGAGTACATCAGACAGGGGAACTTTCCATTAAACAGATGTCTACAGCTTT
GGAATTGTAATAATGGAAGTTCTAACAGGATGTAGAGTAGTGTAGATGATCCAAAACAT
ATCCAGCTGCGGGATCTCCTTAGAGAATTGATGGAGAAGAGAGGCCTGGATTTCATGTCTC
TCATTTCTAGATAAGAAAGTGCCTCCCTGCCCTCGGAATTTCTCTGCCAAGCTCTTCTGT
TTGGCAGGCCGGTGTGCTGCAACGCGGGCAAAGTTAAGACCATCAATGGATGAAGTTTTA
AATACTCTTGAAAGTACTCAAGCCAGCTTGTATTTTGTGTAAGATCCTCCACATCACTA
AAGTCCTTCAGGTGTCTTCTCCTCTATTCTGGAGAATGTACCAAGTATTCAGTGGA
GATGATGAAAGCCAGAATAACAATTTACTACCTTCTGATGAAGGCCTGAGGATAGACAGA
ATGACTCAGAAAACCTCTTTTGAATGCAGCCAGTCTGAGGTTATGTTTCTGAGCTTGGAC
AAAAAGCCAGAGAGCAAGAGAAATGAGGAAGCTTGCAACATGCCAGTTCTTCTTGTGAA
GAAAGTTGGTTCCCAAAGTATATAGTTCCATCCCAGGACTTAAGGCCCTATAAGGTAAAT
ATAGATCCTTCTTCAGAAGCTCCAGGGCATTCTTGCAAGGAGCAGGCCAGTGGAGAGCAGC
TGTTCTCCAAATTTTCTGCGGATGAATATGAACAGTACAAAAAGAATAA

SEQ ID NO: 77_AA840598_M IRAKM_M
ATGTGGAAGAGATTTTTATCAGAACTGGAAGTTCTACTCCTGTTCCGTCACCCCCACATA
CTAGAGCTGGCTGCATATTTACGGAGACTGAGAACTTTGTCTGGTTTATCCCTATATG
AGCAACGGGACGCTTTTCGACAGATTACAGTGCACAAATGGCACAACCCCGCTTCTCTGG
CACGTTTGAATCAGCGTATTGATAGGAATAGCCAAAGCCATCCAATACTTGACAACACT
CAGCCGTGCGCCGTCATCTGTGGCAACGTTTCCAGTGCAAACATACTCTTGGATGACCAG
CTCCAACCCAACTAACGGATTTTGCTGCAGCGCACTTCCGACCCAATCTAGAGCAGCAG
AGTTCTACCATAAATATGACCGGCGGTGGCAGGAAACATCTGTGGTACATGCCAGAAGAA

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FIGURE 2KKK

TACATCAGACAGGGAAGACTTTCCGTTAAAACTGATGTCTACAGCTTCGGAATCGTGATC
ATGGAGGTTCTAACGGGCTGCAAAGTGGTGCTGGATGACCCGAAACACGTTACAGCTGCGG
GACCTCCTCATGGAAGTATGATGGAGAAAAGAGGCCTAGACTCCTGCCTGTCCTTCTTAGAC
AGGAAGATAACCACCTGTCTCGGAAGTTCTCTGCAAAGCTCTTCTCTCTGGCGGGCCGG
TGTGTGGCAACGAAGGCCAAGTTAAGACCCACGATGGACGAAGTCCTGTCTCTCTGGAG
AGCACCAGCCTAGCTTGTATTTTGCAGAAGACCCCTCCACGTCCTTGAAGTCCTTCAGG
TGTCTTCTCCTACTGTTCTTGGATAATGTCCCAAGTATTCCAGTAGAAGATGATGAAAAC
CAGAATAACCATTACGTACCTCCCAAGGAAGTTTGGGGACAGATAGAGTGACTCAGAAA
ACCCCTTTTGAATGCAGCCAGTCTGAGGTACCTTTCTAGGCTTGGACCGAAACAGAGGG
AACAGGGGAAGTGAAGCGGATTGCAACGTGCCAGTTCTTCTCATGAGGAATGCTGGTCC
CCAGAGCTTGTGGCGCCATCCAGGACTTAAGTCCTACTGTGATCAGTTTGGGCTCGTCT
TGGGAAGTACCAGGCCATTCTTATGGGAGCAAGCCAATGGAGAAGAGGTGTTCTCTGGG
CTCTTTTGCAGTGAGCATGAACAGTCCAAAAAGCAGTGAATCCACCAGAAGATCAAGCAA
AAAATAAAAGCAAACGTCACTGAAGGCACTGAGCAAATAGCATCCCCGTGAAAAGACACG
AGCTCTGAGCTCCGTGAGTACAGCCAAGGGACCAACTGATGGAGAATTTGAATGGTGCAG
ATTAGCAGCAAGGAAGTCTATTCTTCTCCTCCAAACAGAATAATTTCAAGAGATGCTTTAT
TCAAGTGACCGCTCTCAGTCAAACCTGAGAAGCTAAACTGGAGCCAATCAGAATTATCC
AAGATTCCGGGTTCTGACAACCAAAACCTAGCAAAGAGTAGCAGGACAAGTCTCTCTCTT
AAGTCTCTCACTCTCTCTCATCATCCGAGTGAGATCTTGGTATAGGTGAACAGAGAACCA
CCCACCTTCCAGAACCAGAACCACCTTCTCCCCAAGCCAGCAGTCAGTCACTCACCATCA
GCAGCCAGTAGTCACCAGCAGCCAATCATGATACAGTGTCACTCTCCCTCTGCGCATGCC
CTACGTCTTTTATAAAACCCAGGTCTTCCAGGGCCCAACCCCTTTCTTTTTTCCATCCTTGCT
CAGAGGCAGCCTTTTGTATACATTCCCTGACCCCAACCCCAATTATATCTCTCATATGATA
TCTGTTGCGTAGTGTGACTTTGTGGCATGACTTGGTTGTGAGATCATTGACACAAGAAC
AGCGAATACACAACAACAAGCCACCATCATTACCACCGGCACCTTAATGCTAGTCTTTC
TGCTAGGGATACTGACAGTCTATTGTCTCCCATGGTCATAGGGAAGTTGCTCAAATGCA
AAGGTTGTAGGGAATGTCTAATTTGTAAATGGCGTCGGGTGCCTTTGGAAGGAATTGTGT
TTTTACAGCCAGTTGCTACTCTTGTTTATCGCTGGTTAAACCGGTCTGTCCGGAAGTGAGC
CAAGTCATCCTTGCTAGGGCTTTTTCTGTGTAGAGAGGGAATTCCAGTCCAAAGTCTGCT
TCTCTGTATTTAAATTCTTAGAAGAGTTGCCTGTGGCATTCCAATTGTTATATAAAAAA
TTATATTAAAGAATTCCAGCACT

SEQ ID NO: 78_AA088547_H

ATGGCGAGTGCGGTCAGGGGGTGGAGGCCGTGGCCCEGGCTGGGGCTCCAGCTCCAGTTCC
GCGGCGCTGCTGCTCGGGACGCTGAGTCCACAGGTTTCATACTCTCAGGCCAGAGAACCTC
CTGCTGGTGTCCACCTTGGATGGAAGTCTCCACGCACTAAGCAAGCAGACAGGGGACCTG
AAGTGGACTCTGAGGGATGATCCCGTCATCGAAGGACCAATGTACGTACAGAAATGGCC
TTTCTCTCTGACCCAGCAGATGGCAGCCTGTACATCTTGGGGACCCAAAAACAACAGGGA
TTAATGAAACTGCCATTACCATCCCTGAGCTGGTTTCATGCCTCTCCCTGCCGCAGCTCT
GATGGGGTCTTCTACACAGGCCGGAAGCAGGATGCCTGGTTTGTGGTGGACCCTGAGTCA
GGGGAGACCCAGATGACACTGACCACAGAGGGTCCCTCCACCCCCCGCCTCTACATTGGC
CGAACACAGTATACGGTCACCATGCATGACCCAAGAGCCCCAGCCCTGCGCTGGAACACC
ACCTACCGCCGCTACTCAGCGCCCCCATGGATGGCTCACCTGGGAAATACATGAGCCAC
CTGGCGTCTGCGGGATGGGCCTGCTGCTCACTGTGGACCCAGGAAGCGGGACGGTGCTG
TGGACACAGGACCTGGGCGTGCCTGTGATGGGCGTCTACACCTGGCACCAGGACGGCCTG
CGCCAGCTGCCGCATCTCACGCTGGCTCGAGACACTCTGCATTTCTCGCCCTCCGCTGG
GGCCACATCCGACTGCCTGCCTCAGGCCCCCGGGACACAGCCACCCTCTTCTCTACCTTG
GACACCCAGCTGCTAATGACGCTGTATGTGGGAAGGATGAACTGGCTTCTATGTCTCT
AAAGCACTGGTCCACACAGGAGTGGCCCTGGTGCCTCGTGGACTGACCCTGGCCCCCGCA
GATGGCCCCACCACAGATGAGGTGACACTCCAAGTCTCAGGAGAGCGAGAGGGCTCACCC

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FIGURE 2LLL

AGCACTGCTGTTAGATACCCCTCAGGCAGTGTGGCCCTCCCAAGCCAGTGGCTGCTCATT
GGACACCACGAGCTACCCCCAGTCCTGCACACCACCATGCTGAGGGTCCATCCCACCCCTG
GGGAGTGGAAGTGCAGAGACAAGACCTCCAGAGAATACCCAGGCCCCAGCCTTCTTCTTG
GAGCTATTGAGCCTGAGCCGAGAGAACTTTGGGACTCCGAGCTGCATCCAGAAGAAAAA
ACTCCAGACTCTTACTTGGGGCTGGGACCCCAAGACCTGCTGGCAGCTAGCCTCACTGCT
GTCCTCCTGGGAGGGTGGATTCTCTTTGTGATGAGGCAGGTGGTGGAGAAGCAGCAGGAG
ACCCCCCTGGCACCTGCAGACTTTGCTCACATCTCCAGGATGCCAGTCCCTGCACTCG
GGGGCCAGCCGAGGAGCCAGAAGAGGCTTCAGAGTCCCTCAAAGCAAGCCAGCCACTC
GACGACCCTGAAGCTGAGCAACTCACCGTAGTGGGGAAGATTTCTTCAATCCCAAGGAC
GTGCTGGGCCGCGGGGAGGCGGGACTTTTCGTTTTCCGGGGACAGTTTGAGGGACGGGCA
GTGGCTGTCAAGCGGCTCCTCCGCGAGTGCTTTGGCCTGGTTCGGCGGGAAGTTCAACTG
CTGCAGGAGTCTGACAGGCACCCCAACGTGCTCCGCTACTTCTGCACCCGAGCGGGGACCC
CAGTTCCACTACATTGCCCTGGAGCTCTGCCGGGCCTCCTTGCAGGAGTACGTAGAAAAC
CCGGACCTGGATCGCGGGGGTCTGGAGCCCCGAGGTGCTGCTGCAGCAGCTGATGTCTGGC
CTGGCCCCACCTGCACTCTTTACACATAGTGACCCGGGACCTGAAGCCAGGAAATATTCTC
ATCACCGGGCCTGACAGCCAGGGCCTGGGCAGAGTGGTGTCTCAGACTTCGGCCTCTGC
AAGAAGCTGCCTGCTGGCCGCTGTAGCTTCAGCCTCCACTCCGGCATCCCCGGCACGGAA
GGCTGGATGGCGCCCGAGCTTCTGCAGCTCCTGCCACCAGACAGTCCTACCAGCGCTGTG
GACATCTTCTCTGCAGGCTGCGTGTCTACTACGTGCTTTCTGGTGGCAGCCACCCCTTT
GGAGACAGTCTTTATCGCCAGGCAAACATCCTCACAGGGGCTCCCTGTCTGGCTCACCTG
GAGGAAGAGGTCCACGACAAGGTGGTTGCCCGGGACCTGGTTGGAGCCATGTTGAGCCCA
CTGCCGCAGCCACGCCCCCTCTGCCCCCAGGTGCTGGCCACCCCTTCTTTTGGAGCAGA
GCCAAGCAACTCCAGTTCTTCCAGGACGTGAGTACTGGCTGGAGAAGGAGTCCGAGCAG
GAGCCCCCTGGTGAGGGCACTGGAGGCGGGAGGCTGCGCAGTGGTCCGGGACAACCTGGCAC
GAGCACATCTCCATGCCGCTGCAGACAGATCTGAGAAAGTTCCGGTCCCTATAAGGGGACA
TCAGTGCGAGACCTGCTCCGTGCTGTGAGGAACAAGAAGCACCCTACAGGGAGCTCCCA
GTTGAGGTGCGACAGGCACTCGGCCAAGTCCCTGATGGCTTCGTCCAGTACTTCACAAAC
CGCTTCCACGGCTGCTCCTCCACACGCACCGAGCCATGAGGAGCTGCGCCTCTGAGAGC
CTCTTCTGCCCCCTACTACCCGCCAGACTCAGAGGCCAGGAGGCCATGCCCTGGGGCCACA
GGGAGGTGA

SEQ ID NO: 79_HGP_6644466

GGAGGGTTTCGAATTGCAACGGCAGCTGCCGGGCGTATGTGTTGGTGCTAGAGGCAGCTGC
AGGGTCTCGCTGGGGGCGCTCGGGACCAATTTTGAAGAGGTACTTGGCCACGACTTATT
TTCACCTCCGACCTTTCTTCCAGGCGGTGAGACTCTGGACTGAGAGTGGCTTTCACAAT
GGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTTATCAGAAAAAAGAAATCTGTATT
ATGTTCAACTCCAATAATAATATCCCGGCCTCTCCGTTTATGCAGAAGCTTGGCTTTGG
TACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCAAGAGGTTTGTCTCATTCTCCTTG
GGCTGTAAAAAAGATTAATCCTATATGTAATGATCATTATCGAAGTGTGTATCAAAAGAG
ACTAATGGATGAAGCTAAGATTTTGAAGAGCCTTCATCATCCAACATTGTTGGTTATCG
TGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTTGCTATGGAATATGGAGGTGAAAA
GTCTCTAAATGACTTAATAGAAGAACGATATAAAGCCAGCCAAGATCCTTTTCCAGCAGC
CATAATTTTAAAAGTTGCTTTGAATATGGCAAGAGGGTTAAAGTATCTGCACCAAGAAAA
GAACTGCTTCATGGAGACATAAAGTCTTCAAATGTTGTAATTAAAGGCGATTTTGAAGC
AATTAAAATCTGTGATGTAGGAGTCTCTTACCCTGGATGAAAATATGACTGTGACTGA
CCCTGAGGCTTGTTACATTGGCACAGAGCCATGGAAACCCAAAGAAGCTGTGGAGGAGAA
TGGTGTATTACTGACAAGGCAGACATATTTGCCTTTGGCCTTACTTTGTGGGAAATGAT
GACTTTTATCGATTCCACACATTAATCTTTCAAATGATGATGATGATGAAGATAAACTTT
TGATGAAAGTGATTTTGTATGATGAAGCATACTATGCAGCGTTGGGAACTAGGCCACCTAT
TAATATGGAAGAACTGGATGAATCATACCAGAAAGTAATTGAACTCTTCTCTGTATGCAC

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FIGURE 2MMM

TAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACACATTGTTGAAGCTCTGGAAACAGA
TGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCCTAAATAACTGTTTATTCCAAAATA
TTTACATAGTTACTATCAGTAGTTATTAGACTCTAAAATTGGCATATTTGAGGACCATAG
TTTCTTGTTAACATATGGATAACTATTTCTAATATGAAATATGCTTATATTGGCTATAAG
CACTTGGAATTGTACTGGGTTTTCTGTAAAGTTTTAGAACTAGCTACATAAGTACTTTG
ATACTGCTCATGCTGACTTAAAACACTAGCAGTAAAACGCTGTAACTGTAACTTAAAT
TGAATGACCATTACTTTTATTAATGATCTTTCTTAAATATTCTATATTTTAAATGGATCTA
CTGACATTAGCACTTTGTACAGTACAAAATAAAGTCTACATTTGTTTAAAACACTGAACC
TTTTGCTGATGTGTTTATCAAATGATAACTGGAAGCTGAGGAGAATATGCCTCAAAAAGA
GTAGCTCCTTGATACTTCAGACTCTGGTTACAGATTGTCTTGATCTCTTGATCTCCTC
AGATCTTTGGTTTTTGTCTTAATTTATTAAATGTATTTTCCATACTGAGTTTAAATTTA
TTAATTTGTACCTTAAGCATTTCAGCTGTGTAAAACAATAAACTCAAATAGGATGA
TAAAGAATAAAGGACACTTTGGGTACCAGAAGGTGTCTCAGCATTATTTTATACTTC

SEQ ID NO: 80_AA449542_M

ATCTCCAAGAGGGTTGTCTCATTTCTCCTTGGGCCGTGAAAAAGATAAGTCTTTTATGCGA
TGATCATTATCGAACTGTGTATCAGAAGAGACTAACTGATGAAGCTAAGATTTTAAAAA
CCTTAATCACCCAAACATTATAGGATATCGTGCTTTTACTGAAGCCAGTGATGGTAGTCT
GTGCCTTGCTATGGAGTATGGAGGTGAAAAGTCTCTGAATGACTTAATAGAAGAGCGGAA
CAAAGACAGTGGAAGTCCTTTTCCAGCAGCTGTAATTCTCAGAGTTGCTTTGCACATGGC
CAGAGGGCTAAAGTACCTGCACCAAGAAAAGAAGCTGCTTCATGGAGACATAAAGTCTTC
AAATGTTGTAATTAAAGGTGATTTTGAACAATTAATAATCTGTGATGTAGGAGTCTCTCT
GCCATTGGATGAAAATATGACTGTGACTGATCCTGAGGCCTGTTATATTGGTACTGAGCC
ATGGAAACCCAAGGAAGCGTTGGAAGAAAATGGCATCATTACTGACAAGGCAGATGTGTT
TGCTTTTGGCCTTACTCTGTGGGAAATGATGACTTTATGTATTCCACACGTCAATCTTCC
AGATGATGATGTTGATGAAGATGCAACCTTTGATGAGAGTGACTTCGATGATGAAGCATA
TTATGCAGCTCTGGGGACAAGGCCATCCATCAACATGGAAGAGCTGGATGACTCCTACCA
GAAGGCCATTGAACTCTTCTGTGTGTGCACTAATGAGGATCCTAAAGATCGCCCGTCTGC
TGCACACATCGTTGAAGCTTTGGAAGTAGATGGCCAATGTTGTGGTCTAAGCTCAAAGCA
TTAACTTGATGGGAAGTGTTAACTAGATATATGTAGTTAATATAACTTATGGTAGCTAG
ATTCTAGAAGTAGCTTTAACACTAGTGACCCCTGTCTAAGATGACTTAAGAATCAAGGGA
CCATTGCTTTGTTACAGATCTTTTATAGATATTCTTGCTTCTTTAGTGGGTACTAAAAAT
TTCCTACGTACATGTGGTACAGATATCTGTCTGCTCATAGTGTGAGTCTTTCAGCTGGC
CTGTCAGCCCATGCGCCCTGGGACTTGAGAAGAGTTTATAAACGTAGCTCCTAGGGTGTCT
TTGCCTCTCTACACTTAGCTTCTAATTTATTACTTTGTTTCTACTGATTGTGTCTTAAGT
CTTTTAAATAAATGTAAGAATAAACAATAAAAGACAGTTTTAGTACCAGG

SEQ ID NO: 81_5R57_10_2_M TESK2_M

GCTGCTGGACAGTGACTTGTATTTACCGTGGACTGTGAGAGTGAACTGGCCTATGGCAT
AGCAGTGGGCCTCAGCTACCTTCACTTCAAAGGCATTTTCCATCGGGACCTCACATCAA
GGTGTGAAGGCTTTGCTTTC

SEQ ID NO: 82_AA232253_H

ATGTCGTCTCTCGGTGCCTCCTTTGTGCAAATTAATTTGATGACTTGCAGTTTTTTGAA
AACTGCGGTGGAGGAAGTTTTGGGAGTGTTTATCGAGCCAAATGGATATCACAGGACAAG
GAGGTGGCTGTAAAGAAGCTCCTCAAAATAGAGAAAGAGGCAGAAATACTCAGTGTCTC
AGTCACAGAAACATCATCCAGTTTTATGGAGTAATTCTTGAACCTCCCAACTATGGCATT
GTCACAGAATATGCTTCTCTGGGATCACTCTATGATTACATTAACAGTAACAGAAGTGAG
GAGATGGATATGGATCACATTATGACCTGGGCCACTGATGTAGCCAAAGGAATGCATTAT
TTACATATGGAGGCTCCTGTCAAGGTGATTACAGAGACCTCAAGTCAAGAAACGTTGTT

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FIGURE 2NNN

ATAGCTGCTGATGGAGTATTGAAGATCTGTGACTTTGGTGCCTCTCGGTTCATAACCAT
ACAACACACATGTCCTTGGTTGGAACCTTCCCATGGATGGCTCCAGAAGTTATCCAGAGT
CTCCCTGTGTGAGAACTTGTGACACATATTCTATGGTGTGGTTCTCTGGGAGATGCTA
ACAAGGGAGGTCCCCTTTAAAGGTTTGGGAAGGATTACAAGTAGCTTGGCTTGTAGTGGAA
AAAAACGAGAGATTAACCATTCCAAGCAGTTGCCCCAGAAGTTTTGCTGAACTGTTACAT
CAGTGTGGGAAGCTGATGCCAAGAAACGGCCATCATTCAAGCAAATCATTTCAATCCTG
GAGTCCATGTCAAATGACACGAGCCTTCCTGACAAGTGTAACCTCATTCTACACAACAAG
GCGGAGTGGAGGTGCGAAATTGAGGCAACTCTTGAGAGGCTAAAGAACTAGAGCGTGAT
CTCAGCTTTAAGGAGCAGGAGCTTAAAGAACGAGAAAGACGTTTAAAGATGTGGGAGCAA
AAGCTGACAGAGCAGTCCAACACCCCGCTGCTGCCTTCCTTTGAGATTGGTGCATGGACG
GAAGACGATGTGTATTGGTGGGTTGAGCAGCTCGTCAGAAAAGGTGACTCTTCAGCAGAG
ATGAGTGTATATGCAAGCTTGTTTAAAGAAAACAACATTACAGGGAAGCGGCTGCTGCTG
CTGGAGGAAGAAGACCTGAAAGACATGGGCATTGTCTCCAAGGGGCATATCATTCACTTC
AAGTCAGCCATTGAGAAATTAACCCATGATTACATAAATTTGTTTCACTTCCCACCACTA
ATTAAGGACTCAGGAGGTGAACCTGAAGAAAATGAGGAAAAAATAGTGAACCTGGAACCTG
GTTTTTGGTTTTTCACTTGAAACCAGGAACTGGCCACAGGATTGTAAGTGGAAAATGTAT
ATGGAGATGGATGGGGATGAAATTGCAATAACCTACATAAAAGATGTGACATTCAACACT
AACCTACCTGATGCGGAGATTTTAAAGATGACAAAGCCACCATTGTGAATGGAGAAGTGG
ATTGTAGGAATAGCAAAAAGTCAGACTGTGGAGTGCCTGTGACATATGAGAGTGATGTT
AGAACTCCAAAAAGCACTAAACATGTCCATTTGATTCAAGTGGAGTAGAACAAAACCTCAG
GATGAAGTGAAAGCAGTCCAACCTTGCCATTGAGACATTATTACCAATTCAGATGGCAAC
CCTGGAAGCAGGTCCGACTCAAGTGCTGATTGCCAGTGGTTAGATACTCTGAGGATGCGG
CAGATTGCATCCAACACTTCTTTACAGCGTTCCAGAGCAATCCTATTCTGGGGTCACCG
TTCTTCTCACACTTTGATGGCCAGGATTCTACGCTGCTGCTGTGAGACGGCCCCAGGTG
CCCATTAAGTATCAACAGATTACACCTGTGAACAGTCCAGAAGCTCGTCTCCTACTCAG
TATGGACTGACCAAAAACCTTCTCTTCTTACATCTCAACTCTAGGGACAGTGGCTTTTCC
AGTGGCAATACTGACACCTCTTCAGAGAGGGGTGATACTCAGACAGAAGCAGGAACAAA
TATGGACGTGGTAGTATATCACTCAATTCTTCTCCTAGAGGAAGATACAGTGGAAAGAGT
CAGCATTCCACTCCATCAAGAGGAAGATACCCTGGAAAGTTCTACAGGGTTTCTCAGTCA
GCACTCAATCCTCACCAGTCGCCTGACTTCAAGAGAAGCCCCAGGGACCTCCACCAACCC
AACACCATAACCAGGGATGCCTTTGCACCCTGAGACTGACTCAAGAGCCAGTGAAGAGGAC
AGCAAAGTCAGCGAAGGGGGCTGGACAAAAGTGGAATACCGGAAAAAGCCCCACAGGCCA
TCTCCCGCCAAAACCAATAAAGAGAGAGCCAGAGGGGACCACCGTGGATGGAGAACTTT
TGA

SEQ ID NO: 83_AI375137_H

ATGGGAAATTATAAATCTAGACCAACCCAACTTGTACTGATGAATGGAAGAAAAAGTC
AGTGAATCATATGTTATCACAATAGAAAGATTAGAAGATGACCTGCAGATCAAGGAAAA
GAACTGACAGAATAAGGAATATATTTGGCTCTGATGAAGCCTTCAGTAAAGTCAATTTA
AATTACCGCACTGAAAATGGGCTGTCTCTACTTCATTTATGTTGCATTTGTGGAGGCAAG
AATCACATATTCGAACTCTTATGTTGAAAGGGCTCCGCCCATCTCGACTGACAAGAAAT
GGATTTACAGCCTTGCAATTAGCAGTTTACAAGGATAATGCAGAATTGATCACTTCTCTG
CTTCACAGTGGAGCTGATATACAGCAGGTTGGATACGGTGGCCTCACTGCCCTCCATATT
GCTACAATAGCTGGCCACCTAGAGGCTGCTGATGTGCTGTTGCAACATGGAGCTAATGTC
AATATTCAAGATGCAGTTTTTTTCACTCCATTGCATATTGCAGCGTACTATGGACATGAA
CAGGTAACCTCGCCTTCTTTTGAATTTGGTGCTGATGTAAATGTAAGTGGTGAAGTTGGA
GATAGACCCCTCCACCTAGCATCTGCAAAGGATTCTTGAATATTGCAAACTCTTGATG
GAAGAAGGCAGCAAAGCAGATGTGAATGCTCAAGATAATGAAGACCATGTCCCACTCCAT
TTCTGTTCTCGATTTGGACACCATGATATAGTTAAGTATCTGCTGCAAAGTGATTTGGAA
GTTCAACCTCATGTTGTTAATATCTATGGAGATACCCCTTACACCTGGCATGCTACAAT

FIGURE 2000

GGCAAATTTGAAGTTGCCAAGGAAATCATCCAAATATCAGGAACAGAAAGTCTGACTAAG
GAAACATCTTCAGTGAAACAGCTTTTCATAGTGCTTGTACCTATGGCAAGAGCATTGAC
CTAGTCAAATTTCTTCTTGATCAGAATGTCATAAACATCAACCACCAAGGAAGGGATGGG
CACACTGGATTACACTCTGCTTGCTACCACGGTCACATTCGCCTGGTTCAGTTCTTACTG
GATAATGGAGCTGATATGAATCTAGTGGCTTGTGATCCCAGCAGGTCTAGTGGTGAAAAA
GATGAGCAGACATGTTTGATGTGGGCTTATGAAAAAGGGCATGATGCCATTGTCACACTC
CTGAAGCATTATAAGAGACCACAAGATGAATTGCCCTGTAATGAATATTCTCAGCCTGGA
GGAGATGGCTCCTATGTGTCTGTTCCATCACCTTGGGGAAGATTAAAAGCATGACAAAA
GAGAAGGCAGATATTCTCCTCCTAAGAGCTGGATTGCCTTCACATTTCCATCTTCAGCTC
TCAGAAATTGAGTTCCATGAGATTATTGGCTCAGGTTCTTTTGGGAAAGTATATAAAGGA
CGATGCAGAAATAAAATAGTGGCTATAAAACGTTATCGAGCCAATACCTACTGCTCCAAG
TCAGATGTGGATATGTTTTGCCGAGAGGTGTCCATTCTCTGCCAGCTCAATCATCCCTGC
GTAATTCAGTTTGTGGGTGCTTGCTTGAATGATCCCAGCCAGTTTGCCATTGTCACTCAA
TACATATCAGGGGGTTCTCTGTTCTCCCTCCTTCATGAGCAGAAGAGGATTCTTGATTTG
CAGTCTAAATTAATTATTGCAGTAGATGTTGCCAAAGGCATGGAGTACCTTCACAACCTG
ACACAGCCAATTATACATCGTGACTTGAACAGTCACAATATTCTTCTCTATGAGGATGGG
CATGCTGTGGTGGCAGATTTTGGAGAATCAAGATTTCTACAGTCTCTGGATGAAGACAAC
ATGACAAAACAACCTGGGAACCTCCGTTGGATGGCTCCTGAGGTGTTACCGCAGTGCCT
CGGTACACCATCAAAGCAGATGTCTTCAGCTATGCTCTGTGTCTGTGGGAAATTCTCACT
GGCGAAATTCCATTGCTCATCTCAAGCCAGCGGCTGCGGCAGCAGACATGGCTTACCAC
CACATCAGACCTCCCATTTGGCTATTCCATTCCCAAGCCCATATCATCTCTGCTGATACGA
GGGTGGAACGCATGTCCTGAAGGAAGACCCGAATTTTCTGAAGTTGTCATGAAGTTAGAA
GAGTGTCTCTGCAACATTGAGCTGATGTCTCCTGCATCAAGTAACAGCAGTGGGTCTCTC
TCACCTTCTTCTTCTTCTGATTGCCTGGTGAACCGGGGAGGACCTGGCCGGAGTCATGTG
GCAGCATTAAAGAGTCGTTTCGAATTGGAATATGCTCTAAATGCAAGGTCTATGCTGCT
TTGTCCCAAAGTGCTGGACAATATTCCTCTCAAGGTCTGTCTTTGGAGGAGATGAAAAGA
AGTCTTCAATACACACCCATTGACAAATATGGCTATGTATCCGATCCCATGAGCTCAATG
CATTTTCATTCTTGCCGAAATAGTAGCAGCTTTGAGGACAGCAGCTGA

SEQ ID NO: 84_H97685_H

ATGATTTCTTGCTGTNATAACCTATGCACTCACAAAGATGAACTCTCTGAGAGGGATGA
GCAAGAGCTTCAGGAAATCCGAAAGTATTTCTCCTTTCTGTATTCTTTTTCAAAGTGCC
GAACTGGGCTCGGAGATAATAGACTCCTCAACCAGGAGAATGGAGAGCGAAAGATCACC
GCTTTATCGCCAGCTAATTGACCTGGGCTATCTGAGCAGCAGTCACTGGAAGTGTGGGGC
TCCTGGCCAGGATACTAAAGCTCAGAGCATGTTGGTGAACAGAGTGAAAAGCTGAGACA
CTTGAGCACATTTTCTCACCAGGTGTTACAGACTCGCCTGGTGGATGCAGCCAAGGCCCT
GAACCTGGTGCCTGCACTGCCACTGCCTTGACATCTTTATTAACCAGGCATTTGACATGCAGCG
GGACCTGCAGATCACTCCCAAACGTCTGGAATATACTCGAAAAAAGGAGAATGAGTTGTA
TGAATCATTGATGAATATTGCCAACCAGGAGGAGGAAATGAAGGATATGATTGTTGA
GACACTTAATACCATGAAGGAGGAACTTCTGGATGATGCTACTAACATGGAGTTTAAAGA
CGTCATTGTCCCTGAGAATGGAGAACCAGTAGGCACCAGAGAGATCAAATGCTGCATCCG
ACAGATCCAGGAACTCATCATCTCCCGACTTAATCAGGCAGTGGCTAATAAGCTGATCAG
CTCAGTGGATTACCTGAGGGAAAGCTTCGTCGGAACCTGGAACGATGTCTGCAGAGCCT
GGAGAAGTCTCAGGATGTCTCAGTTCACATCACAGTAATTATCTCAAACAGATCTTAAA
TGCTGCCTATCATGTTGAAGTCACGTTTCACTCAGGGTCTGTCAGTTACAAGGATGCTATG
GGAGCAAATCAAACAGATCATCCAGCGCATCACATGGGTGAGCCACCTGCCATCACTCT
GGAATGGAAGAGGAAGGTGGCCAGGAAGCCATTGAGAGCCTCAGCGCCTCCAAATTGGC
TAAGAGCATTGTCAGCCAATTCCGACTCGGCTCAATAGTTCCACGAGGCTTTTGCAGC
CTCCTTGCGGCAGCTGGAAGCTGGCCACTCAGGCCGTTAGAGAAAACGGAAGATCTATG
GCTGAGGGTTCGGAAGATCATGCTCCCCGCCTGGCCCCGCTTTCTCTGGAAGCCGTTT

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FIGURE 2PPP

TTTACAGGATGTCTTGCTTCATCGTAAACCTAAACTGGGACAGGAACTGGGCCGGGGCCA
GTATGGTGTGGTATACCTGTGTGACAACTGGGGAGGACACTTCCCTTGTGCCCCCAAATC
AGTTGTCCCTCCAGATGAGAAGCACTGGAATGATCTGGCTTTGGAATTTCACTATATGAG
GTCTCTGCCGAAGCATGAGCGATTGGTGGATCTCCATGGTTTCAGTCATTGACTACAACCTA
TGGTGGTGGCTCCAGCATTGCTGTGCTCCTCATTATGGAGCGGCTACACCGGGATCTCTA
CACAGGGCTGAAGGCTGGGCTGACCCCTGGAGACACGTTTGCAGATAGCACTAGATGTGGT
GGAGGGAATCCGCTTCCTGCACAGCCAGGGACTTGTCCATCGTGATATCAAACCTGAAAAA
TGTGCTGCTGGATAAGCAGAACCGTGCCAAGATCACTGACTTAGGATTCTGCAAGCCAGA
GGCCATGATGTCAGGCAGCATTGTGGGGACACCAATCCATATGGCCCCCTGAACTTTTCAC
AGGGAAGTACGATAATTCCGTGGATGTCTACGCTTTTGGAAATCTTTTCTGGTATATCTG
CTCAGGCTCTGTCAAGCTCCCTGAGGCATTTGAGAGGTGTGCTAGCAAAGACCATCTCTG
GAACAATGTGCGGAGGGGGGCTCGCCCAAGACGTTCTCCTGTGTTTGATGAGGAGTGCTG
GCAGTTGATGGAAGCCTGTTGGGATGGCGACCCCTTGAAGAGGCCTCTCTTGGGCATTGT
CCAGCCCATGCTCCAGGGCATCATGAATCGGCTCTGCAAGTCCAATTCTGAGCAGCCAAA
CAGAGGACTAGATGATTCTACTTGAAAGCAAAGACCTTTCTCTTTCACTCTCTAGTTATT
TCCTTCCCCCTCACCATTGCGCCATGGGGAGAATTTGACATTTATTCACTATAGGACACA
CTCCCAAGGGAACCTGGTGTCTGCTGGGAAACTTGGAACCTTCCAGGCAGGGATGACTCC
TGGACAGTGAAGAGTTGAATGACTGAGCATATTCAGCAGCTCACTGAAGCGCCAAGCTAT
CCCTTTAGCAAAAAAGTGTCTCAGATGTGTAAAGCTGAGGAATGTGGTGTCTGGCTTC
ACAAATGAAAAGGAGGCAGATGTT

SEQ ID NO: 85_W20810_M

TTGATGTCAACCTGAAGGCTTCTAAAGCGAGTGATGTCTACAGCTTTGGGATCCTCGTGT
GGGCAGTGCTGGCTGGCAGAGAAGCTGAGTTGGTAGACAAGACTTCACTAATCCGGGAAA
CAGTGTGTGACAGGCAGAGTCGTCCTCCACTGACAGAGCTGCCTCCAGGTAGCCCTGAGA
CTCCCGGCTTGGA AAAACTGAAGGAGTTAATGATTCAATTGCTGGGGTTCCAGTCCGAAA
ACAGGCCATCCTTCCAGGACTGCGAACC AAAAACC AATGAAGTTTACAATCTGGTAAAGG
ACAAGGTAGATGCTGCTGTCTCCGAGGTAAAGCATTATCTGTCTCAGCACAGAAGCAGCG
GCAGAACTTGTCTGCCAGAGAGCC AAGCC AAGAGGCACAGAAATGGATTGCCCGAGGG
AAACCATGGTTTCTAAATGCTGGACCGCCTGCATTTGGAGGAACCTCCGGACCAGTTC
CTGGAAATGTCTTGAGAGGCAAGCACAGGACACATCAGTTGGGCCTGCCACACCAGCAA
GGACATCTTCTGACCCCGTGGCTGGCACTCCTCAGATTCCACATACTTTACCCTTCAGAG
GCACAACACCTGGGCCAGTCTTTACTGAGACTCCCGGTCTCACCCCCAAAGGAATCAGG
GAGATGGAAGACACGGCACTCCTTGGTATCCCTGGACCCACCGAATCCAATGACAGGGC
CACCGGCTCTCGTCTTCAACAACCTGTTCTGAAGTGCAGATTGGGAACTACAACCTCCTTGG
TAGCACCACCAAGAACTACTGCCTCAAGTTCGGCCAAGTATGACCAAGCACAGTTCGGCA
GGGGTAGGGGCTGGCAGCCCTTCCACAAGTAGACTTCAGAGAATCACTGCAAGAGCCTGA
AGTGTGCCATTACAGCGTGGCAATAAAAAGCACGTTTTTAAGCAACCTGGACTGGCTAAGAC
AGTCCTTGCCACTTCCTGAAGCTCACAACATTCTGTGAGGACAGTTGGACCTACACCCAA
ACTGACTCTTGACCCATCTCCTTAAAGTCAATAAACATAGCATGTTAACTGTG

SEQ ID NO: 86_AA744236_H

ATGGGATCAGAGAACAGTGCTTTAAAGAGCTATACACTGAGAGAACCACCATTTACCTTA
CCCTCTGGACTTGCTGTTTATCCCGCTGTACTGCAAGATGGCAAATTTGCTTCAGTTTTT
GTGTATAAGAGAGAAAATGAAGACAAGGTTAATAAAGCTGCCAAGCATTGGAAGACACTT
CGTACCCCTTGCTTGCTAAGATTTTTATCTTGTACTGTGGAAGCGGATGGCATTTCATCTT
GTCAGTGAGCGAGTACAGCCCCTGGAAGTGGCTTTGGAAACATTGTCTTCTGCAGAGGTC
TGTGCTGGGATCTATGACATATTGCTGGCTCTTATCTTCTTCATGACAGAGGACACCTA
ACACACAATAATGTCTGTTTATCATCTGTGTTTGTGAGTGAAGATGGACACTGGAAGCTA
GGAGGAATGGAACTGTTTGTAAGTTTCTCAGGCCACACCAGAGTTTCTGAGGAGTATT

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FIGURE 2QQQ

CAGTCAATAAGAGACCCAGCATCTATCCCTCCTGAAGAGATGTCTCCAGAATTCACAAC
CTCCCAGAGTGTGATGGACATGCCCGGGATGCCTTTTTCATTTGGAACATTGGTGGAAAGT
TTGCTCACAATCTTAAATGAACAGGTTTCAGCGGATGTTCTCTCCAGCTTTCAACAGACC
TTGCACTCAACTTTGCTGAATCCCATTTCCAAAATGTCGGCCAGCGCTCTGCACCTTACTA
TCTCATGACTTCTTCAGAAATGATTTTCTGGAAGTTGTGAATTTCTTGAAAAGTTTAAAC
TTGAAGAGTGAAGAGGAGAAAACGGAATTCCTTAAATTTCTGCTGGACAGAGTCAGCTGC
TTGTCAGAGGAATTGATAGCTTCAAGGTGGTGCCTCTTCTGCTTAATCAGTTGGTGT
GCAGAGCCAGTGGCTGTTAAGAGTTTTCTTCTTATCTGCTTGGCCCCAAAAAGATCAT
GCGCAGGGAGAAAACCTTGCTTGCTCTCACCAGCCCTGTTCCAGTCACGGGTGATCCCC
GTGCTTCTCCAGTTGTTTGAAGTTCATGAAGAGCATGTGCGGATGGTGTGCTGTCTCAC
ATCGAGGCCCTACGTGGAGCACTTCACTCAGGAGCAGCTGAAGAAAGTCATCTTGCCACAG
GTTTTGCTGGGCCTGCGTGATACTAGCGATTCCATTGTGGCAATTACTCTGCATAGCCTA
GCAGTGCTGGTCTCTCTGCTTGGACCAGAGGTGGTTGTGGGAGGAGAACGAACCAAGATC
TTCAAACGCACTGCCCCAAGTTTACTAAAAATACTGACCTTCTCTAGAAGGCGATCCA
TTTTCTCAGCCTATTAAATTTCCATAAATGGACTCTCAGATGTAAAAATACTTCGGAG
GACAGTGAAAACCTCCCATCAAGTCTAAAAAGTCTGAGGAGTGGCCTGACTGGAGTGAA
CCTGAGGAGCCTGAAAATCAAACGTCAACATACAGATTTGGCCTAGAGAACCTTGTGAT
GATGTCAAGTCCAGTGCCTACCTTGGATGTGGAAGAGTCATCTTGGGATGACTGCGAG
CCCAGCAGCTTAGATACTAAAGTAAACCCAGGAGGTGGAATCACTGCTACAAAACCTGTT
ACCTCAGGGGAGCAGAAGCCTATTCCTGCTTTGCTTTCACTCACTGAAGAGTCTATGCCT
TGGAATCAAGCTTACCCCCAAAAGATTAGCCTTGTAACAAAGGGGGGATGACGCAGACCAA
ATCGAGCCGCCAAAAGTGTATCACAAGAAAGGCCCTTAAGGTTCCATCAGAACTTGGT
TTAGGAGAGGAATTCACCATTCAAGTAAAAAAGAAGCCAGTAAAGATCCTGAGATGGAT
TGGTTTGCTGATATGATCCCAGAAATTAAGCCTTCTGCTGCTTTTCTTATATTACCTGAA
CTGAGGACAGAAATGGTCCCCAAAAGGATGATGTCTCCCCAGTGATGCAGTTTCTCTCA
AAATTTGCTGCAGCAGAAATTACTGAGGGAGAGGCTGAAGGCTGGGAAGAAGAAGGGGAG
CTGAACCTGGGAAGATAATAACTGGTGA

SEQ ID NO: 87_AI052250_H

AGCGGCCGCGGGGCGGGCGGAGGATATGGAGTAAAGCCAGAGTCAGTGGCCAGGCACGAA
GGCAGAGCAGGAACAGCCAGGAGCGTTTATTAGGGGGGCGGGGGGAAAGAGCCCCAGCA
CCGCCCTCCTGGAAGAAGGAAGAGGTAACATACTACCCAATATTGCAGCCATGGAGT
CCATGCTTAATAAATTGAAGAGTACTGTTACAAAAGTCACAGCTGATGTCACTAGTGCGG
TAATGGGAATTCCTGTCACTAGAGAATTTGATGTTGGTCGACACATTGCCAGTGGTTGCA
ATGGGCTAGCTTGGAAGATTTTTAATGGCACAAAAAAGTCAACAAAGCAGGAAGTGGCAG
TTTTTGCTCTTTGATAAAAACTGATTGACAAGTATCAAAAATTTGAAAAGGATCAAATCA
TTGATTCTCTAAACGAGGAGTCCAACAGTTAACTCGGCTTCGACACCCTCGACTTCTTA
CTGTCCAGCATCCTTTAGAAGAATCCAGGGATTGCTTGGCATTTTGTACAGAACCAAGTTT
TTGCCAGTTTAGCCAATGTTCTTGGTAACTGGGAAAATCTACCTTCCCCTATATCTCCAG
ACATTAAGGATTATAAACTTTATGATGTAGAAACCAAATATGGTTTGGCTTCAGGTTTCTG
AAGGATTGTCAATTCTTGATAGCAGTGTGAAAATGGTGCATGGAAATATCACTCCTGAAA
ATATAATTTTGAATAAAAGTGGAGCCTGGAAAATAATGGGTTTTGATTTTTGTGTATCAT
CAACCAATCCTTCTGAACAAGAGCCTAAATTTCTTGTAAAGAATGGGACCCAAATTTAC
CTTCATTGTGTCTTCCAAATCCTGAATATTTGGCTCCTGAATACATACTTTCTGTGAGCT
GTGAAACAGCCAGTGATATGTATTCTTTAGGAACTGTTATGTATGCTGTATTTAATAAAG
GGAAACCTATATTTGAAGTCAACAAGCAAGATATTTACAAGAGTTTCAGTAGGCAGTTGG
ATCAGTTGAGTCGTTTAGGATCTAGTTCACTTACAAATATACCTGAGGAAGTTCGTGAAC
ATGTAAAGCTACTGTTAAATGTAACCTCCGACTGTAAGACCAGATGCAGATCAAATGACAA
AGATTCCCTTCTTTGATGATGTTGGTGCAGTAACACTGCAATATTTTGATACCTTATTCC
AAAGAGATAATCTTCAGAAATCACAGTTTTTCAAAGGACTGCCAAAGGTTCTACCAAAC

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FIGURE 2RRR

TGCCCAAGCGTGTCATTGTGCAGAGAATTTTGCCTTGTTTGA CTTCAGAATTTGTAAACC
CTGACATGGTACCTTTTGT TTTGCCCAATGTTCTACTTATTGCTGAGGAATGCACCAAAG
AAGAATATGTCAAATTAATTCTTCCTGAACTTGGCCCTGTGTTTAAGCAGCAGGAGCCAA
TCCAGATTTTGTTAATTTTCTTACAAAAAATGGATTTGCTACTAACC AAAACCCCTCCTG
ATGAGATAAAGAACAGTGTTCTACCCATGGTTTACAGAGCACTAGAAAGCTCCTTCCATTC
AGATCCAGGAGCTCTGTCTAAACATCATTCCAACCTTTGCAAATCTTATAGACTACCCAT
CCATGAAAAACGCTTTGATACCAAGAATTAAAAATGCTTGCTACAAACATCTTCCCTTGC
GGTTCGTGTAAATTCATTAAACAACATTGGAGCAGACCTTCTGACTGGCAGTGAGTCCG

SEQ ID NO: 88_AA278842_H

GGCGCGCCAGATATCACACGTGCCAAGGGGCTGGCTCAGCCCCGGCTCGGGCGGCCGGAG
GACCCGGAGCTAAGGCGCCCGAACCCGCGGCGGCGGTGGGGACGATGTGGTTCTTTGCC
GGGACCCGGTCCGGGACTTTCCGTTTCGAGCTCATCCCGAGCCCCCAGAGGGCGGCCTGC
CCGGGCCCTGGGCCCTGCACCGCGGCCGCAAGAAGGCCACAGGCAGCCCCGTGTCCATCT
TCGTCTATGATGTGAAGCCTGGCGCGGAAGAGCAGACCCAGGTGGCCAAAGCTGCCTTCA
AGCGCTTCAAAACTCTACGGCACCCCAACATCCTGGCTTACATCGATGGACTGGAGACAG
AAAAATGCCTCCACGTCGTGACAGAGGCTGTGACCCCGTTGGGAATATACTTCAAGGCGA
GAGTGGAGGCTGGTGGCCTGAAGGAGCTGGAGATCTCCTGGGGCTACACCAGATCGTGA
AAGCCCTCAGCTTCTGGTCAACGACTGCAGCCTCATCCACAACAATGTCTGCATGGCCG
CCGTGTTCTGTGGACCGAGCTGGCGAGTGGAAGCTTGGGGGCTGGACTACATGTATTCCG
CCCAGGGCAACGGTGGGGGACCTCCCCGCAAGGGGATCCCCGAGCTTGAGCAGTATGACC
CCCCGGAGTTGGCTGACAGCAGTGGCAGAGTGGTCAGAGAGAAGTGGTCAGCAGACATGT
GGCGCTTGGGCTGCCTCATTTGGGAAGTCTTCAATGGGGCCCTACCTCGGGCAGCAGCCC
TACGCAACCCTGGGAAGATCCCCAAAACGCTGGTGGCCCATTA CTGTGAGCTGGTGGGAG
CAAACCCCAAGGTGCGTCCCAACCCAGCCCGCTTCTTGCAGAACTGCCGGGCACCTGGTG
GCTTCATGAGCAACCGCTTTGTAGAAACCAACCTCTTCTGGAGGAGATT CAGATCAAAG
AGCCAGCCGAGAAGCAAAAATTCTTCCAGGAGCTGAGCAAGAGCCTGGACGCATTCCCTG
AGGATTTCTGTGCGCACAAAGGTGCTGCCCCAGCTGCTGACCGCCTTCGAGTTCGGCAATG
CTGGGGCCGTTGTCCTCACGCCCCCTCTTCAAGGTGGGCAAGTTCCTGAGCGCTGAGGAGT
ATCAGCAGAAGATCATCCCTGTGGTGGTCAAGATGTTCTCATCCACTGACCGGGCCATGC
GCATCCGCTCCTGTCAGCAGATGGAGCAGTTCATCCAGTACCTTGACGAGCCAACAGTCA
ACACCCAGATCTTCCCCACGTCGTACATGGCTTCTTGGACACCAACCTGCCATCCGGG
AGCAGACGGTCAAGTCCATGCTGCTCCTGGCCCCAAAGCTGAACGAGGCCAACCTCAATG
TGGAGCTGATGAAGCACTTTGCACGGCTACAGGCCAAGGATGAACAGGGCCCCATCCGCT
GCAACACCACAGTCTGCCTGGGCAAAATCGGCTCCTACCTCAGTGCTAGCACCAGACACA
GGGTCCTTACCTCTGCCTTCAGCCGAGCCACTAGGGACCCGTTTGCACCGTCCCGGGTTG
CGGGTGTCTGGGCTTTGCTGCCACCCACAACCTCTACTCAATGAACGACTGTGCCCGAGA
AGATCCTGCCTGTGCTCTGCGGTCTCACTGTAGATCCTGAGAAATCCGTGCGAGACCAGG
CCTTCAAGGCCATTTCGAGCTTCTGTCCAAATTGGAGTCTGTGTGCGAGGACCCGACCC
AGCTGGAGGAAGTGGAGAAGGATGTCCATGCAGCCTCCAGCCCTGGCATGGGAGGAGCCG
CAGCTAGCTGGGCAGGCTGGGCCGTGACCGGGGTCTCCTCACTCACCTCCAAGCTGATCC
GTTTCGACCCCAACCACTGCCCCAACAGAAACCAACATTCCCCAAAGACCCACGCCTGAAG
GAGTTCCTGCCCCAGCCCCCACCCTGTTCTGCCCCCTACAACCTCAGGCCACTGGG
AGACGCAGGAGGAGGACAAGGACACAGCAGAGGACAGCAGCACTGCTGACAGATGGGACG
ACGAAGACTGGGGCAGCCTGGAGCAGGAGGCCGAGTCTGTGCTGGCCCAGCAGGACGACT
GGAGCACCGGGGGCCAAGTGAGCCGTGCTAGTCAGGT CAGCAACTCCGACCACAAATCCT
CCAAATCCCCAGAGTCCGACTGGAGCAGCTGGGAAGCTGAGGGCTCCTGGGAACAGGGTT
GGCAGGAGCCAAGCTCCCAGGAGCCACCTCCTGACGGTACACGGCTGGCCAGCGAGTATA
ACTGGGGTGGCCAGAGTCCAGCGACAAGGGCGACCCCTTCGCTACCCTGTCTGCACGTC
CCAGCACCCAGCCGAGGCCAGACTCTTGGGGTGAGGACAACCTGGGAGGGCCTCGAGACTG

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FIGURE 2SSS

ACAGTCGACAGGTCAAGGCTGAGCTGGCCCCGAAGAAGCGCGAGGAGCGGCGGGGAGA
TGGAGGCCAAACGCGCCGAGAGGAAGGTGGCCAAGGGCCCCATGAAGCTGGGAGCCCGGA
AGCTGGACTGAACCGTGGCGGTGGCCCTTCCCGGTGCGGAGAGCCCGCCCCACAGATGT
ATTTATTGTACAAACCATGTGAGCCCGGCCGCCCAGGCCAGGCCATCTCACGTGTACATA
ATCAGAGCCACAATAAATTCTATTTTAC

SEQ ID NO: 89_AA599286_H

ATGGCCTTCATGGAGAAGCCGCCAGCCGGCAAGGTGCTGCTGGACGACACGGTGCCGCTG
ACAGCAGCCATCGAGGCGAGCCAGAGCCTGCAGTCCCACACGGAATATATTATTCGAGTG
CAAGGAGGAATTTCTGTGGAAAACAGCTGGCAGATTGTTAGAAGATACAGTGACTTTGAT
TTGCTTAACAACAGCTTACAGATTGCAGGCCTAAGTCTACCTCTTCCTCCCAAAAATTG
ATTGGTAACATGGATCGTGAATTCATAGCTGAAAGGCAGAAAGGTCTTCAGAACTATCTC
AACGTGATCACAACAAATCATATCTTGTCTAATTGTGAGCTGGTTAAGAAGTTTTTAGAT
CCAAACAACACTATTCGCAAACTATACTGAGATTGCCTTGCAACAGGTTTCCATGTTCTTC
CGATCAGAGCCAAAGTGGGAGGTGGTGGAACTTTGAAAGACATAGGTTGGAGAATAAGG
AAGAAATATTTCTTGATGAAGATTAAAAATCAGCCAAAGGAACGGCTAGTGTAAAGCTGG
GCTGACCTTGGCCCAGACAAGTATTTGTGAGATAAAGATTTTTCAGTGTCTAATCAAACCTT
CTGCCTTCTTGTGTTGACCCCTTACATCTATCGGGTTACCTTTGCCACAGCTAATGAATCC
TCAGCGTTGCTAATTAGGATGTTTAAACGAAAAGGGAACATTGAAGGATCTGATCTACAAG
GCAAAACCAAAAGACCCATTTCTAAAGAAGTACTGCAACCCTAAGAAGATTCAGGGCCTG
GAACTCCAGCAAATAAAAACATATGGACGGCAAATATTAGAGGTACTGAAGTTTCTTCAT
GACAAGGGATTCCCTTATGGGCATCTTCACGCCTCCAATGTGATGCTCGATGGGGACACT
TGCCGGCTGCTGGACCTTGAGAATTCCTTATTGGGCCTGCCTTCCTTCTACCGATCTTAT
TTTTCACAATTCAGGAAAATCAATACATTGGAAAGTGTGGATGTCCACTGCTTTGGCCAC
TACTGTATGAAATGACTTATGGACGACCGCCAGACTCGGTGCCTGTGGACTCCTTCCCT
CCTGCCCCGTCCATGGCTGTGGTGGCCGTGTTGGAGTCTACGCTGTCTTGTGAAGCCTGT
AAAAATGGCATGCCTACCATCTCCCGCTCTTACAGATGCCATTATTACGCGATGTTTTA
CTAACCCTTCTGAAAAACCACAGTTTAAAGATCCCTACAAAGTTAAAGAGGCATTGAGA
ATTGCCAAAGAATGTATAGAGAAGAGACTAATTGAGGAACAGAAACAGATTCACCAGCAT
CGAAGACTGACAAGAGCTCAGTCCCACCATGGATCTGAGGAGGAAAGAAAAAAGAAAG
ATTTTAGCTCGAAAGAAGTCAAAACGATCTGCTCTTGAAAATAGTGAAGAGCATTACGCG
AAGTACAGCAACTCCAATAATTACAGCAGGATCTGGGGCCAGCTCACCTCTCACGTCCCCG
TCATCGCCAACTCCACCCTCTACATCAGGGATATCTGCATTACCTCCACCTCCTCCACCT
CCACCACCACCAGCAGCTCCCTTGCTCCTGCGAGCACCGAGGCACCTGCCAGCTCTCG
TCTCAGGCTGTGAATGGCATGAGCCGAGGGGCTTGCTCAGCTCCATCCAGAATTTCAA
AAAGGAACTTTGAGGAAAGCCAAACCTGTGATCACAGTGCTCCGAAGATCGGCTGAAGCT
TCCTGTTTACACTTGAGGGGAAAAGTTCTTTTTTTATTCTACTACCCCTACCCCCAAC
TACCCTCTTCTGGGAAAGTAATTGCTGAGCCAGTACAGCCACAAACAGTACTATTTTGC
AGATGCTCATGTAAGCAGCTTTTCGAGAGAAATAATTCTTTAAGCAGAATAAAGTTAGGC
TGGCATGCAAAAAAAAAAAAAAAAAAAAAA

SEQ ID NO: 90_AA425725_H

ATGAGCGCCAGCACGGGCGGTGGTGGGGACAGCGGCGGCAGCGGCGGCAGTAGCAGCAGC
TCACAGGCCTCCTGCGGGCCCGAGTCTCGGGCTCCGAACTAGCCCTGGCCACACCGGTG
CCTCAGATGCTGCAGGGCCTTCTGGGCTCCGACGACGAGGAACAGGAAGACCCCAAAGAC
TACTGCAAGGGCGGCTACCACCCTGTGAAGATCGGCGACGTGTTCAATGGGCGGTACCAC
GTGGTGCGCAAACCTGGGCTGGGGCCACTTCTCCACCGTCTGGCTCTGCTGGGACATCCAG
CGCAAGCGCTTTGTGGCCCTCAAAGTGGTGAAGAGTGCGGGGCATTACACGGAGACAGCT
GTGGATGAGATCAAGCTCCTGAAATGTGTCCGGGACAGCGACCCAGTGACCCCAAAGA
GAGACCATTGTCCAGCTCATTGATGACTTCAGGATCTCAGGAGTCAATGGAGTCCATGTG

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FIGURE 2TTT

TGCATGGTGTCTGGAGGTGCTGGGCCACCAGCTCCTCAAATGGATCATCAAGTCCAACTAC
CAGGGCCTGCCCCTGCCCTGCGTGAAGAGCATCGTGAGGCAGGTGCTGCACGGCCTGGAC
TACCTCCACACCAAGTGCAAGATCATCCACACGGACATCAAGCCCCGAGAACATCTTGCTG
TGTGTGGGGGACGCTTACATCAGGCGCCTGGCTGCCGAGGCCACGGAGTGGCAACAGGCA
GGGGCGCCGCCCCCTCCCGCTCCATAGTCAGCACTGCCCCCAGGAGGTCTTGACCGGT
AAGCTGTCCAAAAACAAGAGGAAGAAGATGAGGGCGCAAACCGGAAACAGCAGAAGCGGCTG
CTGGAGGAGCGGCTGCGGGACCTGCAGAGGCTGGAGGCCATGGAGGCTGCCACCCAGGCT
GAGGACTCTGGCTTGAGACTAGACGGGGGCGAGCGGCTCCACATCCTCTTCAGGCTTCTCC
GGCTCCCTCTTCTCTCCTGCCTCCTGCTCCATCCTCTCCGGCTCGTCCAATCAGCGAGAG
ACCGGGGGCCTCCTGTGCGCTAGCACACCATTCCGGTGCCTCGAACCTCCTGGTGAACCCC
CTGGAGCCCCAAAATGCAGATAAGATCAAGATCAAGATCGCAGACCTGGGCAACGCCTGC
TGGGTGCACAAGCACTTCACGGAAGACATCCAGACTCGGCAGTACCGGGCCGTCGAGGTG
CTGATCGGCGCCGAATACGGCCCCCGGCAGACATCTGGAGCACAGCCTGCATGGCCTTC
GAGCTGGCCACTGGTGACTACCTGTTTCGAGCCGCATTCTGGAGAAGACTACAGTCGTGAT
GAGGACCACATCGCTCACATAGTGGAGCTTCTGGGGGACATCCCCCAGCCTTCGCCCTC
TCAGGCCGCTATTCCCGGGAGTTCTTCAACCGGAGAGGAGAGCTGCGGCACATCCACAAT
CTCAAGCACTGGGGCCTGTACGAGGTACTCATGGAAAAGTACGAGTGGCCCCCTAGAGCAG
GCCACACAGTTACGCGCCTTTCTGCTGCCCATGATGGAGTACATCCCCGAAAAGCGGGCC
AGTGCCGCTGACTGCCTCCAGCACCCCTGGCTCAACCCCTAG

SEQ ID NO: 91_SGK022_H

TCTGGCCCTGTCCCTCCCCACCACCCGCCGCTGTGTCCAGACAGAGAATGTTCTAACGCT
GGGGGCGGCTGCGGATGAAGTCCTTGGGGAGAAAAGGAGCAGGCCAAGGGCGATGGTGGGA
GTAGAGCTGCCTCTCAGAGGCAGCATGAGCTGAGAGGGTGATAGGAAGGCGGCGCTAGAC
AGCATGGAGGACTTTCTGCTCTCCAATGGGTACCAGCTGGGCAAGACCATTGGGGAAGGG
ACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAACACCAAAGAAAAGTGGCAATTAAA
GTTATAGACAAGATGGGAGGGCCATCAGAGTTTATCCAGAGATTCTTCCCTCGGGAGCTC
CAAATCGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCT
GCCGACGGGAAAATCTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGC
GTGCTGAATGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTCAGATGGTT
GAGGCCATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAAC
GCCTTGTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCC
AAGTCACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAG
GTGCTGCAGGGCATTCCCCACGATAGCAAAAAGGTGATGTCTGGAGCATGGGTGTGGTC
CTGTATGTCATGCTCTGTGCCAGCCTACCTTTTGACGACACAGACATCCCCAAGATGCTG
TGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATCTGAGCATCTCGGCCGATTGCCAG
GACCTGCTCAAGAGGCTCCTGGAACCCGATATGATCCTCCGGCCTTCAATTGAAGAAGTT
AGTTGGCATCCATGGCTAGCAAGCACTTGATAAAAGCAATGGCAAGTGCTCTCCAATAAA
GTAGGGGGAGAAAGCAA

SEQ ID NO: 92_AA060026_M SGK022_M

CAGACGGAGAATGTTCTAGCCCTGGAGGCAGCTGTGAATGAAGTCCTTGGGGGGAAAAGA
AGCAGGCCGAGGGCGATGGTGGAGTAGAGCTGCCTCGCAGAGGCAGCATGAGCTGAGAGG
GTGACAAGAAGGAGGCGCTACACAGCATGGAGGACTTTCTACTCTCCAATGGGTATCAGC
TGGGCAAGACCATTGGGGAAGGGACCTACTCAAAAGTCAAAGAAGCATTTTCCAAAAAAC
ATCAAAGAAAAGTGGCAATTAAAATTATAGACAAGATGGGAGGGCCAGAAGAGTTTATCC
AGAGATTCTGCCTCGTGAGCTCCAGATTGTCCGTACCCTGGACCACAAAACATCATCC
AGGTGTATGAGATGCTGGAGTCAGCAGATGGAAAAATCTACCTGGTGTATGGAAGTGGCTG
AGGGAGGGGATGTCTTTGACTGTGTGCTGAACGGAGGGCCACTTCCCGAGAGCCGGGCCA
AGGCCCTCTTCCGCCAGATGGTTGAGGCTATTGCTATTGCCATGGCTGTGGCGTGGCC

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FIGURE 2UUU

ACCGGGACCTTAAGTGTGAGAACGCCTTGTTGCAGGGCTTCAACCTGAAGCTGACCGACT
TTGGCTTTGCCAAGGTGCTACCCAAGTCACGCAGGGAGCTGAGCCAGACCTTCTGTGGCA
GCACAGCCTATGCCGCCCCTGAGGTGCTACAGGGCATAACCCCATGATAGCAAGAAAGGTG
ATGTCTGGAGCATGGGTGTGGTCCTGTATGTAATGCTCTGTGCAAGTCTACCTTTTGATG
ACACAGATATCCCCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTCCCCACTCATT
TGGGCATCTCAACCGAATGCCAGGACCTGCTCAAGCGGCTCCTGGAACCAGACATGATAC
TCCGGCCTTCAATCGAAGAAGTTAGTTGGCACCCATGGCTAGCAAGCACTTGATAAAAGC
AATGGCAAGTCCTCCCCAATAAAGTAGGGGGAGAAAGCAAAGTCTG

SEQ ID NO: 93_AA399669_H

CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCCGGCCGCACTTCATTCTCAA
GTTTTGTGGCCAACGATGGATAGGAGGTGGATTGTGATGTATTGCGGAACATGGGACCTTG
AGGAGTTCGTAAACCAAAGGAGAAAGTAACAACAGCCAGTGGAGACAAAAGAACTGCT
TCTCTTTCTTTCCCCCTCCAAGTTCCTAGTGGAGGGCTGAGTCCAGCATCCCAGACTCGT
GTGACTATATAGGCAAGCATTGTTGGGGACCTACTTCACCTTTGATACCTTAGCCTTCAGCAG
CTCAAGGTGTTGGCCTTTGGATAGGAGGCTTCCAAGTAGTAAAGCTCCCTGCTCTCAGCA
AGCCCAACACCATGGGGAAGGGAGATGTCTTAGAGGCAGCACCAACCACACAGCCTACC
ATTCCTCATGGATGAATATGGTTATGAGGTGGGCAAGGCCATTGGCCATGGCTCCTATG
GGTCGGTATATGAGGCTTTCTACACAAAGCAGAAGGTTATGGTGGCAGTCAAGATCATCT
CAAAGAAGAAGGCCTCTGATGACTATCTTAACAAGTTCCTGCCCCGTGAAATACAGGTAA
TGAAAGTCTTGCGGCACAAGTACCTCATCAACTTCTATCGGGCCATTGAGAGCACATCTC
GAGTATACATCATTCTGGAAGTGGCTCAGGGTGGTGATGTCCTTGAATGGATCCAGCGCT
ACGGGGCCTGCTCTGAGCCCCCTTGCTGGCAAGTGGTTCTCCAGCTGACCCTGGGCATTG
CCTACCTGCACAGCAAGAGCATCGTGCACCGGGACTTAAAGTTGGAGAACCTGTTGCTGG
ACAAGTGGGAGAATGTGAAGATATCAGACTTTGGCTTTGCCAAGATGGTGCCTTCTAACC
AGCCTGTGGGTTGTAGCCCTKCTTACCGCCAAGTGAAGTCTTTTCCCACCTCAGCCAGA
CTTACTGTGGCAGCTTTGCTTACGCTTGCCAGAGATCTTACGAGGCTTGCCCTACAACC
CTTTCTGTCTGACACCTGGAGCATGGGCGTCATCCTTTTACACTCTAGTGGTCGCCCATC
TGCCCTTTGATGACACCAATCTCAAAAAGCTGCTAAGAGAGACTCAGAAGGAGGTCACTT
TCCCAGCTAACCATAACCATCTCCCAGGAGTGCAAGGTCCAAGTCTCATTGCCTGTGTGG
CACAATGGAGAAAACTCAGGCAAGACCTCTCTCTCCCTGCTCTAGAACCTGATCCTCC
AGATGCTACGCCAAGCCACTAAGCGTGCCACCATTCTGGACATCATCAAGGATTCTTGGG
TGCTCAAGTTCAGCCTGAGCAACCCACCCATGAGATCAGGCTGCTTGAGGCCATGTGCC
AGCTCCACAACACCACTAAACAGCACCAATCCTTGCAAATTACGACCTGAAAATGGCTGA
GGGAGGGGGCTAAGAGAGGAGCAAAGCAGGAGGTCTTGGGCTAAAAATCTTTTTTACCAA
AAATAAATCTAAGTCTGATTTAGTTTCATCAAAAAA

SEQ ID NO: 94_AA758539_H

GACCATTGACAGCGCTCCGGTAGTGTAATGAGGACAATGCCTGCTGGCCACATGACGG
GGGGATGTAGACGGCAGCGGCGCCAGTCGCTCCTGGCACCATGGACGATGCCACAGTCCT
AAGGAAGAAGGGTTACATCGTAGGCATCAATCTTGGAAGGGTTCTACGCAAAAGTCAA
ATCTGCCTACTCTGAGCGCCTCAAGTTCAATGTGGCTGTCAAGATCATCGACCGCAGGAA
AACACCTACTGACTTTGTGGAGAGATTCTTCTCGGGAGATGGACATCCTGGCAACTGT
CAACCACGGCTCCATCATCAAGACTTACGAGATCTTTGAGACCTCTGACGGACGGATCTA
CATCATCATGGAGCTTGGCGTCCAGGGCGACCTCCTCGAGTTCATCAAGTGCCAGGGAGC
CCTGCATGAGGACGTGGCACGCAAGATGTTCCGACAGCTCTCCTCCGCCGTCAAGTACTG
CCACGACCTGGACATCGTCCACCGGGACCTCAAGTGCGAGAACCTTCTCCTCGACAAGGA
CTTCAACATCAAGCTGTCTGACTTTGGCTTCTCCAAGCGCTGCCTGCGGGACAGCAATGG
GCGCATCATCCTCAGCAAGACCTTCTGCGGGTGGGACGATATGCAGCCCCGAGGTGCT
GCAGAGCATCCCCTACCAGCCCAAGGTGTATGACATCTGGAGCCTGGGCGTGATCCTGTA

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FIGURE 2VVV

CATCATGGTCTGCGGCTCCATGCCCTATGACGACTCCGACATCAGGAAGATGCTGCGTAT
CCAGAAGGAGCACCGTGTGGACTTCCCGCGCTCCAAGAACCTGACCTGCGAGTGCAAGGA
CCTCATCTACCGCATGCTGCAGCCCCGACGTCAGCCAGCGGCTCCACATCGATGAGATCCT
CAGCCACTCGTGGCTGCAGCCCCCAAGCCCAAAGCCACGTCTTCTGCCTCCTTCAAGAG
GGAGGGGGAGGGCAAGTACCGCGCTGAGTGCAAACCTGGACACCAAGACAGGCTTGAGGGCC
CGACCACCGGCCCCGACCACAAGCTTGGAGCCAAAACCCAGCACCGGCTGCTGGTGGTGCC
CGAGAACGAGAACAGGATGGAGGACAGGCTGGCCGAGACCTCCAGGGCCAAAGACCATCA
CATCTCCGGAGCTGAGGTGGGGAAAGCAAGCACCTAGCATGACAATGGCCCCGTTGTGTG
TGGTGGGGGTTCGGGGTTGGGGGGCATGGTGCAGTCGGCCTTCACGTAAACTAAGTAGGCA
GGTAGGATCTGAAGAAGGCACAGGTGCAAGTAAATTCGTCAATTAAACCACTATTTTGA
TT

SEQ ID NO: 95_AA883975_H

ATGTCGGGAGACAACTTCTGAGCGAACTCGGTTATAAGCTGGGCCGCACAATTGGAGAG
GGCAGCTACTCCAAGGTGAAGGTGGCCACATCCAAGAAGTACAAGGGTACCGTGGCCATC
AAGGTGGTGGACCGGCGGCGAGCGCCCCCGGACTTCGTCAACAAGTTCTTGCCGCGAGAG
CTGTCCATCCTGCGGGGCGTGCACACCCGACATCGTGCACGTCTTCGAGTTCATCGAG
GTGTGCAACGGGAACTGTACATCGTGATGGAAGCGGCCGCCACCGACCTGCTGCAAGCC
GTGCAGCGCAACGGGCGCATCCCCGGAGTTCAGGCGCGGACCTCTTTGCGCAGATCGCC
GGCGCCGTGCGCTACCTGCACGATCATCACCTGGTGCACCGCGACCTCAAGTGCGAAAAC
GTGCTGCTGAGCCCCGACGAGCGCCGCGTCAAGCTCACCGACTTCGGCTTCGGCCGCCAG
GCCCATGGCTACCCAGACCTGAGCACCACTACTGCGGCTCAGCCGCCTACGCGTCACCC
GAGGTGCTCCTGGGCATCCCCTACGACCCCCAAGAAGTACGATGTGTGGAGCATGGGCGTC
GTGCTCTACGTCATGGTCACCGGGTGCATGCCCTTCGACGACTCGGACATCGCCGGCCTG
CCCCGGCGCCAGAAACGCGGCGTGCTCTATCCCGAAGGCCTCGAGCTGTCCGAGCGCTGC
AAGGCCCTGATCGCCGAGCTGCTGCAGTTCAGCCCCGTCCGCCAGGCCCTCCGCGGGCCAG
GTAGCGCGCAACTGCTGGCTGCGCGCCGGGACTCCGGCTAG

SEQ ID NO: 96_AA905446_H

CTGGTAGAGAACAGGGGCTGGTGCCAAGGCCCATGGAGATGAGAAAACGGAAGACAGGGA
TCATGGAAAGAATTGTGGGGTCAGGGGACAGTGGCGGGAGGAGCTGGCTCACCACCCTGT
GGACAAATCAGGCCTTATAATTTGTGATTCTGTGGCTTTGTCTAAAAGTCCATAAAGCAC
CTTGATATCCAGTCTCACAGACTGCTCACAACAGTCCACAAGGCTGGTGGGGAGTGCTTC
TTTTGAATGATATACTAACGACAAAAATAATAGAAGTGAACATTCTTTGCAATGTCCAAG
CAGCTAGACACACTTAAGACCATTAAGAAAGCCAAGAAATAAGACCCAGACAAGGTGGGC
AGAAGTTGGAAGGCAGGAGACAGGTGTGAGGAGGTGGGCCCTTTCTGATCTGCCAGCCCAT
CTCTCCTCCCCTTACTTCCTCAGAGTTTATCCAGAGATTCTCCTCCCTCGGGAGCTCCAAAT
CGTCCGTACCCTGGACCACAAGAACATCATCCAGGTGTATGAGATGCTGGAGTCTGCCGA
CGGGAAAATCTGCCTGGTGTATGGAGCTCGCTGAGGGAGGGGATGTCTTTGACTGCGTGCT
GAATGGGGGGGCCACTGCCTGAAAGCCGGGCCAAGGCCCTCTTCCGTGAGATGGTTGAGGC
CATCCGCTACTGCCATGGCTGTGGTGTGGCCACCGGGACCTCAAATGTGAGAACGCCTT
GTTGCAGGGCTTCAACCTGAAGCTGACTGACTTTGGCTTTGCCAAGGTGTTGCCCAAGTC
ACACCGGGAGCTGAGCCAGACCTTCTGCGGCAGTACAGCCTATGCTGCCCCCGAGGTGCT
GCAGGGCATTTCCNNCAAGATGCTGTGGCAGCAGCAGAAGGGGGTGTCTTTCCCCACTCA
TCTGAGCATCTCGGCCGATTGCCAGGACCTGCTCAAGAGGCTCCTGGAACCCGATATGAT
CCTCCGGCCTTCAATTGAAGAAGTTAGTTGGCATCCATGGCTAGCAAGCACTTGATAAAA
GCAATGGCAAGTGCTCTCCAATAAAGTAGGGGGAGAAAGCAAACCC

FIGURE 2WWW

SEQ ID NO: 97_H29974_H

TTACAGCCTGTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCAGTGGC
CGGGCGCAGCGGGGCCCCGGGTGGCGGTCAAGAAGATCCGCTGCGACGCCCCGAGAACGT
GGAGCTGGCGCTGGCTGAATTCTGGGCCCTCACCAGCCTCAAGCGGCGCCACCAGAACGT
CGTGACGTTTGGAGAGTGCCTCCTGCAGCGCAATGGGTTAGCCCAGCGCATGAGTCACGG
CAACAAGAGCTCGCAGCTTTACCTGCGCCTGGTGGAGACCTCGCTGAAAGGAGAAAGGAT
CCTGGGTTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTTCTGTGAAGGTGG
AGACCTGAATCAGTATGTCCTGTCCCGGAGGCCAGACCCAGCCACCAACAAAAGTTTCAT
GCTACAGCTGACGAGCGCCATTGCCTTCCTGCACAAAAACCATATTGTGCACAGGGACCT
GAAGCCAGACAACATCCTCATCACAGAGCGGTCTGGCACCCCCATCCTCAAAGTGGCCGA
CTTTGGACTAAGCAAGGTCTGTGCTGGGCTGGCACCCCCGAGGCAAAGAGGGGCAATCAAGA
CAACAAAAATGTGAATGTGAATAAGTACTGGCTGTCTCAGCCTGCGGTTTCGGACTTCTA
CATGGCTCCTGAAGTCTGGGAGGGACACTACACAGCCAAGGCGGACATCTTTGCCCTGGG
CATTATCATCTGGGCAATGATAGAAAGAATCACTTTTATTGACTCTGAGACCAAGAAGGA
GCTCCTGGGGACCTACATTAAACAGGGGACTGAGATCGTCCCTGTTGGTGAGGCGCTGCT
AGAAAACCCAAAGATGGAGTTGCACATCCCCCAAAAACGCAGGACTTCCATGTCTGAGGG
GATCAAGCAGCTCTTGAAAGATATGTTAGCTGCTAACCACAGGACCGGCCTGATGCCTT
TGAACCTGAAACCAGAATGGACCAGGTACATGTGCTGCTTAAATTTCAGGGCTAAGCAT
TTTGGGTGATTTTAAACTAGGTTCGATTCTCGGGACCCACAGTCTCACCACGTCTCCTCC
AGAGGACGGCAGAGGGTACAGGTGGTGGCCTGGCCGGTTGGCGATCTCCCGACAGCTGGA
TCCGGCAATGTGAAGCTTTTGTGTTGGGTTTCCCCGCTTCTTTTTAGTTTGTCTTTATTN
TNNCCTTTTCTTTTCTTTTTTTNTTNNCCACNTNCCTTTTTTTTAAATTTAAACCATTGAG
ACTTCAGAAGAGCAGGACACAATGCTGTGGACAGGCACCAATTTCTTTAAAGAAATTCAA
TGTGGGCAAGGCATATGTGTAAATTTCACTTTTACTTTTTATAAGGGGTTAGGGAGCTAT
TTTTGGTTTTTGTCTTCACTTCCCTCTGTCTTCCTTCTTTATACTTTTCTCAGTTCTAC
TTATGACACCTCACTTCCCTAGAGAAGGCCTGCCTCCCCATAGGGAATCTGGGGGTANCT
TCTGGAACGGGGCGTGAGGANACAAGGAGCCTCTGGGCCACNCCTCCCTACCAGATGCAG
GAACTCCTGGACTCCTTGGTGGGCTGGCCCTGGCTAGCCCTTGGGCCTCGGAGATGATCA
GAGGTGAAGAACCGCC

SEQ ID NO: 98_AA498104_M H29974_M

CCGTTGCTGCTCCCCCGCCCCCGCAGCCATGGAAACGGGGAAAGAGAACGGAGCCCCG
AGAGGGACAAAAAGCCCGGAGCGGAAAAGGCGAAGCCCAGTCCAGCGGGTACTGTGCGAG
AAGCTGAGGCCGGCGGCCAGGCCATGGATCCGGCTGGGGCCGAGGTCCCGGGCGAGGCC
TTCCTGGCCCCGGCGGCCGCGGATGGCGGCGGGGATGTTCTGACGGCCGCGCTAC
AGCCTCTTGGCGGAGATCGGGCGCGGCAGCTACGGCGTGGTTTATGAGGCTGTGGCTGGG
CGCAGTGGGGCCAGGGTGGCAGTCAAGAAGATCCGCTGCGACGCTCCCGAGAACGTGGAG
TTGGCACTAGCAGAATTCTGGGCCCTCACCAGTCTCAAGCGGCGGCACCAGAATATCGTG
CAGTTTGGAGAGTGCCTCCTACAGCGCAACGGGTTAGCCCAGCGCATGAGTCACGGCAAC
AAGAACTCACAGCTTTACCTGCGCCTGGTGGAGACCTCGCTCAAAGGAGAAAGGATCCTG
GGCTATGCTGAGGAGCCCTGCTATCTCTGGTTTGTTCATGGAGTACTGTGAAGGTGGAGAC
CTCAATCAGTATGTCCTGTCCCGGAGACCTGACCCAGCCACCAACAAAAGTTTTCATGCTA
CAGCTTACAAGCGCCATTGCCTTCCTGCATAAAAACCATCGTGACAGGGACCTAAAG
CCAGACAACATCCTGATCACAGAGCGGTCTGGCACCCCCATCCTCAAGGTGGCAGACTTT
GGACTGAGCAAGGTCTGTGCAGGGCTGGCACCCCCGAGGCAAAGAGGGCAATCAAGATAAC
AAAAATGTGAATGTGAATAAATACTGGCTGTCTCAGCTTGTGGCTCAGACTTCTACATG
GCTCCCGAAGTCTGGGAGGGACACTATACAGCCAAGGCGGACATCTTTGCTCTGGGCATT
ATCATCTGGGCAATGATAGAAAGAATTACCTTTATTGACTCTGAAACCAAGAAGGAGCTC
CTGGGGACCTACATTAAAGCAAGGGACTGAGATCGTCCCTGTTGGTGGAGGCGCTGCTAGAA
AACCCAAAGATGGAGTTGCATATCCCCCAGAAACGTAGGACTTCCATGTCTGAGGGGGTC

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FIGURE 2XXX

AAGCAGCTCTTGAAAGACATGTTAGCTGCTAACCCACAGGACCGACCTGATGCTTTTGAA
CTTGAAACCCGAATGGACCAGGTCACATGTGCTGCTTAAACTCCAGGGCTGAACGTCTTG
GGTGTTTTTTAACTAGGTCGATCCTTCGGGACCCACAGTCTCATCGTGTCTCGGACAGGA
TGGCAGAGGGTACAGGTGGTGGTGATCTCCTGACAGCTGGACCTCCCACAATGTGAAGCT
CACGCTTGGGCTGCCCCTCTACCCTTCTCTTTCTCCTTCAGTAGAATAATAATTGTTTT
TCTAAACATTAAACCATCAAGACTTCTGAAGAGCAGAAGGCTACACTCTG

SEQ ID NO: 99_AA215311_H

CGRCCGCGCTACGGAAGCCGGAGGGGGGCGGGGCGGTCGGCGTAAGGGGGTGTGTCCGC
GCGCACCACGGGGGCGCGCGCCGGCTGCTGACTGGAGGCGGCGGCAGCGGAGGCGCGAGC
TGCCCCGATAATGGCGGCCTGCAGAGCCCATGAGAGGGAGAAGCGGCAGCGTCTACCCTGA
GAAACCTCGACCTTGAAGATGGTGAGTAGCCAGCCAAAGTACGATCTAATACGGGAGGTA
GGCCGAGGTAGTTACGGTGTGTGTATGAAGCAGTCATCAGAAAGACCTCTGCACGGGTG
GCAGTGAAGAAAATTCGATGTACGCACCTGAAAATGTTGAACTAGCCCTTCGTGAGTTC
TGGGCACTAAGCAGTATCAAGAGCCAACTCCAAATGTGATTCACTTGGAGGAATGCATC
CTACAAAAGGATGGGATGGTGCAAAAAGATGTCCACGGCTCTAATTCTTCCCTTTATTTA
CAGCTTGTAGAACTTCATTAAGAGGAGAAATTGCCTTTGATCCCAGAAGCGCCTATTAT
TTGTGGTTTGTGATGGATTTTTGTGACGGAGGAGATATGAATGAGTATCTGTTGTCCAGG
AAGCCCAATCGTAAACTAACACCAGCTTCATGCTTCAGCTGAGCAGTGCCCTGGCTTTC
TTGCATAAAAACCAGATCATCCACCGAGATCTTAAGCCTGATAACATCCTGATTTCTCAA
ACCAGGTTGGATAACAGTGACTTGGAACTACCCTCAAAGTGGCTGATTTTGGTCTAAGT
AAAGTTTGTTCAGCCTCTGGGCAGAACCAGAAACCTGTGAGTGTAACAAGTGTTC
CTTTCCACAGCATGTGGAACAGATTTTTTACATGGCTCCTGAAGTTTGGGAAGGACATTAC
ACAGCAAAAGCTGACATCTTTGCTCTGGGGATTATCATCTGGGCAATGCTGGAAAGGATC
ACATTCATAGACACAGAGACAAAGAAGGAACCTCTGGGGAGTTATGTAAACAAGGAAC
GAGATTGTGCCTGTTGGGGAGGCACTTCTGAAAATCCCAAATGGAACTTCTCATTCTC
GTGAAGAAAAAATCTATGAATGGGCGAATGAAACAACCTGATTAAGGAAATGCTGGCTGCA
AACCTCAGGATCGTCCAGATGCTTTTGAAGTAGAAGTACAGATTAGTACAAATTGCATTT
AAAGATAGCAGCTGGGAAACGTGACACATATTATTTGCAAATACCATGGATGATATGCTG
CTTCTGTTTAAACAGTGATGCAACATTATGTGGCTGAAAAAGAAATATAAAAAGCTAGACTC
TACCCTCTAAGGGTTTAGATTTTTTTGTGGGATTTTTTTTTTCTCATTCTTAAATCC
AAGTTGGCCGTTTTATTAGTATGTTTCAAATGTGTATTACCAATGTGGGTGTAAATTTTT
AAAAAATGATTATTGATAGAAGTTTGGCAGGAAAATCTTTAAGAGCTAACAAAGAGAAGA
GAGTCCAGTTTTCTGGAAATATGTCTTTAAGTATTTTAGACATTCCTCGTCAGTATTAGG
AATTTCCATGGGAAAAGAGGTTTGCATGCTGGTAATGCAACCTTTGAAACTTTGTAAAGG
AAACATATATGTATATATTTATGTATATGTAAGTATGTGAATGTGCGCATTTTGCATTCC
ATATGAAAAAATGCCACGTCTGTTTAAATTATTTGATGTAGGTTTGGGTTTTTGTAGATT
TGCTGGTGAAGTCAGTGACGAAAAATAAACCTTCCCTTATCTTCCTACTCTGCCCCCTCCC
CCTAATGAAATCATATTAAGTNGTTTTTCTNNTTTTTTTTGTAAATATACAGCTTTTTTTTT
TAAGGCATCATTTTCGAGGGTCTAAAATTATCTGGTAAAACAAATGAAATTAAGTGATCC
AAAGCTGCTGAAGTATGTTTGAAGTCTCCAGTGCCCTATAGCTGCAAGAGTTGAATTAGT
CATGCAGTCATATGGCAGCAGGTTGGTGATT

SEQ ID NO: 100_AA018361_H

GCGGGGCTCCGTATCCCCACGTGGGCGCTGCAGGAACTGGCGGGGCGCGTGACCCGGCG
AGGCCAGAGACAGGGGAGGGGCGCCGGGAGCCGGGCGGATCCGCGTCCCCGATGCGCGC
TGCAATTCGGCGGGGCGCGCTGGGGGCGAGCTGGAGCCACCCAGTGCTCGGCCCGCCCC
GCAACCCGCCGGAACCGCCCGCCGCGAGCGAGGAAGCGCCCGCGGGGCGCAGGCGGCCGG
AATGGCGGGGCGCGCTGGGGTCCCCGCGCCTGGACGGCTTCATCCTCACCGAGCGCCT
GGGCAGCGGCACGTACGCCACGGTGTACAAGGCCTACGCCAAGAAGGACACTCGTGAAGT

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FIGURE 2YYY

GGTAGCCATAAAGTGTGTAGCCAAGAAAAGTCTGAACAAGGCATCGGTGGAGAACCTCCT
CACGGAGATTGAGATCCTCAAGGGCATTGACATCCCCACATTGTGCAGCTGAAAGACTT
TCAGTGGGACAGTGACAATATCTACCTCATCATGGAGTTTTCGCGAGGGGGCGACCTGTC
TCGCTTCATCCATACCCGAGGATTCTGCCTGAGAAGGTGGCGCGTGTCTTCATGCAGCA
ATTAGCTAGCGCCCTGCAATTCTGTCATGAACGGAATATCTCTCACCTGGATCTGAAGCC
ACAGAACATTCTACTGAGCTCCTTGGAGAAGCCCCACCTAAAAGTGGCAGACTTTGGTTT
CGCACAAACATGTCCCCGTGGGATGAGAAGCACGTGCTCCGTGGCTCCCCCTCTACAT
GGCCCCCGAGATGGTGTGCCAGCGGCAGTATGACGCCCGCGTGGACCTCTGGTCCATGGG
GGTCATCCTGTATGAAGCCCTCTTCGGGCAGCCCCCTTTGCCTCCAGGTCTTCTCGGA
GCTGGAAGAGAAGATCCGTAGCAACCGGGTCATCGAGCTCCCCTTGCGGCCCTGCTCTC
CCGAGACTGCCGGGACCTACTGCAGCGGCTCCTGGAGCGGGACCCAGCCGTCGCATCTC
CTTCCAGGACTTCTTTGCGCACCCCTGGGTGGACCTGGAGCACATGCCAGTGGGGAGAG
TCTGGGGCGAGCAACCGCCCTGGTGGTGCAGGCTGTGAAGAAAGACCAGGAGGGGGATT
AGCAGCCGCTTATCACTCTACTGCAAGGCTCTGGACTTCTTTGTACCTGCCCTGACTA
TGAAGTGGATGCCCAGCGGAAGGAGGCAATTAAGGCAAAGGTGGGGCAGTACGTGTCCCG
GGCTGAGGAGCTCAAGGCCATCGTCTCCTCTTCCAATCAGGCCCTGCTGAGGCAGGGGAC
CTCTGCCCGAGACCTGCTCAGAGAGATGGCCCGGGACAAGCCACGCCTCCTAGCTGCCCT
GGAAGTGGCTTCAGCTGCCATGGCCAAGGAGGAGGCCGCCGGCGGGGAGCAGGATGCCCT
GGACCTGTACCAGCACAGCCTGGGGGAGCTACTGCTGTTGCTGCGGAGCCCCCGGGCCGG
AGGCGGGAGCTGCTTCACACTGAGGTTGAGAACCTCATGGCCCGAGCTGAATACTTGAAG
GAGCAGATGAGGGAATCTCGCTGGGAAGCTGACACCCTGGACAAAGAGGGACTGTGCGAA
TCTGTTCTGTAGCTCTTGACCCCTTCAGTGACCCTAGAAGAATGATTGGACAGATGTGAGC
CATCTGGAGCAGAGGGGCACTAACCAGGCTGACGCCAAGAATGAAGTGGCCCACTGCAG
CCCTGGCGAGCAGGCTTCTTGGATGGACAGTGTGAGACCCCATATCCCAGAGTCCCCA
GCCTCCCTCAGGTTACTCTGCACCCACAGATGGTTTGATGGCTGTGCTGTATACTGGAG
GGGAGGGCAGGACTCTGGGAGAACAGCACTTCTTTCATGAGACCTTTGTTACTCGGTGGT
TACTGGGTCTGTGCCTGTCCGTTTTGGGGCATGCAGCCCTCTATCATTTTTGGCTCCGA
GAAGAGGGCAAGGGGCCCCCGCAGGGTACTTCTGTGCTTGCCCTCGCCCTGCCAGCAGGC
AGCTGTGCCCTGGCCTGCCCTTCCCGGACCCCTTATTCCAACCTCAGCTCCTCTTTGCA
CTGGAATGGGGCACTCCAACACCCCTCAGGGACCACTCCCCACAGTATGCACTCAGCC
CCACAGAACCCACCAGTCTTTCTGGGAACCTCACACCTGCCCGCCATCTTGGTACTTTAGG
TTAATCCCTCAAGCATGAAAGCTGGATCTTTTGGGGTTTAAGAAGCCCAAGCCTTGTTCC
TGCCCTGGCCTAGGGAGCACTCAGGAGGGTTCCTTGGTCTCATCTCTCCACCTCCGTT
CCCTCTGGGCCCCACACTAGCCACAGCGEGGGCCTTGTGCTGGAGTTTGAGCCTGGGACA
GGGAGAGGGAGGCTTGGAGACAGTCTGACCCAGTGCCCTCTAGGCCACCCACTTCTAGGC
CTGCCCTGCCGCCGTGGAGCCCTGGGCAAGCTCTTTCCTCTTCTGGGCCCTGGGTCTCCC
CATCTCTTCAATGGGGCTGATACCTTCACAGCCACAGCATGGGCACCTTATGAGGACAAA
GTGAATTTAACCCTGGAAGAAGATGTATTTGAGAGTTTCTTTTAAATAATCAGCGGGTGT
GGTGATTTGTAGCCCTTCTGCCCTTAAATGCTTCTTGGGCAAGAGCTGTCTGTCTCTCC
TGCAGGAGGCTGAGTGTGAAGAGTATCATTCATTGTTTCTCTATTAAATTATTTCTCT

SEQ ID NO: 101_AA311714_H

TGGACCTGTCCTGAGGCAGAGGCCGAGATGCGCGCAACCGCGGGAGCAGCCAAGTGGACT
GGACTCTTTTCTTGAAGTAGCTACCAGGAGCTAGAGATGCTGTTATTCTATCGTATGTGA
GAAGTCGGCCCCAGAGATGGAAAACCTTTATTCTGTATGAGGAGATCGGAAGAGGAAGCAAG
ACTGTTGTCTATAAAGGGCGACGGAAGGGAACAATCAATTTTGTAGCCATTCTTTGTACT
GATAAGTGCAGAAGGCCTGAAATAACCAACTGGGTCCGTCTCACCCGTGAAATAAAACAC
AAGAATATTGTAACCTTTTCATGAATGGTATGAAACAAGCAACCACCTCTGGCTAGTGXAT
GAAAACCTCCCAGAAGATGTTGTGAGAGAATTTGGAATTGACCTGATTAGTGGATTACAT
CATCTTCATAAACTTGGCATTCTCTTTGTGACATTTCTCCTAGGAAGATACTCTTGAA

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FIGURE 2ZZZ

GGGCCTGGCACACTGAAGTTTAGCAACTTTTGCTTGGCAAAAGTGGAAGGTGAAAATTTG
GAAGAGTTCTTTGCTTTGGTGGCAGCAGAGGAAGGAGGAGGTGATAATGGGGAAAATGTC
CTGAAGAAAAGCATGAAAAGTAGAGTCAAAGGATCTCCTGTATATACAGCACCAGAAGTT
GTGAGGGGTGCTGACTTTTCCATCTCCAGTGACCTCTGGTCTTTGGGCTGTCTGCTTTAT
GAAATGTTTTTCAGGAAAACCTCCATTCTTCTCAGAAAAGTGTTTCAGAATTAAGTAAAAG
ATCTTATGTGAAGATCCTTTGCCACCTATTCCGAAAGATTCTTCTCGTCCTAAAGCTTCT
TCAGATTTTATTAATTTGCTTGATGGGTACTTCAAAGAGATCCTCAGAAAAGATTGACT
TGGACAAGGCTACTGCAGCATTCAATTTTGAAGAAAGCTTTTGCTGGAGCAGATCAGGAA
TCAAGCGTCGAAGATCTCAGTCTCAGCAGAAACACTATGGAGTGTTCTGGGCCACAAGAT
TCCAAGGAGCTTTTGCGAAGCTCTCAGAGTAGACAAGCAAAGGGCACAAGAGTGGTCAA
CCACTAGGTCAGTCTTTTCAGACTAGAAAATCCAAGTGGCTTTCGGCCTAAGAGTACTCTT
GAGGGTCAATTGAATGAATCCATGTTTCTTCTCAGTCTCTCGTCCTACTCCCAGAACTAGC
ACTGCAGTGGAAAGTAAGTCCCTGGTGAGGATATGACTCACTGTTTACCACAGAAGACTTCT
CCTCTGACCAAGATTACAAGTGGACACCTGAGTCAGCAGGACCTGGAATCCCAGATGAGA
GAGCTTATCTACACGGACTCAGATCTTGTGTGACCCCCATTATCGACAATCCAAAGATA
ATGAAACAGCCACCAGTTAAATTTGATGCAAAAATATTGCATCTACCAACATATTAGTG
GATAAGTTATTATTTCTGAAAGATCAAGATTGGAATGACTTTTTTGCAACAAGTGCTCG
CAGATCGACTCCACTGAGAAGAGCATGGGGGCCTCCCGAGCCAAGCTGAATCTCCTTTGC
TATTTGTGCGTGGTGGCTGGTCACCAGGAGGTGGCCACCAGGCTCCTCCATTCCCCCTG
TTCCAATTGCTAATCCAGCATTTGCGGATAGCTCCAAACTGGGATATACGGGCCAAGGTT
GCTCACGTGATTGGTTTACTGGCTTCGCACACAACTGAGCTCCAGGAAAATACACCTGTT
GTTGAGACTACAAGCTCCATTGGAATCGGGATTTTGAAGTGTCTTGTTCACACTCCACT
CCAGTGCCTAGACAGTGCCTTGTGTATGTATAGATACTGACAAATATTTCAAATAAATA
AAACTGTATCAGCATT

SEQ ID NO: 102_SGK384_H

TCTTTGGCCACGTGCTGAGGGCGCGGCAGATCCTGACGGAGCCAGAAGTGCGCGACTAC
CTGCGGGGCCTGGTCAGCGCCTGCGCTACCTGCACCAGCGGTGCATCCTGCACCGC

SEQ ID NO: 103_AA210451_M SGK384_M

GGTCTGCTGCATGGATAATGGACTGGAACACAGAAAGACCATGCAGGGTTCGGCTGTAGA
AGGCCAGTATCTCCAGAGGCCAGAAGACACCATCAGATCTCCTGGGACTGGAGTTATAGA
GGTTGTGAGCTGCCATGTTGAACCAAGCAGGTCACTGAGGGACACAGGCATGTGGATGGA
AACCCTGCTGGGAGAAAAAAGAACTGCTGAAGGGACTGACATGGGACAGCAACATGGAA
CCAGGAATGGTCTCACGCATAGAGAGCTCCCCGGGGCGTGGGGCTGCTGCTCGCCATGG
CCCTTATGAACGTGGCGCTCTACCTCTGCCTTGATCAGCTTTTTCATCTCCCCTGGACGAT
CCACCGCGGACTCTAGGCGCTGTCTCCGGGCTACTTCAGAATGGGGCGGATGAGAACT
GCTCACGCTGGCTGTCTGTGAAGAGCTGAGGACAGAAGTCAGGCAGCTGAAGCGCGTTG
GGGAGGGAGCCGTGAAGAGAGTCTTTCTGTCTGAATGGAAGGAACACAAAGTCGCTCTCT
CCCGGCTCACCAGGCTGGAGATGAAGGAGGACTTCCTGCATGGGCTGCAGATGCTGAAGT
CTCTACAGAGTGAGCACGTGGTCACGCTGGTGGGCTACTGTGAGGAAGATGGCACTATT
TCACCGAATATCACCCCTTAGGTTCTTTGAGCAACCTGGAAGAAACACTAAACCTTTCAA
AGTACCAAGACGTGAACACTTGGCAGCACAGGCTGCAGCTGGCCATGGAGTACGTCAGCA
TCATTAAGTATCTGCATCACAGCCCCCTGGGCACGAGGGTCATGTGTGACTCTAACGACC
TGCCCAAACATTGTCCCAGTACCTGCTAACAAGTAACTTCAGCATTGTGGCAAACGACC
TGGACGCTCTGCCCCCTGGTAGACCATGACTCTGGGGTACTTATAAAGTGTGGCCACAGAG
AGCTCCATGGGGATTTTGTGGCTCCAGAGCAGCTGTGGCCCTACGGAGAAGACACGCCCT
TCCAAGACGATCTCATGCCTTCTTACAATGAGAAGGTTGACATCTGGAAGATTCCAGATG
TCTCCAGTTTCTTGTGGGCACGTGGAAGGGAGTGATATGGTTAGATTCCATTTGTTT
ATATCCATAAGGCGTGCAAGAGCCAGATCCCGGCAGAAAGACCCACTGCTCAGAACGTGC

FIGURE 2AAAA

TAGACGCTTACCAGAGGGTTTTCCATTCACTCCGAGACACTGTGATGTGCGCAGACGAAAG
AAATGCTGTAAAAATGAGCCATCGAGTGACGTGCTTGATGGCTGAATGGCATCCCAGCTG
TTCCGCTCTTGATGATGGAAGAGCTTTGCATGGATGGATGTTGACCCTGGCTGTTTCAGCC
ACGTAGGCCTCCTCTACGTCTGCCTGCATGTTTGAGTGTTCTGCTCTCCTGGCAGCCCGG
ATGGAAGCTGCCAAGCGAGAAAGCCTGGCTTCAGGATGCTCCCTGGTGAAGATGCAGAGG
ATTCTGATCTGCATAGTTTTCAAGGGAGTGATCAAACGGTGACCTTGAAGACATGCTGCC
TGCCTTGGTAACTTTTTATAGACTAGTAGGAAACAGAAATCTTTTGGGGGAGGGGGGGAC
AACCCACTAGTTCCTCAGAGACAATTTCTTCTCATTAGAAAGCCCTGTTGGAAGCTGGG
GATGTTTTAACTCCGTGGCAGGGCACTTGCTTAGTTGTGTGCAAAGCCTTGGATCTGACC
CATGGCATGTGCACACACAAATGCTCAAAGAAAATCCCAGACGCCAGAAGTGTGCCCC
TTTCTTGTCAATAAGGTCATTGTTCAGTACCGGAGATGATTTTTTTTTATGAAGCGTTTATG
CTGACTCGTGTCACTGAGCCAAGTGTGCATGGTCGTTAGCTACTTTGTGGGTCTTCTTT
CTTTCTACCCTACTTCTTCCCTTTCCACCCCTAACACTAGATAGGAGAGAGGAGAGAGA
AAGGAAAGTGGGCACTGTTATATTGTTGGACGACTTCTTGCTGATTAAAGGGTGTGAGT
TCCTTGGAGCAATGATCTTTGCTGCCAAGATATCTCATTCTTCTTGTCTTCTTCTCGCC
CACGACCCTTCACAAACACCGACCAACAGCAAACAACCCACCCCGCTTCTCGGGGG
CCCTAGCACTTATGTACTTCTGAAAAGTCCCCAGAAATTCCAATCATCACACTCAGAG
AACTGTCTGCTGCTGCGAAACTACACCCCTGCTAGAGCATGAGGCAAATCATAGTCAG
CTGCTGTGGACAGTCTGAAGCAGCCTGGCATCCACACCTGAGATTAAACAAAAACATT
CTTACCTGTGTTTTGTTTTGTTTTAAGAAACCAAAGTGCACCAAGATAGCATGCTCTTG
AGATTGTGGCTGTCTAGAGATTTTTGGAACAGCAAGTTGAAGGAACCTTCTTACCTGCCT
TGAATGGTGCTTTGAACTTCCTGCTGACCTGGAGTTTCTGTGTGAATATTTCTATCCAGT
GTCCCCCTGTACCGGAAAGTACAAAGTCTGCTCTGGGCTTGTCATGCCTGAACACTTTAA
ACACTGTGGAGCCAGGAATAATGGTACCCACCTGTAATCCCAGCACCTGGGAGACAGGAG
GAACCAGGAGTTCAGGGTTATCCTGGGCTATATACCGTGACCCTGTCTACCCCCACACCC
CAATAAAAAACAAAAAGGTC

SEQ ID NO: 104_SGK071_2_H

GAGGTGGTGGCTGTGCAGATGATGGTGGAATGCATGGATGACCATTACGCCAGTCAGGCC
CTGGAGGAGCTGATGCCACTGCTGAAGCTGCGGCACGCCCACATCTCTGTGTACCAGGAG
CTGTTTCATCACGTGGAATGGGGAGATCTCTTCTCTGTACCTCTGCCTGGTGATGGAGTTC
AATGAGCTCAGCTTCCAGGAGGTCATTGAGGATAAGAGGAAGGCAAAGAAAATCATTGAC
TCTGAGTGGATGCAGAAATGTGCTGGGCCAGGTGCTGGACGCGCTGGAATACCTGCACCAT
TTGGACATCATCCACAGGAATCTCAAACCTCCAACATCATCTCATCAGCAGTGACCAC
TGCAAACCTGCAGGACCTGAGTTCCAATGTGCTAATGACAGACAAAGCCAAATGGAATATT
CGTGCGGAGGAAGACCCCTTTCGTAAGTCTGGATGGCCCCCTGAAGCCCTCAACTTCTCC
TTCAGCCAGAAATCAGACATCTGGTCCCTGGGCTGCATCATTCTGGACATGACCAGCTGC
TCCTTCATGGATGGCACAGAAGCCATGCATCTGCGGAAGTCCCTCCGCCAGAGCCCAGGC
AGCCTGAAGGCCGTCTGAAGACAATGGAGGAGAAGCAGATCCCGGATGTGGAAACCTTC
AGGAATCTTCTGCCCTTGATGCTCCAGATCGACCCCTCGGATCGAATAACGATAAAGGAC
GTGGTGCACATCACCTTCTTGAGAGGCTCCTTCAAGTCTCTCGTGCGTCTCTCTGACCCTG
CACCGGCAGATGGTGCCTGCGTCCATCACCGACATGCTGTTAGAAGGCAACGTGGCCAGC
ATTTTAGGTGATGCTGGGGACACAAAGGGGGAGCGTGCCCTGAAGCTCCTGTCCATGGCC
TTGGCATCCTATTGTTTAGTTCCAGAGGGTTCATTATTTATGCCCCTGGCCTTGCTCCAC
ATGCACGACCAGTGGCTCAGCTGTGACCAGGACAGAGTCCCTGGGAAGAGAGACTTTGCC
TCCCTGGGGAAACTAGGGAAGCTGTTGGGCCCATCCCAAAGGGTCTGCCGTGGCCCCCG
GAGCTGGTGGAGGTGGTGGTCACGACCATGGAGCTACATGACAGGGTCTCGATGTCCAG
CTGTGTGCCTGCTCCCTGCTGCTGCACCTCCTGGGCCAAGCGCTGGTGCACCACCCGGAA
GCCAAGGCTCCCTGCAACCAAGCCATCACCTCCACCTGCTGAGTGCTCTTCAGAGCCAC
CCCGAGGAGGAGCCACTTCTGTTCATGGTCTACAGCCTGCTAGCCATCACCAACCCAG

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FIGURE 2BBBB

GAGTCAGAGTCACTGTCAGAGGAGCTGCAGAACGCTGGGCTGCTGGAGCACATCCTGGAG
CACCTCAACAGCTCCCTCGAAAGCAGGGACGTCTGCGCCAGCGGCCTGGGCCTGCTCTGG
GCCCTCCTGCTGGACGACCCCATCTTGGCACTCCAGCGCCCCAGGAAAAAGAGAGCTCCA
AACCACGGAAAGCCCCGGGAAACCCAAGAACCCTGCCAGCACCCAAAGTATCATTGTGAAC
AAGGCCCCCTTGGAGAAGGTCCCCGACCTCATCAGCCAGGTGTTGGCCACCTACCCTGCG
GATGGGGAAATGGCAGAAGCCAGCTGCGGAGTCTTCTGGCTGCTGTCCCTGCTGGGCTGC
ATCAAGGAGCAGCAGTTTGAACAAGTGGTGGCGCTGCTCCTGCAAAGCATCCGGCTGTGC
CAGGACAGAGCCCTGCTGGTGAACAATGCCTACCGGGGACTGGCCAGCCTGGTGAAGGTG
TCAGAGCTGGCGGCCCTTCAAGGTGGTGGTGCAGGAGGAGGGCGGCAGTGGCCTCAGCCTC
ATCAAGGAGACCTACCAGCTCCACAGGGACGACCCGGAGGTGGTGGAGAACGTGGGCATG
CTGCTGGTCCACCTGGCTTCCCTATGAGGAGATCCTGCCGGAGCTGGTGTCCAGTAGTATG
AAGGCCCTGCTCCAGGAGATCAAGGAGCGCTTACCTCCAGCCTGGTGAGTGACAGCAGC
GCCTTCAGCAAACCAGGCCTCCCTCCAGGTGGAAGCCCCCAGCTGGGGTGCACCACGTCT
GGGGGACTGGAATAG

SEQ ID NO: 105_AA118352_M SGK071_M

CAGAAGAAGACCCCTGCCAGAAGTCTGGATGGCTCCTGAAGCTCTCAAATTCTCCTTCT
CCACCAAATCCGACATCTGGTCTCTGGGCTGCATCATTCTAGACATGGCCACTTGCTCCT
TCCTGAACGACACAGAAGCCATGCAACTGCGGAAGGCCATCCGCCATCATCCAGGCAGCC
TGAAGCCCATCCTGAAAACCATGGAGGAGAAGCAAATCCCTGGTACAGATGTCTACTATT
TGCTTCTGCCCTTCATGTTGCATATCAACCCCTCCGATCGACTGGCAATCAAGGATGTGA
TGCAAGTCACCTTCATGAGCAACTCCTTCAAAGCTCCTCTGTTGCGCTGAATATGCAGC
GGCAGAAGGTCCCCATCTTCATCACTGACGTGCTGCTTGAAGGCAACATGGCCAAACATCT
TAGGCAGCTGGCTGTGTGCTTCCCTTGTGAACGACAGCAGGCACTGTGACTCAGGGATTG
GCTCGCAGAGACTTGGGTTTGATTTTCAGTCAGTCTCTTGGACAGAGCACCTCTGAAAG
ATGTCATGCAGAATTTCTCCAGTCGACCAGAGGTCCAGCTCAGAGCCATTAACAAGTTGT
TGACAATGCCAGAGGACCAGCTAGGGCTGCCATGGCCCACAGAGCTGCTGGAAGAGGTGA
TCAGCATCATAAAGCAGCATGGGCGGATCCTGGATATTCTGCTCAGCACCTGCTCCCTTC
TGCTGCGTGTTCTTGGCCAAGCACTGGCAAAGGACCCAGAAGCTGAGATCCCAAGGAGCA
GTTTGATCATCTCCTTCCTGATGGATACTTGGCGGAGCCATCCTAACTCTGAAAGGCTTG
TTAATGTGGTCTACAACGTGCTTGCCATTATTTCCAGCCAAGGACAGATCTCAGAAGAGC
TGGAAGAGGAGGGGTTGTTTCAGCTTGCCCCAAGAGAACCTGGAGCACTTCCAAGAGGACA
GGGACATCTGCCTCTCTATCCTGAGCCTGCTCTGGTCCCTCCTGGTAGATGTTGTCACTG
TGGACAAAGAGCCCTTGGAGCAGCTCTCTGGCATGGTCACCTGGGTGCTGGCTACTCATC
CGGAGGACGTGGAAATAGCAGAGGCTGGCTGTGCGGTGCTCTGGCTGCTGTCTTGTGG
GCTGCATAAAGGAGAGTCACTTTGAGCAGGTGGTAGTGCTGCTCCTGAGAAGCATCCAGC
TGTGCCCTGGCAGAGTACTGCTGGTGAACAATGCATTCCGTGGCTTGGCCAGCCTCGCAA
AGGTGTCCGAACCTGGTGGCCTTCCGAATAGTAGTACTGGAAGAGGGCAGCAGCGGCCTCC
ACCTCATCCAAGATATCTACAAGCTCTACAAGGATGACCCTGAGGTGGTGGAGAACCTCT
GCATGCTGTTGGCCCATCTGACCTCCTACAAGGAGATCCTGCCAGAGATGGAGTCTGGAG
GCATCAAAGACCTAGTCCAGGTGATCCGGGGGCGCTTTACCTCCAGCCTGGAGCTGATTT
CTTACGCTGATGAGATACTCCAGGTACTGGAAGCAAATGCACAACCTGGCCTCCAGGAGG
ATCAGCTTGAGCCTCCTGCAGGGCAGGAAGCCCCACTGCAGGGAGAGCCCCTCTTCAGGC
CCTGACATGCTGCCCTTCTGGTCTGTGGTAAGAGAAAGTATCACTAGGTCCAGTATTAA
TTTCGTACCCCATGGTGACTAATAAAAGAAGCCCTAGGCTGTTTCTGGC

SEQ ID NO: 106_018653.9_H

GGCCGGGGTTCGGGGCGCGGGGCATGCGCGCGGGCTGGGCAGGGGGCCGGCGGGGGCGCAGA
GCGGAGCCGCCCTCGGAGCCTGAGCCGCCCGGGGCGGGGAGCCGCGCGGGGGCCG
GCCGGCCGGGGGAGGGGAGCGATGCGGCGCCGGCGGGCGGCAGTGGCCGCGGGTTTCTG

FIGURE 2CCCC

CGCCTCCTTCCTGCTGGGCTCCGTCCTCAACGTGCTCTTCGCTCCGGGTTCGGAGCCTCCG
AGGCCAGGCCAGTCCCCTGAGCCTTCGCCGGCCCCGGGTGCGGGCCGTGCGGGGGCCGC
GGGGAGCTGGCCCCGGCAGATCCGGGCGCGCTACGAGGAGGTGCAGCGCTATTCCCGCGGG
GGCCCCGGGCCCCGGGGCGGGCCGGCCGGAGCGGCGGCGCCTGATGGACCTGGCTCCGGGC
GGGCCCCGGCCTGCCGCGCCCCCGGCCCCCTTGGGCCCCGGCCCCCTGTCCGACGGCGCCCCA
GGCTGGCCCCCGGCTCCCCGGCCAGGCTCCCCCGGCCCGGGCCCCGCGCCTGGGCTGCGCC
GCGCTTCGCAACGTGTCCGGCGCGCAGTACATGGGCTCAGGCTACACCAAGGCCGTGTAC
CGGGTCCGCCTGCCCGGCGGTGCCGCGGTGGCGCTCAAGGCGGTGGACTTTAGCGGCCAC
GATCTGGGCAGCTGCGTGCGCGAGTTCGGGGTACGGAGGGGTGCTATCGGCTGGCGGCC
CACAAGCTGCTTAAGGAGATGGTGTGCTGGAGCGGCTGCGGCACCCCAACGTGCTGCAG
CTCTATGGCTACTGCTACCAGGACAGCGAGGACATCCCAGACACCCTGACCACCATCAG
GAGCTGGGCGCCCCCTGTAGAAATGATCCAGCTGCTGCAAACCTTCCTGGGAGGATCGATT
CGAATCTGCCTGAGCCTGGGCGCCTCCTCCACCACCTGGCCCACTCCCCACTGGGCTCC
GTCACTCTGCTGGACTTCCGCCCTCGGCAGTTTGTGCTGGTGGATGGGGAGCTCAAAGTG
ACGGACCTGGATGACGCACGTGTGGAGGAGACGCCGTGTGCAGGCAGCACCGACTGCATA
CTCGAGTTTCCGGCCAGGAACCTTCACCCTGCCCTGCTCAGCCCAGGGCTGGTGCAGAGGC
ATGAACGAGAAGCGGAACCTCTATAATGCCTACAGGTTTTTCTTCACATACCTCCTGCCT
CACAGTGCCCCGCCTTCACTGCGTCCTCTGCTGGACAGCATCGTCAACGCCACAGGAGAG
CTCGCCTGGGGGTGGACGAGACCCTGGCCAGCTGGAGAAGGTGCTGCACCTGTACCGG
AGCGGGCAGTATCTGCAGAACTCCACGGCAAGCAGCAGTACCGAGTACAGTGTATCCCA
GACAGCACCATCCCCCAGGAAGACTACCGCTGCTGGCCATCCTACCACCACGGGAGCTGC
CTCCTTTTCAGTGTTCAACCTGGCTGAGGCTGTGGATGTCTGTGAGAGCCATGCCAGTGT
CGGGCCTTTGTGGTCACCAACCAGACCACCTGGACAGGTCGGCAGCTGGTCTTTTTTCAAG
ACTGGATGGAGCCAAGTGGTCCCTGATCCCAACAAGACCACATATGTGAAGGCCTCTGGC
TGACCTATCTGAGGGCTCGGCTGACCAGCTGACTATCCTCAGCAGCTGGGCTTGCCTGTG
GAGGGAGTGAATGCACTGGCAGCACTGCATGTACCTGGGAACCCCTGCAGACAAAGCT
AACATCCCAGACAGACAGATGTGACCAGGACAAACGTGCAATAATGCCAAATGTTAAAAT
GTGAGTTTACCAGCCTAGCTATGGGACTGCTGGCTCCTAGTCCAGGAATCATGGGGGTAT
GACTGCCTCTCCAACCCTGTGGGCTGTAAGCAAGCTCAGGCTAGTCTCCCCACTGGGGGC
TGTGCCCTTCCCTGGGACGGTTCGCTGGGCGAGCCCCATCACTGTGTTCAATAGTGTGAGA
ATGTAGCTAAAGCCCCTGCTGCTGCTGCTGCACATGCCACAGCAGGCGGTGGGGGCTGCG
TGGGGACAATCCATCGTGGAGTGTTCTCTCAGCTTAGGTCTGGACAGGAGACTTGGCGGG
AGATGCTCCAGGATGTGGGTGATTCTGTACCTGGGGAGGCTATCTCTGACCTCCCGACAG
GGGACACTCCCAGGCCAGCCAGGGGTACGGGGCAGAGGTGCACACCTCAGCATGAGCCA
AGACTGGGGTCAGGGAGCAGGTGTGGTTTGGAGCCAGGACCTGGGGCGGGGGTGGGGCCGG
GGCCTTTCTGCCTCATTTGCTTTCAATGAAAGCCTCAAAGCAGCCAAAACCAGGCTTTCC
CCCTTCTCGAGTTTGAATATCCAGAATCTTTTGTACTTCTTGTGGTTAAATTGTTTAT
TTTTGTAAAAATAAAATAAAATTAGTTAATAAAATGATGTTTCACAGCAAACCTCTCCC
T

SEQ ID NO: 107_AA396601_M

CCACGCGTCCGGGCTGCGCCGCGCTCCGCAACGTGTCTGGCGCGCAGTACGTGGGCTCAG
GCTACACTAAGGCTGTGTACCGGGTCCGCTGCCCCGGCGCGCCGCGGTGGCGCTTAAAG
CAGTGGACTTCAGCGGCCACGATCTGGGCAGCTGCGTGCGCGAGTTCGGGGCGCGAAGGG
GCTGCTATCGCTGGCGGCCACAAGCTGCTCAAAGAGATGGTGTGCTGGAGCGGCTGC
GGCACCCCAACGTGCTGCAGCTCTATGGCTATTGCTACCAGGACAGTGAGGGCATCCCAG
ACACGCTGACCACCATCACAGAGCTGGGTGCCCTGTGGAGATGATCCAGCTGTTGCAGA
CTTCCTGGGAGGATCGATTCCGAATCTGCCTCAGCCTTGGCCGCTCCTCCACCACCTGG
CCCACTCCCCGCTGGGCTCGGTACCCCTGCTTGACTTCCGCCCTCGGCAGTTTGTGCTAG
TGAACGGGGAGCTGAAAGTGACAGACCTGGATGATGCCCCGCGTGGAAGAGACACCGTGCA

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FIGURE 2DDDD

CCAGCAGTGCCGACTGCACGCTAGAGTTTCCAGCCAGGAACCTTCAGCCTGCCCTGCTCGG
CCCAGGGCTGGTGCAGGGGCATGAATGAGAAACGGAACCTCTACAATGCCTACAGGTTCT
TCTTCACATACCTCCTGCCACACAGTGCCCCGCCTTCCCTCCGACCTCTCCTGGATAGCA
TCGTCAATGCCACGGGAGAGCTCGCCTGGGGGGTGGATGAGACCCTGGCCCAGCTGGAGA
CAGCGCTACACTTGTTCCGAAGTGGGCAGTACCTGCAGAACTCTACAAGCAGCAGGGCTG
AGTACCAGCGCATCCCGGACAGTGCCATCACACAGGAGGACTATCGCTGCTGGCCATCCT
ATCACCACGGCGGCTGCCTCCTGTCCGTGTTCAACCTGGCTGAGGCTATAGATGTCTGTG
AGAGCCATGCTCAGTGTCGTGCCTTTGTGGTCAACCAACCAGACCACCTGGACAGGTCCGA
AGCTGGTCTTTTTTTAAGACTGGATGGAACCAAGTGGTCCCTGATGCCGGCAAGACCACAT
ATGTGAAGGCCCCCTGGTTGACTGGTTGTGGGCTCAGCTGACCAGCTGGGCTTGCTGTG
CAGGCGTGACTTGCATCCACCTGGGAACCCCTGCAGACAAAAGCTAGCTCCCAGAGCAA
CTGATGTGACCAGGACAAAACGTGCAATATGCAAAAATGTTAAATGTGAGTTTGCCAGC
TTCAGTCCCAGACTGGTTGGAACCCGATTGCCTCTCTGGAGCTGTAGGCTGTGAGCAGGG
CTCAGGCTGGTCTTAAGTGGGACAGTCCCGTGGGCAGCCATTACTGCATTTCATGCTTTG
AGAATGTAGCCAGAACACTGCTGCTGCATAAGCCACCGTGGGCAGGAGCTGCCTGGGGAC
AACCAGTCTCAGAGTGCTCTCTCAGCTCAGCTCCGCTCCAAATGGAGAGCGCGGGATGCG
GAGATGTGAGTGAACCAGCACTGGGAAGAAGGCTCTCGGGCCTCTCCCTAGAGGTTGCTC
CTAGGCCAGCCCCGAGGCGTGGGCAGCAGTGCTCGCATCCATATGAGCCAAGACTAGAG
TGGAGGAGCAGATTGCATTTGAGCCAGGACTGGGGTGGGGGTAGGGTTCGGGGCCTCTCTG
CCTCATTTGCTTTTCACTGAAAGCCAGGGAGCAGCCGCAGCCAGGCTCCTCCCACTCCTGG
AGGCCAGGCTCCTCCCCCTCCTGGAGGCCAGGCTCCTCCCCCTCCTGGAGTTTGCGTACC
CAGAAGCTTTTATACTTCTCGTTCAATTAAATTGTTTATTTTTGTAAAAAAAATAAT
CAATTAATAAAATGATGTTTTGTGAC

SEQ ID NO: 108_VRK3_H

ATGATCTCCTTCTGTCCAGACTGTGGCAAAAGTATCCAAGCGGCATTCAAATTCTGCCCC
TACTGTGGAATTTCTTTGCCTGTAGAGGAGCATGTAGGGTCCCAGACCTTTGTCAATCCA
CATGTGTCATCCTTCCAAGGCTCAAAGAGAGGGCTGAACTCCAGTTTTGAAACCTCTCCT
AAGAAAGTGAAATGGTCCAGCACCGTCACCTCTCCCCGATTATCCCTCTTCTCAGATGGT
GACAGTTCTGAGTCTGAAGATACTCTGAGTTCCTCTGAGAGATCCAAAGGCTCCGGGAGC
AGACCCCCAACCCCCAAAAGCAGCCCTCAGAAGACCAGGAAGAGCCCTCAGGTGACCAGG
GGTAGCCCTCAGAAGACCAGCTGTAGCCCTCAGAAGACCAGGCAGAGCCCTCAGACGCTG
AAGCGGAGCCGAGTGACCACCTCACTTGAAGCTTTGCCCCACAGGGACAGTGCTGACAGAC
AAGAGTGGGCGACAGTGGAAGCTGAAGTCCTTCCAGACCAGGGACAACCAGGGCATTCTC
TATGAAGCTGCACCCACCTCCACCCTCACCTGTGACTCAGGACCACAGAAGCAAAAGTTC
TCACTCAAACCTGGATGCCAAGGATGGGCGCTTGTTCAATGAGCAGAACTTCTTCCAGCGG
GCCGCCAAGCCTCTGCAAGTCAACAAGTGGAGAAGCTGTACTCGACCCCACTGCTGGCC
ATCCCTACCTGCATGGGTTTTCGGTGTTACCAGGACAAATACAGGTTCTTGGTGTACCC
AGCCTGGGGAGGAGCCTTCAGTCGGCCCTGGATGTGAGCCCAAAGCATGTGCTGTCAGAG
AGGTCTGTGCTGACAGGTGGCCTGCCGGCTGCTGGATGCCCTGGAGTTCTTCCATGAGAAT
GAGTATGTTTATGGAATGTGACAGCTGAAAATATCTTTGTGGATCCAGAGGACCAGAGT
CAGGTGACTTTGGCAGGCTATGGCTTCGCCTTCCGCTATTGCCCAAGTGGCAAACACGTG
GCCTACGTGGAAGGCAGCAGGAGCCCTCACGAGGGGGACCTTGAGTTTATTAGCATGGAC
CTGCACAAGGGATGCGGGGCCCTCCCGCCGCAGCGACCTCCAGAGCCTGGGCTACTGCATG
CTGAAGTGGCTCTACGGGTTTTCTGCCATGGACAAATTGCCTTCCCAACACTGAGGACATC
ATGAAGCAAAAACAGAAGTTTGTGATAAGCCGGGGCCCTTCGTGGGACCCTGCGGTAC
TGGATCAGGCCCTCAGAGACCCTGCAGAAGTACCTGAAGGTGGTGATGGCCCTCACGTAT
GAGGAGAAGCCGCCCTACGCCATGCTGAGGAACAACCTAGAAGCTTTGCTGCAGGATCTG
CGTGTGTCTCCATATGACCCCATTTGGCCTCCCGATGGTGCCCTAG

FIGURE 2EEEE

SEQ ID NO: 109_S71575_M VRK3_M

CCATCCCCACCTGTATCGGCTTTGGCATTACACCAGGACAAGTACAGGTTCCCTAGTATTCC
CCAGCCTGGGGAGGAGCCTTCAGTCAGCCCTGGATGACAACCCAAAGCATGTGGTATCAG
AGAGATGTGTGCTTCAGGTGGCCTGCAGGCTGCTGGATGCTCTGGAGTATCTCCATGAAA
ATGAGTATGTTACGGGAACCTGACAGCTGAGAAATGTCTTTGTGAATCCAGAGGATCTGA
GCCAGGTGACCTGGTGGGCTATGGCTTCACCTACCGATACTGCCCAGGTGGCAAACACG
TGGCCTACAAAGAAGGCAGCAGGAGTCCACACGATGGGGACTTGGAGTTCATTAGCATGG
ACCTGCACAAGGGATGCGGACCCTCCCGCCGAGCGATCTCCAGACCTTGGGCTACTGTA
TGCTCAAGTGGCTTTATGGGTCCCTGCCATGGACAAATTGCCTTCCCAACACCGAAAAGA
TAACTAGGCAGAAGCAGAAGTATCTGGACAGCCCCGAGCGCCTCGTGGGACTGTGTGGCC
GCTGGAACAAGGCCTCAGAGACCCTGCGGGAGTACCTGAAGGTGGTGTATGGCCCTCAATT
ATGAGGAGAAGCCACCCTATGCCACGCTGAGGAACAGCCTAGAAGCTCTGCTGCAGGATA
TGCGGGTGTACCCCTATGACCCTCTGGACCTCCAGATGGTGCCTTAGATGGAATCCAGAG
CTTCCGACTTGACGCTTGAAGTAGAACATGAAGTAGTGTGACTGGAGGCCTGTTTGAAC
CATAGCTCCTAAAAGAATCCCTTGAATGTGCATTCTCACCGCTCCCTTAGGACATATGAA
TCAGCACTTGTGTTGGGGAACCTGAGTCATGTATGAATGTGAAACTCCTCCCTGTCTC
AGCTCTGGCAGCTGTGGATGGAGGTAAGTGGATGCTGGCGGCGGCGGCGGCAGCAGCCAC
TCCACTCCCTATGGCATTCTGTGTATGGCATAATAAACTGTTTTTAATC

SEQ ID NO: 110_AA45427_H

ATGGGGCCACGCGCTGTGTGTCTGCTCTCGGGGAACGTGTCATCATTGACAATAAGCGCTAC
CTCTTCATCCAGAACTGGGGGAGGGTGGGTTTCACTATGTGGACCTAGTGGAAGGGTTA
CATGATGGACACTTCTACGCCCTGAAGCGAATCCTGTGTACGAGCAGCAGGACCGGGAG
GAGGCCCAGCGAGAAGCCGACATGCATCGCCTCTTCAATCACCCCAACATCCTTCGCCTC
GTGGCTTACTGTCTGAGGGAACGGGGTGCTAAGCATGAGGCCTGGCTGCTGCTACCATTC
TTCAAGAGAGGTACGCTGTGGAATGAGATAGAAAGGCTGAAGGACAAAGGCAACTTCCTG
ACCGAGGATCAAATCCTTTGGCTGCTGCTGGGGATCTGCAGAGGCCTTGAGGCCATTCAT
GCCAAGGGTTATGCCCCAGAGACTTGAAGCCCACCAATATATTGCTTGGAGATGAGGGG
CAGCCAGTTTTAATGGACTTGGGTTCCATGAATCAAGCATGCATCCATGTGAGGGCTCC
CGCCAGGCTCTGACCCTGCAGGACTGGGCAGCCAGCGGTGCACCATCTCCTACCGAGCC
CCAGAGCTCTTCTCTGTGCAGAGTCACTGTGTATCGATGAGCGGACTGATGTCTGGTCC
CTAGGCTGCGTGCTATATGCCATGATGTTTGGGGAAGGCCCTTATGACATGGTGTTC
AAGGGTGACAGTGTGGCCCTTGCTGTGCAGAACCAACTCAGCATCCCAACAAAGCCCCAGG
CATTCTTCAGCATTGCGGCAGCTCCTGAACTCGATGATGACCGTGGACCCGCATCAGCGT
CCTCACATTCTCTCCTCCTCAGTCAGCTGGAGGCGCTGCAGCCCCCAGCTCCTGGCCAA
CATACTACCCAAATCTGA

SEQ ID NO: 111_H05721_H

CCCTGAGGCACCGCCCCAAGTTTGGTGTGACCGGCGGGGGACGCCGGTGGTGGCGGCAGC
GACGGCTGCGGGGGACCGGGCCGCGGCGCCACCATGGCGGTGCGACAGGCGCTGGGCCG
CGCCTGACAGCTGGGTGAGCGCTGCTGCTGCGCTTACGGGCAAGCCCCGGCCGGGCCTA
CGGCTTGGGGCGGCCGGGCCCGGCGGCGGGCTGTGTCCGCGGGGAGCGTCCAGGCTGGGC
CGCAGGACCGGGCGCGGAGCCTCGCAGGGTCGGGCTCGGGCTCCCTAACCGTCTCCGCTT
CTTCCGCCAGTCGGTGGCCGGGCTGGCGGCGCGGTTGCAGCGGCAGTTCGTGGTGCGGGC
CTGGGGCTGCGCGGGCCCTTGCGGCGGGCAGTCTTTCTGGCCTTCGGGCTAGGGCTGGG
CCTCATCGAGGAAAAACAGGCGGAGAGCCGGCGGGCGGTCTCGGCCTGTGAGGAGATCCA
GGCAATTTTTTACCCAGAAAAGCAAGCCGGGGCCTGACCCGTTGGACACGAGACGCTTGCA
GGGCTTTCGGCTGGAGGAGTATCTGATAGGGCAGTCCATTGGTAAGGGCTGCAGTGCTGC
TGTGTATGAAGCCACCATGCCTACATTGCCCCAGAACCTGGAGGTGACAAAGAGCACC
GTTGCTTCCAGGGAGAGGCCAGGTACAGTGCACCAGGAGAAGGGCAGGAGCGAGCTCC

FIGURE 2FFFF

GGGGGCCCCTGCCTTCCCCTTGGCCATCAAGATGATGTGGAACATCTCGGCAGGTTCTC
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SEQ ID NO: 112_AI086865_H

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FIGURE 2HHHH

ACTGTCTGTGTGACTGATGAGGGTCAGCTCTATGCCTTCGGATCAGATTATTATGGCTGC
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SEQ ID NO: 114_R86668_H, MKK6_H

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FIGURE 2III

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SEQ ID NO: 115_PAK6_H

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FIGURE 2JJJJ

GACCTCCGGAAGCAACAGAGACGAGAACTGCTTTTCAATGAGGTCGTGATCATGCGGGAT
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SEQ ID NO: 116_SURTK106_H

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FIGURE 2KKKK

GAACATTCAACATGTATTGTTTCATTAAGCTAGCTTCCTAGTTCGATTAGACTAAGGAGA
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SEQ ID NO: 117_AA098024_M

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CAGAGAAAGAAAATCATGAAGAGACCCAGCAGCTGCTCACATGCCATGTACAACATCATG
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SEQ ID NO: 118_SGK2ALPHA_H

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CAGCCCTCCAGGGCCAATGGGAACATCAACCTGGGGCCTTCAGCCAACCCAAATGCCAG
CCCACGGACTTCGACTTCTCAAAGTCATCGGCAAAGGGAACCTACGGGAAGGTCCTACTG
GCCAAGCGCAAGTCTGATGGGGCGTTCTATGCAGTGAAGGTACTACAGAAAAAGTCCATC
TTAAAGAAGAAAGAGCAGAGCCACATCATGGCAGAGCGCAGTGTGCTTCTGAAGAACGTG
CGGCACCCCTTCCCTCGTGGGCCTGCGCTACTCCTTCCAGACACCTGAGAAGCTCTACTTC
GTGCTCGACTATGTCAACGGGGGAGAGCTCTTCTTCCACCTGCAGCGGGAGCGCCGGTTC
CTGGAGCCCCGGGCCAGGTTCTACGCTGCTGAGGTGGCCAGCGCCATTGGCTACCTGCAC
TCCCTCAACATCATTTACAGGGATCTGAAACCAGAGAACATTCTCTTGAGCTGCCAGGGA
CACGTGGTGCTGACGGATTTTGGCCTCTGCAAGGAAGGTGTAGAGCCTGAAGACACCACA

FIGURE 2LLLL

TCCACATTCTGTGGTACCCCTGAGTACTTGGCACCTGAAGTGCTTCGGAAAGAGCCTTAT
GATCGAGCAGTGGACTGGTGGTGCTTGGGGGCAGTCCTCTACGAGATGCTCCATGGCCTG
CCGCCCTTCTACAGCCAAGATGTATCCCAGATGTATGAGAACATTCTGCACCAGCCGCTA
CAGATCCCCGGAGGCCGGACAGTGGCCGCCTGTGACCTCCTGCAAAGCCTTCTCCACAAG
GACCAGAGGCAGCGGCTGGGCTCCAAAGCAGACTTTCTTGAGATTAAGAACCATGTATTC
TTCAGCCCCATAAACTGGGATGACCTGTACCACAAGAGGCTAACTCCACCCTTCAACCCA
AATGTGACAGGACCTGCTGACTTGAAGCATTTTGACCCAGAGTTCACCCAGGAAGCTGTG
TCCAAGTCCATTGGCTGTACCCCTGACACTGTGGCCAGCAGCTCTGGGGCCTCAAGTGCA
TTCCTGGGATTTTCTTATGCGCCAGAGGATGATGACATCTTGGATTGCTAGAAGAGAAGG
ACCTGTGAACTACTGAGGCCAGCTGGTATTAGTAAGGAATTACCTTCAGCTGCTAGGAA
GAGCGACTCAAATAACAATGGCTTCAACGAGAAGCAGGTTTATTTTTTCCAGCACATAA
AAGAAAAATAATGTTTCGGAGTCCAGGACTGGCAGGACAGGTCATCAGATACTCAGAGGC
TGTATCTCTGCCCTGCCAACCTTGACAAATGGCTTCCAATGTTAGGTTTGCTACAAGATG
GTTACTGGAGCTCTAGCTGCCTATTTTGTGTTTAGGGAAGGGAAAATGGAGGAAAGGGGA
GAAGAGCAAAGGGCGCTTTTAAAGAGCTTCCCAAAGCTCCCCCAATGACTTTTGCTT
CCATCTCACTAACCACCCACCCCTACCTGGAATGGAGGCTGGGAAATGTGGCTTATTTGC
TGGGTACGTGACTATCCCTAATAACAAAGGGGTTTTGACCCTAAGACATTAGGGGAGAAT
GTTGGGTAGGCAGCCAGCCCTCTTTTACCATAGGGCCTCCTGGTGTTTGGATTTTGATCT
CAATGTGTAAATGACAGAGATGTAACAAGCTCATAGGGTATCAATATCTCTTATTGTTC
TATGTTGAAAAA

SEQ ID NO: 120_CCRK_H

ATGGACCAGTACTGCATCCTGGGCGCATCGGGGAGGGCGCCACGGCATCGTCTTCAAG
GCCAAGCACGTGGAGACTGGCGAGATAATTGCCCTCAAGAAGGTGGCCCTAAGGCGGTG
GAAGACGGCTTCCCTAACCAGGCCCTGCGGGAGATTAAGGCTCTGCAGGAGATGGAGGAC
AATCAGTATGTGGTACAACCTGAAGGCTGTGTTCCACACGGTGGAGGCTTTGTGCTGGCC
TTTGAGTTTCATGCTGTGCGGATCTGGCCGAGGTGGTGCGCCATGCCAGAGGCCACTAGCC
CAGGCACAGGTCAAGAGCTACCTGCAGATGCTGCTCAAGGGTGTGCGCTTCTGCCATGCC
AACAACATTGTACATCGGGACCTGAAACCTGCCAACCTGCTCATCAGCGCCTCAGGCCAG
CTCAAGATAGCGGACTTTGGCCTGGCTCGAGTCTTTTCCCAGACGGCAGCCGCCTCTAC
ACACACCAGGTGGCCACCAGGTCTGTGGGCTGCATCATGGGGGAGCTGTTGAATGGGTCC
CCCCTTTTCCCGGGCAAGAACGATATTGAACAGCTTTGCTATGTGCTTCGCATCTTGGGC
ACCCCAAACCCTCAAGTCTGGCCGGAGCTCACTGAGCTGCCGGACTACAACAAGATCTCC
TTTAAGGAGCAGGTGCCCATGCCCTGGAGGAGGTGCTGCCTGACGTCTCTCCCAGGCA
TTGGATCTGCTGGGTCAATTCCTTCTCTACCCCTCCTCACCAGCGCATCGCAGCTTCCAAG
GCTCTCCTCCATCAGTACTTCTTCACAGCTCCCCTGCCTGCCCATCCATCTGAGCTGCCG
ATTCTCAGCGTCTAGGGGGACCTGCCCCCAAGGCCCATCCAGGGCCCCCCCCACATCCAT
GACTTCCACGTGGACCGGCCTCTTGAGGGAGTCGCTGTTGAACCCAGAGCTGATTTCGGCC
CTTCATCCTGGAGGGGTGAGAAGTTGGCCCTGGTCCCGTCTGCCTGCTCCTCAGGACCAC
TCAGTCCACCTGTTCTCTGCCACCTGCCTGGCTTCACCCCTCAAGGCCTCCCCATGGCC
ACAGTGGGCCCCACACCACCTTGCCCCTTAGCCCTTGCGAGGGTTGGTCTCGAGGCAGA
GGTCATGTTCCCAGCCAAGAGTATGAGAACATCCAGTCGAGCAGAGGAGATTTCATGGCCT
GTGCTCGGTGAGCCTTACCTTCTGTGTGCTACTGACGTACCCATCAGGACAGTGAGCTCT
GCTGCCAGTCAAGGCCTGCATATGCAGAAATGACGATGCCTGCCTTGGTGCTGCTTCCCC
GAGTGCTGCCTCCTGGTCAAGGAGAAGTGACAGAGAGTAA

SEQ ID NO: 121_TESK2_H

GAATTCGCGGCCGCTCGACGCTCAGCAGAGCTACCAGCTGCCCTGTTGGCTTCGCTGGTC
GGATCGTCTCCTGGCCCCGCCAAACAGGCGAGCGGCCCGACTGTGGGGCATGGCAGTA
GTCTCCTCGTTCTCCGCCGCCGCTAGCCTAGCTGAGTCGCCGGCTTCTGCGCTAGGGGCT

FIGURE 2MMMM

CCCACCGCCTCCGCAGGCTAAGGAGCCGCTGCCACCAACGAGCTGTGAGGGTTACTATGC
TCCCTCTTTGCCGCCGTCTCCTCCTCTTGCCCGCGCAGGCACCCCTCTGGCTGCTCAGTC
CTGCCTCAGTGTCAAACCAGAAGAGAAGTAAAATTCAACAAAAATTTATGTGTGGAGTTC
CTTCTTAAAAGAAGAAAAAAGTGATTATTTAGACTATGGATCGGAGCAAACGGAATTCAA
TTGCAGGATTTCTCCACGTGTGGAGCGTCTTGAAGAGTTTGAAGGAGGTGGTGGAGGAG
AAGGAAATGTGAGCCAGGTGGGAAGAGTTTGGCCATCTTCGTATCGAGCTCTTATAAGTG
CCTTTTCCAGACTGACGCGTTTGGATGATTTACCTGTGAAAAAATAGGGTCTGGCTTCT
TTTCTGAAGTGTTCAAGGTACGACACCGAGCTTCTGGTCAGGTGATGGCTCTTAAGATGA
ACACATTGAGCAGTAACCGGGCAAACATGCTGAAAGAAGTACAGCTCATGAATAGACTCT
CCCATCCCAACATCCTTAGGTATATCAACTCCGGGAACCTGGAACAGTTGCTAGACAGTA
ACCTGCATTTGCCTTGGACTGTGAGGGTAAACTGGCCTATGACATAGCAGTGGGCCTCA
GCTACCTTCACTTCAAAGGCATTTTTTCATCGGGACCTCACATCTAAGAACTGCCTGATAA
AGAGGGATGAGAATGGTTACTCTGCAGTGGTAGCTGACTTTGGCCTGGCTGAGAAGATCC
CCGATGTCAGCATGGGGAGTGAGAAGCTGGCCGTGGTGGGTCCCCATTCTGGATGGCAC
CTGAGGTTCTCCGAGATGAGCCCTATAATGAAAAGGCAGATGTGTTCTCTTATGGTATCA
TCCTCTGCGAGATCATCGCCCGCATCCAGGCCGATCCGGAATCTTCCCCGCACAGAGA
ATTTCCGGCTGGACTATGATGCTTTCCAGCACATGGTGGGAGACTGTCCCCAGATTTTC
TGCAACTTACTTTCAACTGCTGTAACATGGATCCCAAACCTGCGCCCATCTTTTGTGGAGA
TTGGGAAGACCCTGGAGGAAATCTGAGCCGCCTACAGGAAGAAGAGCAGGAGAGGGATA
GGAAGCTGCAGCCACAGCCAGGGGACTCTTGAGAAAGCACCTGGGGTGAAGCGACTAA
GCTCACTGGATGACAAGATCCCCACAAGTCACCATGCCCAAGACGTACCATCTGGCTGT
CTCGAAGCCAGTCAGATATCTTTTCCCGTAAGCCCCACGTACAGTGAGTGTCTTGGACC
CATACTACCGGCCACGAGATGGTGCTGCCCGCACCCCCAAAGTCAACCCTTTTAGTGCTC
GCCAGGACCTCATGGGGGGCAAGATCAAGTTTTTTGACCTGCCCAGCAAGTCTGTCTATCT
CTCTGGTATTTGACCTGGATGCACCAGGGCCCGGAACATATGCCCTGGCTGACTGGCAGG
AGCCCCCTGGCCCCACCTATTCGCCGGTGGCGTTCTTGCCTGGTTCGCCTGAGTCTTGC
ATCAAGAGGCTTGTCCATTTGTGGGCCGGGAAGAATCGCTATCTGATGGGGCCCCACCAC
GCCTAAGTAGTCTCAAGTACAGAGTTAAAGAGATCCCAACATTCCGGGCATCTGCCCTAC
CAGCTGCTCAAGCCCATGAGGCTATGGACTGCTCCATTCTCCAGGAAGAAAATGGTTTTG
GGTCCAGGCCCCAGGGGACCAGTCCATGCCCTGCGGGTGTCTTCTGAGGAGATGGAGGTAG
AAGAAAGGCCAGCAGGCTCAACTCCAGCCACCTTCTCCACCTCAGGCATAGGCCTGCAAA
CCCAGGGAAAGCAGGATGGGTGAGGGGGTTTAGTCCCTGCCTCACCTTGGGGATGGACCT
TCAGCTGAAACCATATGGCCCCCTAGGTGCACAGCCTTGATTCTTCCCTGGAGCCTACAG
AGCAGGCAGGCTAGGCCAAGCCAGGCTCAACTTCTGGGCTECCAGTGCCCATTTGGCTGTG
TATGACGGGAGGCAGCAGTGAGAGGCCCTTCTAGTTAGGGCCAACAGCTGATACCAAGCC
TCTGAAATCCAGCAAGGAGGTCTGCCTCCCACCAGACCCTCTCCAGTGTACTTCCCCAGA
TAGGACCAGAGGATGTCTAGTTCTAGGCTGAGCTGGCAGGCAGCTATTACCCCGGTTCTT
TCCCCACCCCAGGTCTGTCTCTTGCCTTTTCTTGGGGCATATAAGCTACTGAGTGGAACA
TGGAGCTGATCAAGAGGCCGTAATGGTTCATGGCTGTTTCCAGACCTGAATATTGGGTGCT
TCTTGCCAGTATTCTAAGACATTTGAGTAATTGCTGTTTGCATTAAGTGCATGGTCAGAC
CACGTCACTACATTTCTATGCAAGGGGACAGCAAGGCAGCGTGGTGGTTCATGGCTCTTAG
CTAACCTATTCAAAGACCTTTTCTGTTGATTAATCTATTTTCATATTTATAAAGGAGTC
TTAATGTTCTGCCCCATAAGACTTTCAACCTTGTGGTTGGGAGTGGGGCTGGTTTTGTAG
GCCCTAGGGCCTGCTTCTATGTATTTATCAACATGTGATACATTCAATTGGTTAAATGGT
TTATACAGGGACTGATTTGCTTCCCTTCCCTGCCATGGCTGGAGCTTTGGGAACAGTCTGT
CCTTACAGAGCTGCAATAAGAAATAACCAAAGATGAAGCTGGTCAAATATTTTCATAACT
TGCTTCTGTTGATTTTTTTTTGTAAACTTTCCCAAGACATTTTCAGACTTAAAAATAA
AGTCAGTGTACAGGT

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(54) Title: PROTEIN KINASES

(57) Abstract: The present invention relates to kinase polypeptides, nucleotide sequences encoding the kinase polypeptides, as well as various products and methods useful for the diagnosis and treatment of various kinase-related diseases and conditions.

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A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/54 C12N9/12 C12N15/11 C12N5/12 C07K16/40
A61K38/00 G01N33/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

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EPO-Internal, WPI Data, PAJ, EMBL, MEDLINE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

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X	DATABASE EMBL 'Online! Accession Number W90839, 9 July 1996 (1996-07-09) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:420441 5' similar to gb:M80359 putative serine/threonine protein kinase." XP002165856 abstract DOC. AGAINST INV. 31 (SEQ.IDs. 152, 34) ---	1, 2, 4, 6, 7, 10-13, 16
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A	<p>WO 98 35015 A (GERHOLD DAVID L ;MERCK & CO INC (US)) 13 August 1998 (1998-08-13) SEQ.IDs.2 and 3 DOC. AGAINST INV. 50 (SEQ.IDs. 171, 53) DOC. AGAINST INV. 114 (SEQ.IDs. 235, 117)</p>	1-30, 35-38

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X	DATABASE EMBL 'Online! Accession Number AA387681, 25 June 1997 (1997-06-25) MARRA M. ET AL.: "Mus musculus cDNA clone." XP002167898 abstract DOC. AGAINST INV. 70 (SEQ.IDs. 191, 73) ---	6,7
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X	DATABASE EMBL 'Online! Accession Number AA270784, 28 March 1997 (1997-03-28) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:736476." XP002167971 abstract DOC. AGAINST INV. 80 (SEQ.IDs. 201, 83) ---	6,7
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X	<p>DATABASE EMBL 'Online! Accession Number AF027406, 6 January 1999 (1999-01-06) BRENNER V. ET AL.: "Homo sapiens muscle-specific serine kinase 1 (MSSK1) mRNA." XP002168230 abstract DOC. AGAINST INV. 85 (SEQ.IDs. 206, 88)</p>	1-14
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X	<p>DATABASE EMBL 'Online! Accession Number AI553938, 25 March 1999 (1999-03-25) STAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2090493 3' similar to TR:015367 TSK_1." XP002168388 abstract DOC. AGAINST INV. 86 (SEQ.IDs. 207, 89) DOC. AGAINST INV. 87 (SEQ.IDs. 208, 90) DOC. AGAINST INV. 91 (SEQ.IDs. 212, 94)</p>	1,2,4-7, 10-14,25

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X	DATABASE EMBL 'Online! Accession Number AI651075, 5 May 1999 (1999-05-05) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2304078 3' similar to TR:060679 serum inducible kinase." XP002169145 abstract DOC. AGAINST INV. 97 (SEQ.IDs. 218, 100) ---	1,2,4-7, 10-14,25
X	DATABASE EMBL 'Online! Accession Number W08549, 27 April 1996 (1996-04-27) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:332593." XP002169146 abstract DOC. AGAINST INV. 98 (SEQ.IDs. 219, 101) ---	6,7
X	DATABASE EMBL 'Online! Accession Number AC002355, 24 July 1997 (1997-07-24) HAWKINS T. L. ET AL.: "Homo sapiens chromosome 9 clone 107G20 map 9q34" XP002169147 abstract DOC. AGAINST INV. 99 (SEQ.IDs. 220, 102) ---	1-7
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X	<p>DATABASE EMBL 'Online! Accession Number AI638161, 29 April 1999 (1999-04-29) STRAUSBERG R.: "Homo sapiens cDNA clone IMAGE:2239185 3' similar to SW:PAK3_Human 075914 serine/threonine-protein kinase." XP002169314 abstract DOC. AGAINST INV.110 (SEQ.IDs. 231, 113)</p>	<p>1,2,4-7, 10-14</p>
P, X	<p>NAGASE T. ET AL.: "PREDICTION OF THE CODING SEQUENCES OF UNIDENTIFIED HUMAN GENES. XV. THE COMPLETE SEQUENCES OF 100 NEW CDNA CLONES FROM BRAIN WHICH CODE FOR LARGE PROTEINS IN VITRO" DNA RESEARCH, vol. 6, 29 October 1999 (1999-10-29), pages 337-345, XP000865804 ISSN: 1340-2838 -& DATABASE EMBL 'Online! Accession Number AB033090, 11 November 1999 (1999-11-11) OHARA O. ET AL.: "Homo sapiens mRNA for KIAA1264 protein." XP002169637 abstract DOC. AGAINST INV.110 (SEQ.IDs. 231, 113)</p>	<p>1-14</p>

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X	<p>DATABASE EMBL 'Online! Accession Number H29272, 19 July 1995 (1995-07-19) HILLIER L. ET AL.: "Homo sapiens cDNA clone IMAGE:49948." XP002169315 abstract DOC. AGAINST INV.111 (SEQ.IDs. 232, 114)</p>	6,7
P,X	<p>WO 99 64589 A (ZENECA LTD) 16 December 1999 (1999-12-16)</p> <p>the whole document DOC. AGAINST INV.111 (SEQ.IDs. 232, 114) DOC. AGAINST INV.112 (SEQ.IDs. 233, 115)</p>	1-14,23, 26-30, 35-38
X	<p>DATABASE EMBL 'Online! Accession Number AA098024, 27 October 1996 (1996-10-27) MARRA M. ET AL.: "Mus musculus cDNA clone IMAGE:550913 5' similar to SW:DROME P18475 tyrosine-protein kinase receptor torso precursor." XP002169442 abstract DOC. AGAINST INV.112 (SEQ.IDs. 233, 115)</p>	1-4, 6-13,23
X	<p>DATABASE EMBL 'Online! Accession Number Z98752, 23 August 1997 (1997-08-23) RAMSAY H.: "Human DNA sequence from clone RP1-138B7 on chromosome 20q13.12." XP002169443 nts. 43893 - 62413 DOC. AGAINST INV.113 (SEQ.IDs. 234, 116)</p>	1-14
X	<p>DATABASE EMBL 'Online! Accession Number AF035013, 4 January 1999 (1999-01-04) JIANG Y. AND ZHAO K.: "Homo sapiens cell cycle related kinase mRNA, complete cds." XP002169444 abstract DOC. AGAINST INV.114 (SEQ.IDs. 235, 117)</p>	1-14,24

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Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☒ Claims Nos.: 31-34
because they do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
~~see FURTHER INFORMATION sheet PCT/ISA/010~~
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
- X
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos. 1-19 (partially), 20-22 (completely), 23-38 (partially), 39 and 40 (partially), 41 and 42 (completely), 43 and 44 (partially), 45 and 46 (completely), 47 and 48 (partially), 49 and 50 (completely), 51 and 52 (partially), 53 and 54 (completely), 55 and 56 (partially), 57 and 58 (completely), 59 and 60 (partially), 61 and 62 (completely), 63 and 64 (partially), 65 and 66 (completely), 67 and 68 (partially), 69 and 70 (completely), 71 and 72 (partially), 73 and 74 (completely), 75 and 76 (partially), 77 and 78 (completely), 79 and 80 (partially), 81 and 82 (completely), 83 and 84 (partially), 85 and 86 (completely), 87 and 88 (partially), 89 and 90 (completely), 91 and 92 (partially), 93 and 94 (completely), 95 and 96 (partially), 97 and 98 (completely), 99 and 100 (partially).
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☒ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: Invention 1: Claims 1-14,26-38 (all partially)

A nucleic acid molecule encoding a kinase polypeptide as represented by SEQ.ID.122 or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide as represented by SEQ.ID.122 or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a kinase polypeptide as represented by SEQ.ID.122.

2. Claims: Inventions 2-78: Claims 1-20, 23-38 (all partially and as far as applicable)

A nucleic acid molecule encoding a kinase with a polypeptide sequence selected from SEQ.IDs.123-199, wherein invention 2 is limited to SEQ.ID. 123, invention 3 is limited to SEQ.ID. 124,, and invention 78 is limited to SEQ.ID.199, or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide as represented by a polypeptide sequence selected from SEQ.IDs.123-199 or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a kinase polypeptide represented by a polypeptide sequence selected from SEQ.IDs.123-199.

3. Claims: Invention 79: Claim 21 (completely) and Claims 1-14,26-38 (all partially)

A nucleic acid molecule encoding a kinase polypeptide as represented by SEQ.ID.200 or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide as represented by SEQ.ID.200 or a fragment thereof; an antibody or antibody fragment having

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a kinase polypeptide as represented by SEQ.ID.200.

4. Claims: Invention 80: Claim 22 (completely) and Claims 1-14, 26-38 (all partially)

A nucleic acid molecule encoding a kinase polypeptide as represented by SEQ.ID.201 or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide as represented by SEQ.ID.201 or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a kinase polypeptide as represented by SEQ.ID.201.

5. Claims: Inventions 81-121: Claims 1-20, 23-38 (all partially and as far as applicable)

A nucleic acid molecule encoding a kinase with a polypeptide sequence selected from SEQ.IDs.202-242, wherein invention 81 is limited to SEQ.ID. 202, invention 82 is limited to SEQ.ID. 203,, and invention 121 is limited to SEQ.ID.242, or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide as represented by a polypeptide sequence selected from SEQ.IDs.202-242 or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a kinase polypeptide represented by a polypeptide sequence selected from SEQ.IDs.202-242.

6. Claims: Inventions 122-136: Claims 15-20, 23-25 (all partially) and claims 1-14, 26-38 (if applicable)

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

A nucleic acid molecule encoding a kinase polypeptide as represented by a 'gene name' selected from 'AA980090', 'AA045601', 'AA297313', 'N23936', '5R72-18-1', '5R79-54-1', '5R65-16-1', 'AA065538', 'H17727', 'W08549', 'AA430250', 'AA139478', 'R87679', 'W65887', 'AA948538', '5R69-23-3', and '5R69-26-2', wherein invention 122 is limited to 'AA980090', invention 123 is limited to 'AA045601', and invention 136 is limited to '5R69-26-2', or a domain thereof; a vector and a recombinant cell comprising said nucleic acid molecule; a nucleic acid probe for the detection of said nucleic acid molecule; a polypeptide encoded by said nucleic acid molecule or a fragment thereof; an antibody or antibody fragment having specific binding affinity to said polypeptide; a hybridoma which produces said antibody; methods for identifying a substance that modulates the kinase activity of said polypeptide; methods for treating a disease or disorder by administering such a substance; and methods for the detection of a said polypeptide.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Continuation of Box I.2

Claims Nos.: 31-34

The search was based on the sequence listing furnished in computer readable form, the numbering of which differs from the numbering in the figures.

Claims 31-34 refer to a 'substance that modulates the activity of a kinase' without giving a true technical characterization. Moreover, no such specific compounds are defined in the application. In consequence, the scope of said claims is ambiguous and vague, and their subject-matter is not sufficiently disclosed and supported (Art. 5 and 6 PCT). No search can be carried out for such purely speculative claims whose wording is, in fact, a mere recitation of the results to be achieved.

The applicant's attention is drawn to the fact that claims, or parts of claims, relating to inventions in respect of which no international search report has been established need not be the subject of an international preliminary examination (Rule 66.1(e) PCT). The applicant is advised that the EPO policy when acting as an International Preliminary Examining Authority is normally not to carry out a preliminary examination on matter which has not been searched. This is the case irrespective of whether or not the claims are amended following receipt of the search report or during any Chapter II procedure.

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